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GenCore version 5.1.6
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December 2, 2004, 00:55:08 ; Search time 204.612 Seconds
(without alignments)
7003.964 Million cell updates/sec

Run on: US-09-989-293A-376_COPY_92_364

Title: 1 atgacattttttctgact.....gtgtaagaaaaaacacttag 273
Sequence: IDENTITY NUC
Scoring table: Gapop 10.0 , Gapext 1.0
                4134886 segs, 2624710521 residues
                Minimum DB seq length: 0
                Maximum DB seq length: 2000000000
                Post-processing: Minimum Match 0%
                               Maximum Match 100%

Database : Listing first 1500 summaries
1: _Geneseq 23Sep04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description
RESULT 1
ID AAC91481 standard; cDNA; 712 BP.
DE Human PRO1159 cDNA.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 5; Length 712;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 2
ID AAZ65094 standard; cDNA; 713 BP.
DE Membrane-bound protein PRO1159 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 5; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 3
ID AAC58634 standard; cDNA; 713 BP.
DE Human cDNA sequence encoding for PRO1159 polypeptide.
PN WO200140466-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 4
ID AAS21480 standard; cDNA; 713 BP.
DE Human cDNA sequence encoding for PRO1159 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 4; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 5
ID AAF44240 standard; cDNA; 713 BP.
DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 273; DB 5; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 6
ID ACA64409 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 7
ID ACA03839 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 8
ID ABX89377 standard; cDNA; 713 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1159.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 9
ID ABX80868 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 10
ID ACD44377 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 11
ID ACD42031 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #237.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 12
ID ABX79548 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 13
ID ACA93569 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 14
ID ABX81251 standard; DNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 15
ID ACA04260 standard; cDNA; 713 BP.
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DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 473.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 16
ID ACA93067 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 17
ID ABX17151 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 18
ID ACA68006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002171164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 19
ID ACA88455 standard; cDNA; 713 BP.
DE Human secreted and transmembrane polypeptide PRO1159 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 20
ID ACB81962 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 21
ID ADA45992 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 22
ID ADA76423 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 23
ID ADA19073 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 24
ID ADA61696 standard; cDNA; 713 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 25
ID ADB19481 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 26
ID ADB28022 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 27
ID ADA86501 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 28
ID ADB16065 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 29
ID ADA37887 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 30
ID ADA47951 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 31
ID ADA21573 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1159.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 32
ID ADA10360 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1159.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 33
ID ADA67646 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;

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RESULT 34
ID ADB30653 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 35
ID ADA85949 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 36
ID ADA17904 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 37
ID ADA97161 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 38
ID ADA79465 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 39
ID ADA87604 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 40
ID ADB16806 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 41
ID ADA28012 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 42
ID ADA91898 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 43
ID ADB14961 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 44
ID ADB18922 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 45
ID ADA94137 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 46
ID ADB20033 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 47
ID ADB13345 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 48
ID ACD98660 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 49
ID ADA94592 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 50
ID ADA74599 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 51
ID ADB24832 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 52
ID ADA82356 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082701-A1.
PD 01-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 53
ID ADA75319 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 54
ID ADA85397 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 55
ID ADA84845 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 56
ID ADB3101 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 57
ID ADA80629 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 58
ID ADA75871 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 59
ID ADA38817 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 60
ID ADA47096 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 61
ID ADB25392 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 62
ID ADA93568 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 63
ID ADB26918 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 64
ID ADB31205 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 65
ID ADA92938 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 66
ID ADA61133 standard; cDNA; 713 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 67
ID ADB24280 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 68
ID ADA96609 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 69
ID ADA81181 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 70
ID ADA96057 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 71
ID ADA96057 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;

ID ADB26366 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 72
ID ADB21851 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 73
ID ADA77630 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 74
ID ADB18370 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 75
ID ADA87053 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082769-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 76
ID ADA88156 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 77
ID ADA46544 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 78
ID ADB28574 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 79
ID ADB29126 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 80
ID ACH65523 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 81
ID ADA77078 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 82
ID ADA22499 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1159.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 83
ID ADA88708 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 84
ID ADA97713 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 85
ID ADB27470 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US200302239-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 86
ID ADB22403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 87
ID ACD39513 standard; cDNA; 713 BP.
DE Human cDNA encoding PRO1124.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 88
ID ADA06665 standard; cDNA; 713 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #118.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 89
ID ADA39358 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 273; DB 9; Length 713;
Pred. No. 3.3e-75;
RESULT 90
ID ADA67094 standard; cDNA; 713 BP.

DE Human PRO polynucleotide #237.
PD US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 91
ID ADB22955 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 92
ID ADB23728 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 93
ID ADA92450 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 94
ID ADB15513 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 95
ID ADB38765 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 96
ID ADE96384 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 97
ID ADB38213 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 98
ID ADB66685 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 99
ID ADB89765 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082698-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 100
ID ADB90497 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 101
ID ADB39598 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 102
ID ADB47221 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 103
ID ADB86828 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 104
ID ADB77433 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 105
ID ADB34590 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 106
ID ADB35694 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 107
ID ADB34038 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 108
ID ADB35142 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077718-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 109
ID ADB36246 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 110
ID ADB46641 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 111
ID ADC57856 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 112
ID ADC55220 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 113
ID ADC12087 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 114
ID ADC56509 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 115
ID ADC07564 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 116
ID ADC11554 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 117
ID ADC50514 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 118
ID ADC72061 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092107-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 119
ID ADC60040 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 120
ID ADC51047 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 121
ID ADC57401 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 122
ID ADC60592 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 123
ID ADC51067 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 124
ID ADC65594 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 125
ID ADC54692 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 126
ID ADC53653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 127
ID ADC59176 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087359-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 128
ID ADC56054 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 129
ID ADC58624 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 130
ID ADC14676 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 131
ID ADD08208 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 132
ID ADD03298 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 133
ID ADC90290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 134
ID ADC82033 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 135
ID ADC69709 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 136
ID ADC48598 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 137

ID ADD10127 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 138
ID ADD07675 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 139
ID ADD04702 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 140
ID ADC82566 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 141
ID ADC80658 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 142
ID ADL1165 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 143
ID ADC48046 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 144
ID ADD08746 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 145
ID ADC80106 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 146
ID ADD06995 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193300-A1.

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PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 147
ID ADD09575 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 148
ID ADC83242 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 149
ID ADD41288 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 150
ID ADD52427 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 151
ID ADD53167 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 152
ID ADD53719 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 153
ID ADD55349 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 154
ID ADD56307 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 155
ID ADD51875 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 156
ID ADD02674 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 157
ID ADD02108 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 158
ID ADD54290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 159
ID ADD54745 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 160
ID ADD92607 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 161
ID ADD91503 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 162
ID ADE04117 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 163
ID ADE26899 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 164
ID ADE32414 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 165
ID ADE22346 standard; cDNA; 713 BP.
```

DE cDNA encoding human PRO polypeptide #237.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 166
ID ADE19027 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 167
ID ADE42106 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 168
ID ADE17923 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 169
ID ADE92055 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 170
ID ADE33518 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 171
ID ADE34070 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 172
ID ADE80122 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 173
ID ADD93159 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 174
ID ADE19579 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.

PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 175
ID ADE19027 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 176
ID ADE43223 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 177
ID ADD96012 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 178
ID ADE22898 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 179
ID ADD79016 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 180
ID ADE26366 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 181
ID ADE32966 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 182
ID ADE42658 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 183
ID ADE80674 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207418-A1.
PD 06-NOV-2003.

ID ADH81484 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 203
ID ABX77952 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 204
ID ABX80364 standard; cDNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 205
ID ACA69270 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 206
ID ACD24089 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 207
ID ABX90341 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 208
ID ABX64187 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 209
ID ACA67230 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 10; Length 713;
Result 210
ID ADM82653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 11; Length 713;
Result 211
ID ADN16052 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087353-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 11; Length 713;
Result 212
ID ADN16681 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 11; Length 713;
Result 213
ID ADN15500 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 11; Length 713;
Result 214
ID ADN14948 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 11; Length 713;
Result 215
ID ADC81210 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
Result 216
ID ADD76658 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
Result 217
ID ADD88022 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
Result 218
ID ADD86426 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
Result 219
ID ADE75874 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
Result 220
ID ADE23450 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092108-A1.
PD 15-MAY-2003.


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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 221
DE ADE24002 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 222
ID ADE24645 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 223
ID ADD87470 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 224
ID ADE89336 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 225
ID ADE18475 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 226
ID ADE88784 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 227
ID ADE94804 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 228
ID ADE91215 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 229
ID ADF35502 standard; cDNA; 713 BP.
DE CDNA encoding human PRO1159 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
100.0%; Score 273; DB 12; Length 713;

Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 230
ID ADE95356 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 231
ID ADE93466 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 232
ID ADF35047 standard; cDNA; 713 BP.
DE CDNA encoding human PRO polypeptide #237.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 233
ID ADE92362 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 234
ID ADE90663 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 235
ID ADE91810 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 236
ID ADG11752 standard; cDNA; 713 BP.
DE CDNA encoding human PRO1159 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 237
ID ADG02389 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 238
ID ADG22175 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 273; DB 12; Length 713;
RESULT 239
ID ADF35502 standard; cDNA; 713 BP.
DE CDNA encoding human PRO1159 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
100.0%; Score 273; DB 12; Length 713;
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RESULT 239
ID ADG20245 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 240
ID ADF98151 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 241
ID ADG24368 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 242
ID ADF98722 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 243
ID ADG03553 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 244
ID ADF99274 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 245
ID ADG16859 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 246
ID ADG05318 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 247
ID ADG19585 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 248
ID ADG07855 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 249
ID ADG08479 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 250
ID ADG15649 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 251
ID ADF97047 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 252
ID ADG06322 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 253
ID ADG23816 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 254
ID ADG04105 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 255
ID ADG25006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 256
ID ADG07303 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 257
ID ADG07855 standard; cDNA; 713 BP.
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DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 258
ID ADG55350 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 259
ID ADG61014 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 260
ID ADG62118 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 261
ID ADG82319 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 262
ID ADG57558 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 263
ID ADG57006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 264
ID ADG53902 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 265
ID ADG58662 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 266
ID ADG71028 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 267
ID ADG58110 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 268
ID ADG53694 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 269
ID ADG71580 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 270
ID ADG81767 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 271
ID ADH19622 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 272
ID ADH30729 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 273
ID ADH12096 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 274
ID ADG52518 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 275
ID ADG54246 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.

RESULT 294
ID ADM27837 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 295
ID ADM42561 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 296
ID ADM28423 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004077084-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 273; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
RESULT 297
ID AAK81282 standard; DNA; 5709 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 273; DB 4; Length 5709;
Best Local Similarity 100.0%; Pred. No. 7e-75;
RESULT 298
ID AAX01260 standard; cDNA; 741 BP.
DE Human DC3' protein coding sequence.
PN JP11001497-A.
PD 06-JAN-1999.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 51.3%; Score 140; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
RESULT 299
ID AAZ07533 standard; cDNA; 1018 BP.
DE Human SDCMP4 polypeptide encoding cDNA.
PN WO9947673-A2.
PD 23-SEP-1999.
PA (ISCHE) SCHERING CORP.
Query Match 51.3%; Score 140; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
RESULT 300
ID ADF60937 standard; cDNA; 1018 BP.
DE Human long Schering dendritic cell membrane protein 4 (SDCMP4) cDNA.
PN US2003162955-A1.
PD 28-AUG-2003.
PA (CHAL/) CHALUS L.
PA (QUAN/) QUAN A. B.
PA (BATE/) BATES E E M.
PA (GORM/) GORMAN D M.
PA (SAEL/) SAELEND S.
PA (LEBE/) LEBECQUE S J E.
PA (PHIL/) PHILLIPS J H.
Query Match 51.3%; Score 140; DB 10; Length 1018;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
RESULT 301
ID ABV73351 standard; cDNA; 1153 BP.
DE LIR-J24-2 polypeptide encoding cDNA.
PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 51.3%; Score 140; DB 10; Length 1153;
Best Local Similarity 100.0%; Pred. No. 2e-33;
RESULT 302
ID AAS31409 standard; cDNA; 1281 BP.

DE Human cDNA encoding a novel extracellular matrix protein, Seq ID NO 223.
PN WO20015368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 51.3%; Score 140; DB 4; Length 1281;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
RESULT 303
ID ABQ66733 standard; cDNA; 1281 BP.
DE Human polynucleotide SEQ ID NO 223.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 51.3%; Score 140; DB 6; Length 1281;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
RESULT 304
ID ADC10755 standard; cDNA; 1281 BP.
DE Human cDNA from extracellular matrix gene 66 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 51.3%; Score 140; DB 10; Length 1281;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
RESULT 305
ID ABZ24041 standard; DNA; 1606 BP.
DE Human Dectin-1 polypeptide encoding DNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 51.3%; Score 140; DB 8; Length 1606;
Best Local Similarity 100.0%; Pred. No. 2.2e-33;
RESULT 306
ID ABV73363 standard; cDNA; 138 BP.
DE LIR-J24-stalk peptide encoding cDNA.
PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 50.5%; Score 138; DB 10; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.9e-33;
RESULT 307
ID AAK81284 standard; DNA; 336 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36096.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.4%; Score 113; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.7e-25;
RESULT 308
ID AAV42548 standard; cDNA; 2298 BP.
DE Mouse Dectin-1 cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 28.4%; Score 77.6; DB 2; Length 2298;
Best Local Similarity 73.1%; Pred. No. 9.4e-14;
RESULT 309
ID ABZ24043 standard; DNA; 2298 BP.
DE Mouse Dectin-1 polypeptide encoding DNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 28.4%; Score 77.6; DB 8; Length 2298;
Best Local Similarity 73.1%; Pred. No. 9.4e-14;
RESULT 310
ID AAV42551 standard; cDNA; 528 BP.
DE Mouse Dectin-1 extracellular domain cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 27.5%; Score 75.2; DB 2; Length 528;
Best Local Similarity 77.2%; Pred. No. 3.1e-13;

RESULT 311
ID AAC24137 standard; cDNA; 85 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 28212.
PN EP1033401-A2.
PA (GEST) GENSET.
Query Match 27.1%; Score 74; DB 3; Length 85;
Best Local Similarity 97.4%; Pred. No. 3.9e-13;
RESULT 312
Query Match 13.8%; Score 37.8; DB 6; Length 110000;
Best Local Similarity 53.8%; Pred. No. 1.2;
RESULT 313
Query Match 13.8%; Score 37.8; DB 6; Length 110000;
Best Local Similarity 53.8%; Pred. No. 1.2;
RESULT 314
ID AALJ5354 standard; cDNA; 930 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 696.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 34.4; DB 4; Length 930;
Best Local Similarity 57.4%; Pred. No. 2.4;
RESULT 315
ID ABX58342 standard; cDNA; 930 BP.
DE cDNA encoding novel human musculoskeletal system antigen #686.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.6%; Score 34.4; DB 8; Length 930;
Best Local Similarity 57.4%; Pred. No. 2.4;
RESULT 316
ID ADJ28069 standard; DNA; 930 BP.
DE Human musculoskeletal system-associated contig DNA - SEQ ID 696.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 34.4; DB 12; Length 930;
Best Local Similarity 57.4%; Pred. No. 2.4;
RESULT 317
ID ABK43739 standard; cDNA; 1446 BP.
DE DNA encoding novel central nervous system protein #319.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 34.4; DB 4; Length 1446;
Best Local Similarity 57.4%; Pred. No. 2.8;
RESULT 318
ID ADI54126 standard; cDNA; 1446 BP.
DE cDNA encoding novel human protein seq id 329.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.6%; Score 34.4; DB 12; Length 1446;
Best Local Similarity 57.4%; Pred. No. 2.8;
RESULT 319
ID ADB63593 standard; cDNA; 1969 BP.
DE Human cDNA encoding clone THYMU20034790.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.6%; Score 34.4; DB 10; Length 1969;
Best Local Similarity 57.4%; Pred. No. 3.1;
RESULT 320
ID AAL37066 standard; DNA; 2086 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3431.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.

Query Match 12.6%; Score 34.4; DB 4; Length 2086;
Best Local Similarity 57.4%; Pred. No. 3.2;
RESULT 321
ID ABX60054 standard; cDNA; 2086 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2398.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.6%; Score 34.4; DB 8; Length 2086;
Best Local Similarity 57.4%; Pred. No. 3.2;
RESULT 322
ID ADJ30804 standard; DNA; 2086 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3431.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 12.6%; Score 34.4; DB 12; Length 2086;
Best Local Similarity 57.4%; Pred. No. 3.2;
RESULT 323
ID ABL99813 standard; cDNA; 4045 BP.
DE Human secretory polynucleotide (sptm) 68.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.6%; Score 34.4; DB 6; Length 4045;
Best Local Similarity 57.4%; Pred. No. 4.1;
RESULT 324
ID ADC92020 standard; DNA; 696 BP.
DE E. faecium DNA sequence SEQ ID 1647.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 34.2; DB 10; Length 696;
Best Local Similarity 54.3%; Pred. No. 2.5;
RESULT 325
Query Match 12.5%; Score 34.2; DB 5; Length 110000;
Best Local Similarity 50.3%; Pred. No. 15;
RESULT 326
ID AAS98600 standard; DNA; 140036 BP.
DE Human genomic DNA for PHIP/NDRP.
PN WO200185785-A2.
PD 15-NOV-2001.
PA (ROZA/) ROZAKIS-ADCOCK M.
PA (FARH/) FARHANG-FALLAH J.
PA (CHEN/) CHENG A.
Query Match 12.5%; Score 34; DB 6; Length 140036;
Best Local Similarity 52.9%; Pred. No. 20;
RESULT 327
ID ABK91073 standard; DNA; 5144 BP.
DE Gene encoding Arabidopsis thaliana SOS2 serine/threonine protein kinase.
PN US2002095032-A1.
PD 18-JUL-2002.
PA (UYAR-) UNIV ARIZONA.
Query Match 12.4%; Score 33.8; DB 6; Length 5144;
Best Local Similarity 50.3%; Pred. No. 6.8;
RESULT 328
ID ABN77024 standard; cDNA; 321 BP.
DE Human ORF1971 cDNA, SEQ ID NO:3941.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 33.6; DB 6; Length 321;
Best Local Similarity 56.2%; Pred. No. 2.9;
RESULT 329
ID ABL33689 standard; DNA; 9646 BP.
DE Human immune system associated gene SEQ ID NO: 1662.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 12.3%; Score 33.6; DB 6; Length 9646;
Best Local Similarity 48.9%; Pred. No. 9.9;

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RESULT 330
ID ABL33948 standard; DNA; 18218 BP.
DE Human immune system associated gene SEQ ID NO: 1921.
PN WO200200928-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 12.3%; Score 33.6; DB 6; Length 18218;
Best Local Similarity 50.6%; Pred. No. 12;
RESULT 331
ID ADB62949 standard; cDNA; 1990 BP.
DE Human cDNA encoding clone PLACE60175640.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.2%; Score 33.4; DB 10; Length 1990;
Best Local Similarity 54.5%; Pred. No. 6.5;
RESULT 332
ID ADO47190 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004029249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 12.2%; Score 33.4; DB 12; Length 200000;
Best Local Similarity 55.7%; Pred. No. 34;
RESULT 333
ID AAC39967 standard; DNA; 2928 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26555.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 33; DB 3; Length 2928;
Best Local Similarity 51.0%; Pred. No. 9.9;
RESULT 334
ID AAL05628 standard; DNA; 32176 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8316.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.1%; Score 33; DB 4; Length 32176;
Best Local Similarity 46.1%; Pred. No. 24;
RESULT 335
ID AEN16359 standard; cDNA; 435 BP.
DE Human OREX polynucleotide sequence SEQ ID NO: 1195.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 32.8; DB 6; Length 435;
Best Local Similarity 57.4%; Pred. No. 5.8;
RESULT 336
ID ABL32657 standard; DNA; 9832 BP.
DE Human immune system associated gene SEQ ID NO: 630.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 12.0%; Score 32.8; DB 6; Length 9832;
Best Local Similarity 59.8%; Pred. No. 18;
RESULT 337
ID ACH2923 standard; cDNA; 489 BP.
DE Human adult ovary cDNA #1303.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 11.9%; Score 32.6; DB 9; Length 489;
Best Local Similarity 48.9%; Pred. No. 7;
RESULT 338
ID ACA28755 standard; DNA; 1209 BP.
DE Prokaryotic essential gene #10412.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 32.6; DB 8; Length 1209;
Best Local Similarity 54.6%; Pred. No. 9.6;
RESULT 339
ID AAK74053 standard; DNA; 39567 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 28865.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.9%; Score 32.4; DB 4; Length 39567;
Best Local Similarity 50.0%; Pred. No. 39;
RESULT 340
ID ABZ74429 standard; DNA; 39567 BP.
DE Secreted protein gene 286 genomic fragment HRGBD54, SEQ ID NO: 1576.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.9%; Score 32.4; DB 8; Length 39567;
Best Local Similarity 50.0%; Pred. No. 39;
RESULT 341
ID ABZ67986 standard; DNA; 39567 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO: 1509.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.9%; Score 32.4; DB 10; Length 39567;
Best Local Similarity 50.0%; Pred. No. 39;
RESULT 342
ID ABV06453 standard; cDNA; 366 BP.
DE Human prostate expression marker cDNA 6444.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.7%; Score 32; DB 5; Length 366;
Best Local Similarity 48.4%; Pred. No. 9.7;
RESULT 343
ID ACD92876 standard; cDNA; 695 BP.
DE Human colon cancer cell expressed cDNA #1288.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 11.7%; Score 32; DB 10; Length 695;
Best Local Similarity 48.6%; Pred. No. 12;
RESULT 344
ID ADM29365 standard; DNA; 1414 BP.
DE Human novel protein NOV22b coding sequence.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 32; DB 11; Length 1414;
Best Local Similarity 51.4%; Pred. No. 16;
RESULT 345
ID ADM29363 standard; DNA; 1432 BP.
DE Human novel protein NOV22a coding sequence.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 32; DB 11; Length 1432;
Best Local Similarity 51.4%; Pred. No. 16;
RESULT 346
ID ADC14278 standard; DNA; 1529 BP.
DE Human enzyme ENZM-31 gene.
PN WO2003042357-A2.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 32; DB 10; Length 1529;
Best Local Similarity 51.4%; Pred. No. 16;
RESULT 347
ID ABL58125 standard; cDNA; 1889 BP.
DE Human RNA helicase 12 coding sequence.
PN CN1331331-A.
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PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 11.7%; Score 32; DB 6; Length 1889;
Best Local Similarity 47.1%; Pred. No. 17;
RESULT 348
ID AAD09939 standard; cDNA; 1931 BP.
DE Human drug metabolising enzyme (DME-4) cDNA.
PN WO200151638-A2.
PD 19-JUL-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 32; DB 4; Length 1931;
Best Local Similarity 51.4%; Pred. No. 18;
RESULT 349
ID ADN04961 standard; cDNA; 2114 BP.
DE Antipsoriatic cDNA sequence #695.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 11.7%; Score 32; DB 12; Length 2114;
Best Local Similarity 51.4%; Pred. No. 18;
RESULT 350
ID ADM29367 standard; DNA; 2183 BP.
DE Human novel protein NOV22c coding sequence.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 32; DB 11; Length 2183;
Best Local Similarity 51.4%; Pred. No. 18;
RESULT 351
ID AAS87446 standard; cDNA; 2265 BP.
DE DNA encoding novel human diagnostic protein #23250.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 32; DB 5; Length 2265;
Best Local Similarity 51.4%; Pred. No. 19;
RESULT 352
ID ABQ60988 standard; cDNA; 2504 BP.
DE 7 alpha hydroxylase sequence encoding sequence.
PN WO20023111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 32; DB 6; Length 2504;
Best Local Similarity 51.4%; Pred. No. 19;
RESULT 353
ID ABK45465 standard; cDNA; 506 BP.
DE CDNA encoding colon tumour protein, SEQ ID No 1016.
PN WO200212328-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 11.6%; Score 31.8; DB 6; Length 506;
Best Local Similarity 56.1%; Pred. No. 13;
RESULT 354
ID ABK55395 standard; cDNA; 713 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 865.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 11.6%; Score 31.8; DB 6; Length 713;
Best Local Similarity 56.1%; Pred. No. 14;
RESULT 355
ID AAH33427 standard; cDNA; 851 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:483.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.6%; Score 31.8; DB 4; Length 851;
Best Local Similarity 56.1%; Pred. No. 15;
RESULT 356
ID ADF82256 standard; DNA; 983 BP.
DE Leukaemia-related DNA sequence #2812.
PN WO2003039443-A2.
PD 15-MAY-2003.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 11.6%; Score 31.8; DB 10; Length 983;
Best Local Similarity 58.7%; Pred. No. 16;
RESULT 357
ID ACA2448 standard; DNA; 2648 BP.
DE Human encoding human PNM-33.
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.6%; Score 31.8; DB 10; Length 2648;
Best Local Similarity 56.1%; Pred. No. 23;
RESULT 358
ID ABX04178 standard; cDNA; 2680 BP.
DE Human mRNA differentially expressed in mesenchymal cells #25.
PN WO200271927-A2.
PD 19-SEP-2002.
PA (BGM-) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 11.6%; Score 31.8; DB 6; Length 2680;
Best Local Similarity 56.1%; Pred. No. 23;
RESULT 359
ID AAQ81792 standard; DNA; 8478 BP.
DE B subtilis biotin operon and flanking sequences.
PN EP635572-A2.
PD 25-JAN-1995.
PA (HOFF-) HOFFMANN LA ROCHE & CO AG F.
Query Match 11.6%; Score 31.8; DB 2; Length 8478;
Best Local Similarity 56.1%; Pred. No. 35;
RESULT 360
Query Match 11.6%; Score 31.8; DB 8; Length 110000;
Best Local Similarity 54.8%; Pred. No. 89;
RESULT 361
ID AAV75482 standard; DNA; 299 BP.
DE Staphylococcus aureus contig SEQ ID #1171.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.6%; Score 31.6; DB 2; Length 299;
Best Local Similarity 50.7%; Pred. No. 12;
RESULT 362
ID AAZ56348 standard; DNA; 1665 BP.
DE Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:18.
PN WO9961458-A1.
PD 02-DEC-1999.
PA (UNSY-) UNIV SYDNEY.
Query Match 11.6%; Score 31.6; DB 3; Length 1665;
Best Local Similarity 49.4%; Pred. No. 22;
RESULT 363
ID ABL34627 standard; DNA; 5539 BP.
DE Human metastasis associated gene SEQ ID NO: 180.
PN WO20017376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.6%; Score 31.6; DB 6; Length 5539;
Best Local Similarity 48.9%; Pred. No. 34;
RESULT 364
ID ABL32728 standard; DNA; 14307 BP.
DE Human immune system associated gene SEQ ID NO: 701.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.6%; Score 31.6; DB 6; Length 14307;
Best Local Similarity 51.4%; Pred. No. 48;
RESULT 365
ID ADH30232 standard; DNA; 161671 BP.
DE Human FLOD2 DNA.
PN US2003124535-A1.
PD 03-JUL-2003.
PA (VITI-) VITIVITY INC.
Query Match 11.6%; Score 31.6; DB 12; Length 161671;

Best Local Similarity 54.2%; Pred. No. 1.2e+02;
RESULT 366
ID ABL92288 standard; DNA; 6156 BP.
DE Chemically treated DNA repair gene fragment#49.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 11.5%; Score 31.4; DB 6; Length 6156;
Best Local Similarity 61.7%; Pred. No. 41;
RESULT 367
ID ABL9359 standard; DNA; 6156 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 59.
PN WO20017377-A2.
PD 18-OCT-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 11.5%; Score 31.4; DB 6; Length 6156;
Best Local Similarity 61.7%; Pred. No. 41;
RESULT 368
ID AAK10546 standard; DNA; 536 BP.
DE Human brain expressed single exon probe SEQ ID NO: 10537.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 11.4%; Score 31.2; DB 4; Length 536;
Best Local Similarity 50.7%; Pred. No. 20;
RESULT 369
ID ABS36095 standard; DNA; 536 BP.
DE Human liver single exon probe, SEQ ID No 11085.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 11.4%; Score 31.2; DB 4; Length 536;
Best Local Similarity 50.7%; Pred. No. 20;
RESULT 370
ID AAK58497 standard; cDNA; 559 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3557.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31.2; DB 4; Length 559;
Best Local Similarity 49.7%; Pred. No. 20;
RESULT 371
ID AXB63053 standard; cDNA; 1072 BP.
DE Human cDNA #53 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 11.4%; Score 31.2; DB 8; Length 1072;
Best Local Similarity 66.2%; Pred. No. 25;
RESULT 372
ID ABL45638 standard; DNA; 1202 BP.
DE Human ubiquitin protein ligase E3A gene fragment SEQ ID NO: 4.
PN WO200192582-A1.
PD 06-DEC-2001.
PA (GENA-) GENAITSANCE PHARM INC.
Query Match 11.4%; Score 31.2; DB 6; Length 1202;
Best Local Similarity 51.4%; Pred. No. 26;
RESULT 373
ID ACA04691 standard; cDNA; 1760 BP.
DE cDNA encoding human membrane associated protein fragment #139.
PN US6492505-B1.
PD 10-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.4%; Score 31.2; DB 8; Length 1760;
Best Local Similarity 66.2%; Pred. No. 30;
RESULT 374
ID ABK43427 standard; cDNA; 1911 BP.
DE DNA encoding novel central nervous system protein #7.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31.2; DB 4; Length 1811;
Best Local Similarity 66.2%; Pred. No. 31;
RESULT 375
ID ADI53814 standard; cDNA; 1811 BP.
DE cDNA encoding novel human protein seq id 17.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 11.4%; Score 31.2; DB 12; Length 1811;
Best Local Similarity 66.2%; Pred. No. 31;
RESULT 376
ID AAS41019 standard; cDNA; 1854 BP.
DE cDNA encoding novel human enzyme polypeptide #235.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31.2; DB 4; Length 1854;
Best Local Similarity 66.2%; Pred. No. 31;
RESULT 377
ID AAZ00354 standard; DNA; 2885 BP.
DE Nucleotide sequence of human hspATP6.
PN WO9936537-A2.
PD 22-JUL-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.4%; Score 31.2; DB 2; Length 2885;
Best Local Similarity 60.7%; Pred. No. 36;
RESULT 378
ID ADD69636 standard; cDNA; 2899 BP.
DE Human REMAP cDNA - SEQ ID 65.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.4%; Score 31.2; DB 10; Length 2899;
Best Local Similarity 66.2%; Pred. No. 36;
RESULT 379
ID AAQ82847 standard; DNA; 3142 BP.
DE P-selectin gene.
PN WO9506118-A1.
PD 02-MAR-1995.
PA (OKLA) UNIV OKLAHOMA STATE.
Query Match 11.4%; Score 31.2; DB 2; Length 3142;
Best Local Similarity 66.2%; Pred. No. 37;
RESULT 380
ID ADI31764 standard; cDNA; 3142 BP.
DE Human cDNA #1090.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 11.4%; Score 31.2; DB 11; Length 3142;
Best Local Similarity 66.2%; Pred. No. 37;
RESULT 381
ID ADP13425 standard; DNA; 3142 BP.
DE Renal cell carcinoma differentially expressed gene #161.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN) TWINE N C.
PA (BURC) BURCZYNSKI M E.
PA (TREP) TREPICCHIO W L.
PA (DORN) DORNER A.
PA (STOV) STOVER J A.
PA (SLOW) SLOWI D K.
Query Match 11.4%; Score 31.2; DB 12; Length 3142;
Best Local Similarity 66.2%; Pred. No. 37;
RESULT 382
ID ADN95547 standard; DNA; 3199 BP.
DE Human BEC/LEC-related gene sequence SeqID470.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 11.4%; Score 31.2; DB 11; Length 3199;

Best Local Similarity 66.2%; Pred. No. 38;
RESULT 383
ID AAH72583 standard; cDNA; 3246 BP.
DE Human cervical cancer marker nucleic acid 3857.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 31.2; DB 4; Length 3246;
Best Local Similarity 66.2%; Pred. No. 38;
RESULT 384
ID AAD57202 standard; DNA; 3660 BP.
DE Rice homologue of petunia restorer (Rhrpr2) DNA.
PN WO2003057859-A2.
PD 17-JUL-2003.
PA (CORR) CORNELL RES FOUND INC.
Query Match 11.4%; Score 31.2; DB 9; Length 3660;
Best Local Similarity 53.8%; Pred. No. 40;
RESULT 385
ID ABL28550 standard; DNA; 4324 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37123.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.4%; Score 31.2; DB 4; Length 4324;
Best Local Similarity 58.7%; Pred. No. 42;
RESULT 386
ID ABL33065 standard; DNA; 6074 BP.
DE Human immune system associated gene SEQ ID NO: 1038.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31.2; DB 6; Length 6074;
Best Local Similarity 52.3%; Pred. No. 47;
RESULT 387
ID ABL07258 standard; cDNA; 19754 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16256.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.4%; Score 31.2; DB 4; Length 19754;
Best Local Similarity 58.7%; Pred. No. 73;
RESULT 388
ID ABN83124 standard; DNA; 172637 BP.
DE Human voltage-activated ion channel transporter protein gene.
Query Match 11.4%; Score 31.2; DB 6; Length 172637;
Best Local Similarity 54.3%; Pred. No. 1.6e+02;
RESULT 389
ID AAK73896 standard; DNA; 396 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28708.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 4; Length 396;
Best Local Similarity 50.3%; Pred. No. 20;
RESULT 390
ID ADL62560 standard; DNA; 397 BP.
DE Human ovarian cancer DNA marker #20772.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 31; DB 5; Length 397;
Best Local Similarity 52.8%; Pred. No. 20;
RESULT 391
ID ADI70673 standard; DNA; 400 BP.
DE Human ovarian cancer DNA marker #3415.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 31; DB 5; Length 400;
Best Local Similarity 52.8%; Pred. No. 21;
RESULT 392
ID ADI76991 standard; DNA; 400 BP.
DE Human ovarian cancer DNA marker #9733.

PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 31; DB 5; Length 400;
Best Local Similarity 52.8%; Pred. No. 21;
RESULT 393
ID ADI42227 standard; DNA; 494 BP.
DE Human ovarian cancer DNA marker #16117.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.4%; Score 31; DB 5; Length 494;
Best Local Similarity 52.8%; Pred. No. 22;
RESULT 394
ID AAK59117 standard; cDNA; 519 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4177.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 4; Length 519;
Best Local Similarity 51.5%; Pred. No. 23;
RESULT 395
ID AAS92837 standard; cDNA; 823 BP.
DE DNA encoding novel human diagnostic protein #28641.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.4%; Score 31; DB 5; Length 823;
Best Local Similarity 48.6%; Pred. No. 27;
RESULT 396
ID AAC59176 standard; cDNA; 1885 BP.
DE Human secreted protein cDNA sequence #20.
PN WO200055201-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 3; Length 1885;
Best Local Similarity 52.8%; Pred. No. 36;
RESULT 397
ID AAS61454 standard; DNA; 4233 BP.
DE Human gene regulation-associated gene oligonucleotide #409.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 6; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 398
ID ABZ10093 standard; DNA; 4233 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #233.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 8; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 399
ID ABZ09989 standard; DNA; 4233 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #129.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 8; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 400
ID ABZ10239 standard; DNA; 4233 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #379.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 8; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 401
ID ABZ10135 standard; DNA; 4233 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #275.
PN WO20027272-A2.

PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 8; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 402
ID ADE84073 standard; DNA; 4233 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #9.
FN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 10; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 403
ID ADE84149 standard; DNA; 4233 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #85.
FN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.4%; Score 31; DB 10; Length 4233;
Best Local Similarity 49.1%; Pred. No. 48;
RESULT 404
ID AAA9265 standard; DNA; 5433 BP.
DE Plasmidium yoeiii YM MAEBL genomic DNA sequence SEQ ID NO:1.
FN US6120770-A.
PD 19-SEP-2000.
PA (UNOT) UNIV NOTRE DAME DU LAC.
Query Match 11.4%; Score 31; DB 3; Length 5433;
Best Local Similarity 52.8%; Pred. No. 53;
RESULT 405
ID AZB67645 standard; DNA; 8960 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1168.
FN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 10; Length 8960;
Best Local Similarity 55.0%; Pred. No. 63;
RESULT 406
ID AZB67644 standard; DNA; 8965 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1167.
FN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 10; Length 8965;
Best Local Similarity 55.0%; Pred. No. 63;
RESULT 407
ID AAK68939 standard; DNA; 28180 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23751.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 4; Length 28180;
Best Local Similarity 51.0%; Pred. No. 95;
RESULT 408
ID AAS26795 standard; DNA; 32248 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1769.
FN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 4; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 409
ID AAL37122 standard; DNA; 32248 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3487.
FN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 4; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 410
ID ABA20412 standard; DNA; 32248 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12743.
FN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 8; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 411
ID ABX74144 standard; DNA; 32248 BP.
DE Human novel polynucleotide #972.
FN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 11.4%; Score 31; DB 8; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 412
ID ABX60110 standard; cDNA; 32248 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2454.
FN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 11.4%; Score 31; DB 8; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 413
ID ADJ30860 standard; DNA; 32248 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3487.
FN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.4%; Score 31; DB 12; Length 32248;
Best Local Similarity 50.3%; Pred. No. 1e+02;
RESULT 414
ID ADB12769 standard; DNA; 139308 BP.
DE Human PRKR DNA.
FN DE10128838-A1.
PD 02-JAN-2003.
PA (GENP-) GENPROFILE AG.
Query Match 11.4%; Score 31; DB 8; Length 139308;
Best Local Similarity 51.0%; Pred. No. 1.7e+02;
RESULT 415
ID ABV17415 standard; cDNA; 353 BP.
DE Human prostate expression marker cDNA 17406.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.3%; Score 30.8; DB 5; Length 353;
Best Local Similarity 48.3%; Pred. No. 23;
RESULT 416
ID ABV47209 standard; cDNA; 450 BP.
DE Human prostate expression marker cDNA 47200.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.3%; Score 30.8; DB 5; Length 450;
Best Local Similarity 48.3%; Pred. No. 25;
RESULT 417
ID ABT09214 standard; DNA; 705 BP.
DE Phase-1 Rat CT gene SEQ ID NO 302.
FN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 11.3%; Score 30.8; DB 6; Length 705;
Best Local Similarity 50.0%; Pred. No. 29;
RESULT 418
ID ADG45603 standard; DNA; 705 BP.
DE Liver inflammatory predictive gene related DNA sequence.
FN WO2003095624-A2.
PD 20-NOV-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 11.3%; Score 30.8; DB 12; Length 705;
Best Local Similarity 50.0%; Pred. No. 29;
RESULT 419
ID ACA22540 standard; DNA; 1236 BP.

DE Prokaryotic essential gene #4197.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.3%; Score 30.8; DB 8; Length 1236;
Best Local Similarity 54.4%; Pred. No. 36;
RESULT 420
ID ACAS2653 standard; DNA; 1794 BP.
DE Prokaryotic essential gene #34310.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.3%; Score 30.8; DB 8; Length 1794;
Best Local Similarity 51.4%; Pred. No. 41;
RESULT 421
ID AAS81340 standard; cDNA; 1873 BP.
DE DNA encoding novel human diagnostic protein #17144.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.3%; Score 30.8; DB 5; Length 1873;
Best Local Similarity 48.3%; Pred. No. 41;
RESULT 422
ID ADJ40188 standard; cDNA; 2469 BP.
DE Plant cDNA #1188.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI P.
PA (KREP/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RICK D.
PA (ZHUT/) ZHU T.
Query Match 11.3%; Score 30.8; DB 12; Length 2469;
Best Local Similarity 57.1%; Pred. No. 46;
RESULT 423
ID AAK91497 standard; DNA; 5314 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5073.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 30.8; DB 4; Length 5314;
Best Local Similarity 51.4%; Pred. No. 60;
RESULT 424
ID AAK64723 standard; DNA; 5314 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19535.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 30.8; DB 4; Length 5314;
Best Local Similarity 51.4%; Pred. No. 60;
RESULT 425
ID AAK75611 standard; DNA; 5314 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30423.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.3%; Score 30.8; DB 4; Length 5314;
Best Local Similarity 51.4%; Pred. No. 60;
RESULT 426
ID AD157166 standard; DNA; 76272 BP.
DE Oryza minuta P19 locus genomic DNA sequence.
PN US2004006788-A1.
PD 08-JAN-2004.
PA (WANG/) WANG G.
PA (LIUG/) LIU G.
Query Match 11.3%; Score 30.8; DB 12; Length 76272;
Best Local Similarity 52.3%; Pred. No. 1.6e+02;

RESULT 427
ID ADB55776 standard; DNA; 475 BP.
DE Toxicity-related gene, SEQ ID 802.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 11.2%; Score 30.6; DB 10; Length 475;
Best Local Similarity 55.0%; Pred. No. 29;
RESULT 428
ID ADB50356 standard; DNA; 475 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:898.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 11.2%; Score 30.6; DB 10; Length 475;
Best Local Similarity 55.0%; Pred. No. 29;
RESULT 429
ID ABL90179 standard; cDNA; 1000 BP.
DE Human polynucleotide SEQ ID NO 741.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.2%; Score 30.6; DB 6; Length 1000;
Best Local Similarity 49.7%; Pred. No. 38;
RESULT 430
ID AAH34864 standard; cDNA; 1587 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1946.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.2%; Score 30.6; DB 4; Length 1587;
Best Local Similarity 52.8%; Pred. No. 45;
RESULT 431
ID ADB62875 standard; cDNA; 2377 BP.
DE Human cDNA encoding clone OCBF20177910.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.2%; Score 30.6; DB 10; Length 2377;
Best Local Similarity 50.3%; Pred. No. 52;
RESULT 432
ID ABZ35894 standard; cDNA; 2775 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 58.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.2%; Score 30.6; DB 8; Length 2775;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 433
ID ADB62455 standard; cDNA; 2942 BP.
DE Human cDNA encoding clone FEBRA20038330.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.2%; Score 30.6; DB 10; Length 2942;
Best Local Similarity 50.3%; Pred. No. 56;
RESULT 434
ID ADQ25068 standard; DNA; 3807 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7888.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.2%; Score 30.6; DB 12; Length 3807;
Best Local Similarity 50.3%; Pred. No. 62;
RESULT 435
ID AAG46736 standard; DNA; 6292 BP.
DE Tumour suppressor gene derived chemically modified sequence #460.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EFIG-) EFIGENOMICS AG.
Query Match 11.2%; Score 30.6; DB 4; Length 6292;

Best Local Similarity 60.0%; Pred. No. 74;
RESULT 436
ID ADH56913 standard; DNA; 68571 BP.
DE Human CARD4 genomic DNA sequence SeqID 1.
PN US2003219810-A1.
PD 27-NOV-2003.
PA (BARN/) BARNES G.
PA (BERT/) BERTIN J.
Query Match 11.2%; Score 30.6; DB 12; Length 68571;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
RESULT 437
ID RAD58431 standard; DNA; 322101 BP.
DE Human PRAD1 genomic DNA.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 11.2%; Score 30.6; DB 10; Length 322101;
Best Local Similarity 45.3%; Pred. No. 3e+02;
RESULT 438
ID ADI35046 standard; DNA; 322101 BP.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) genomic DNA sequence.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 11.2%; Score 30.6; DB 12; Length 322101;
Best Local Similarity 45.3%; Pred. No. 3e+02;
RESULT 439
ID ABX53718 standard; cDNA; 324 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3647.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 11.1%; Score 30.4; DB 8; Length 324;
Best Local Similarity 50.7%; Pred. No. 29;
RESULT 440
ID ABX49849 standard; cDNA; 375 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #15014.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 11.1%; Score 30.4; DB 8; Length 375;
Best Local Similarity 48.8%; Pred. No. 31;
RESULT 441
ID AAL02531 standard; cDNA; 612 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2532.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.4; DB 4; Length 612;
Best Local Similarity 57.3%; Pred. No. 37;
RESULT 442
ID ABL97297 standard; cDNA; 612 BP.
DE Human testicular antigen encoding cDNA SEQ ID NO: 965.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.4; DB 4; Length 612;
Best Local Similarity 57.3%; Pred. No. 37;
RESULT 443
ID ABV53438 standard; cDNA; 619 BP.
DE Human prostate expression marker cDNA 53429.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.1%; Score 30.4; DB 5; Length 619;
Best Local Similarity 54.5%; Pred. No. 37;
RESULT 444

ID ABZ71606 standard; cDNA; 1031 BP.
DE Breast specific nucleic acid # SEQ ID 66.
PN WO20028375-A2.
PD 07-NOV-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 11.1%; Score 30.4; DB 8; Length 1031;
Best Local Similarity 57.3%; Pred. No. 45;
RESULT 445
ID ADF85848 standard; cDNA; 1031 BP.
DE Human breast specific nucleic acid (BSNA) cDNA, SEQ ID NO:66.
PN WO200309989-A2.
PD 04-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 11.1%; Score 30.4; DB 12; Length 1031;
Best Local Similarity 57.3%; Pred. No. 45;
RESULT 446
ID ADL62875 standard; DNA; 1721 BP.
DE Human ovarian cancer DNA marker #21087.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.1%; Score 30.4; DB 5; Length 1721;
Best Local Similarity 52.3%; Pred. No. 54;
RESULT 447
ID ACA48024 standard; DNA; 2538 BP.
DE Prokaryotic essential gene #29661.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.1%; Score 30.4; DB 8; Length 2538;
Best Local Similarity 50.7%; Pred. No. 62;
RESULT 448
ID ABA18222 standard; DNA; 26241 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8553.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.4; DB 5; Length 26241;
Best Local Similarity 59.1%; Pred. No. 1.4e+02;
RESULT 449
ID AAC54789 standard; DNA; 490 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79098.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 30.2; DB 3; Length 490;
Best Local Similarity 52.8%; Pred. No. 39;
RESULT 450
ID AAC38648 standard; DNA; 492 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21740.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 30.2; DB 3; Length 492;
Best Local Similarity 52.8%; Pred. No. 39;
RESULT 451
ID ABV55148 standard; cDNA; 622 BP.
DE Human prostate expression marker cDNA 55139.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 11.1%; Score 30.2; DB 5; Length 622;
Best Local Similarity 60.2%; Pred. No. 43;
RESULT 452
ID ADK14348 standard; DNA; 771 BP.
DE Candida maltosa CYP gene upstream regulator region DNA SEQ ID NO:77.
PN WO2004016756-A2.
PD 26-FEB-2004.
PA (COGN-) COGNIS CORP.
Query Match 11.1%; Score 30.2; DB 12; Length 771;
Best Local Similarity 51.9%; Pred. No. 46;
RESULT 453
ID ABQ76298 standard; cDNA; 896 BP.
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 21.
PN WO200264766-A2.

PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 11.1%; Score 30.2; DB 6; Length 896;
Best Local Similarity 49.1%; Pred. No. 49;
RESULT 454
ID AAX04331 standard; DNA; 987 BP.
DE Human secreted protein gene 21 clone HWT275.
PN WO9856804-A1.
PD 17-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.2; DB 2; Length 987;
Best Local Similarity 49.0%; Pred. No. 51;
RESULT 455
ID ADH23603 standard; DNA; 1199 BP.
DE Baker's yeast small non-coding amplicon between H2a/H2b SeqID 236.
PN WO2003097868-A1.
PD 27-NOV-2003.
PA (MICR-) MICROBIOGEN PTY LTD.
Query Match 11.1%; Score 30.2; DB 12; Length 1199;
Best Local Similarity 49.1%; Pred. No. 54;
RESULT 456
ID AAS62692 standard; cDNA; 1217 BP.
DE cDNA sequence #479 encoding novel human secreted protein.
PN WO200177251-A2.
PD 18-OCT-2001.
PA (GENY) GENETICS INST INC.
Query Match 11.1%; Score 30.2; DB 6; Length 1217;
Best Local Similarity 58.2%; Pred. No. 55;
RESULT 457
ID ADC93856 standard; DNA; 1308 BP.
DE E. faecium DNA sequence SEQ ID 3483.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.1%; Score 30.2; DB 10; Length 1308;
Best Local Similarity 53.9%; Pred. No. 56;
RESULT 458
ID AAS69875 standard; cDNA; 15031 BP.
DE DNA encoding novel human diagnostic protein #5679.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HVSE-) HVSEQ INC.
Query Match 11.1%; Score 30.2; DB 5; Length 15031;
Best Local Similarity 51.9%; Pred. No. 1.4e+02;
RESULT 459
ID ABU17834 standard; DNA; 23203 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4975.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.1%; Score 30.2; DB 4; Length 23203;
Best Local Similarity 51.1%; Pred. No. 1.6e+02;
RESULT 460
ID AAL04361 standard; DNA; 32192 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7049.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.2; DB 4; Length 32192;
Best Local Similarity 53.9%; Pred. No. 1.8e+02;
RESULT 461
ID ABQ67005 standard; DNA; 33053 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 35.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.1%; Score 30.2; DB 6; Length 33053;
Best Local Similarity 51.9%; Pred. No. 1.8e+02;
RESULT 462
ID ADA02609 standard; DNA; 96598 BP.
DE Mouse Nfkb1 carcinoma associated gene, SEQ ID NO:1127.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 30.2; DB 9; Length 96598;
Best Local Similarity 47.2%; Pred. No. 2.7e+02;
RESULT 463
ID ADB72347 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene.
PN WO200308583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 11.1%; Score 30.2; DB 10; Length 96598;
Best Local Similarity 47.2%; Pred. No. 2.7e+02;
RESULT 464
ID ADE82941 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene genomic DNA sequence.
PN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 11.1%; Score 30.2; DB 10; Length 96598;
Best Local Similarity 47.2%; Pred. No. 2.7e+02;
RESULT 465
ID ADE95857 standard; DNA; 96598 BP.
DE Mouse Nfkb1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 11.1%; Score 30.2; DB 10; Length 96598;
Best Local Similarity 47.2%; Pred. No. 2.7e+02;
RESULT 466
ID AAH25483 standard; DNA; 180 BP.
DE Nucleotide fragment of ribulose-1,5-bisphosphate carboxylase cDNA.
PN WO200141559-A1.
PD 14-JUN-2001.
PA (UNIC-) UNICROP LTD.
Query Match 11.0%; Score 30; DB 4; Length 180;
Best Local Similarity 50.7%; Pred. No. 32;
RESULT 467
ID ABZ08556 standard; cDNA; 306 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8547.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 11.0%; Score 30; DB 6; Length 306;
Best Local Similarity 55.9%; Pred. No. 38;
RESULT 468
ID AAK63313 standard; cDNA; 381 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8373.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 30; DB 4; Length 381;
Best Local Similarity 55.9%; Pred. No. 42;
RESULT 469
ID ADF02426 standard; DNA; 624 BP.
DE Bacterial polynucleotide #2711.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.0%; Score 30; DB 10; Length 624;
Best Local Similarity 52.4%; Pred. No. 50;
RESULT 470
ID AAD09356 standard; DNA; 1134 BP.
DE Human beta-1,3-galactosyltransferase homologue, ZNSSP8 degenerate DNA.
PN WO200144479-A1.
PD 21-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.0%; Score 30; DB 5; Length 1134;
Best Local Similarity 23.8%; Pred. No. 62;
RESULT 471
ID AAX61837 standard; DNA; 1212 BP.
DE B. burgdorferi antigenic protein coding sequence, f04A.nt BB011.
PN WO9853071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMMUNE INC.
Query Match 11.0%; Score 30; DB 2; Length 1212;
Best Local Similarity 45.7%; Pred. No. 63;
RESULT 472
ID ACA44604 standard; DNA; 1575 BP.
DE Prokaryotic essential gene #26261.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.0%; Score 30; DB 8; Length 1575;
Best Local Similarity 59.3%; Pred. No. 69;
RESULT 473
ID ADF02276 standard; DNA; 1590 BP.
DE Bacterial polynucleotide #2561.
FN US605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.0%; Score 30; DB 10; Length 1590;
Best Local Similarity 59.3%; Pred. No. 70;
RESULT 474
ID AAC76388 standard; cDNA; 1671 BP.
DE Human ORFX ORF1943 polynucleotide sequence SEQ ID NO:3885.
FN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 11.0%; Score 30; DB 3; Length 1671;
Best Local Similarity 50.7%; Pred. No. 71;
RESULT 475
ID ABK75003 standard; DNA; 1917 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #2294.
FN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 11.0%; Score 30; DB 6; Length 1917;
Best Local Similarity 54.5%; Pred. No. 74;
RESULT 476
ID ADA73195 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 6521.
FN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 11.0%; Score 30; DB 8; Length 2000;
Best Local Similarity 51.5%; Pred. No. 76;
RESULT 477
ID AAN91624 standard; DNA; 2160 BP.
DE 5' flanking sequence of sigma-gamma-4 switch sequence for Cx gene upstream.
FN WO8903425-A.
PD 20-APR-1989.
PA (MITK) MITSUI TOATSU CHEM INC.
PA (MITH) MISTUI PHARM INC.
PA (EDUC-) EDUCATION FOUNO FUJITA.
PA (FUJI-) FUJITA GAKYEN GH.
PA (FUJI-) FUJITA GAKYEN GH.
Query Match 11.0%; Score 30; DB 1; Length 2160;
Best Local Similarity 52.4%; Pred. No. 78;
RESULT 478
ID ABL21333 standard; DNA; 3144 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15472.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.0%; Score 30; DB 4; Length 3144;
Best Local Similarity 53.4%; Pred. No. 89;
RESULT 479
ID ADQ22350 standard; DNA; 3741 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5170.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.0%; Score 30; DB 12; Length 3741;
Best Local Similarity 55.9%; Pred. No. 95;

RESULT 480
ID ABL21332 standard; DNA; 5641 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15469.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.0%; Score 30; DB 4; Length 5641;
Best Local Similarity 53.4%; Pred. No. 1.1e+02;
RESULT 481
ID AAX56763 standard; DNA; 7432 BP.
DE Mouse odorant binding protein MWOBF1A genomic DNA.
FN DE19756678-C1.
PD 20-MAY-1999.
PA (FORS/) FORSSMANN W.
Query Match 11.0%; Score 30; DB 2; Length 7432;
Best Local Similarity 49.4%; Pred. No. 1.2e+02;
RESULT 482
ID ABZ10124 standard; DNA; 7809 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #264.
FN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 11.0%; Score 30; DB 8; Length 7809;
Best Local Similarity 49.4%; Pred. No. 1.2e+02;
RESULT 483
ID AAK84636 standard; DNA; 8911 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39448.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 30; DB 4; Length 8911;
Best Local Similarity 55.9%; Pred. No. 1.3e+02;
RESULT 484
ID AAK84635 standard; DNA; 8911 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39447.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.0%; Score 30; DB 4; Length 8911;
Best Local Similarity 55.9%; Pred. No. 1.3e+02;
RESULT 485
ID AAN40141 standard; DNA; 11866 BP.
DE Sequence of human factor IX genomic DNA.
FN WO8400560-A.
PD 16-FEB-1984.
PA (NATR) NAT RES DEV CORP.
PA (BROW/) BROWNLEE G G.
Query Match 11.0%; Score 30; DB 1; Length 11866;
Best Local Similarity 57.4%; Pred. No. 1.4e+02;
RESULT 486
ID AAN40176 standard; DNA; 11873 BP.
DE Sequence of human factor IX genomic DNA.
FN GB2125409-A.
PD 07-MAR-1984.
PA (NATR) NAT RES DEV CORP.
Query Match 11.0%; Score 30; DB 1; Length 11873;
Best Local Similarity 57.4%; Pred. No. 1.4e+02;
RESULT 487
ID AAX99556 standard; DNA; 14066 BP.
DE Nucleic acid sequence from U. urealyticum.
FN WO9939007-A1.
PD 05-AUG-1999.
PA (UABR-) UAB RES FOUND.
Query Match 11.0%; Score 30; DB 2; Length 14066;
Best Local Similarity 55.9%; Pred. No. 1.5e+02;
RESULT 488
ID ACA52811 standard; DNA; 14067 BP.
DE Prokaryotic essential gene #34468.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.0%; Score 30; DB 8; Length 14067;
Best Local Similarity 55.9%; Pred. No. 1.5e+02;

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RESULT 489
ID AAX20255 standard; DNA; 18359 BP.
DE Borrelia burgdorferi polynucleotide sequence #8.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 2; Length 18359;
Pred. No. 1.7e+02;
RESULT 490
ID AAK89418 standard; DNA; 28588 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2394.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 4; Length 28588;
Pred. No. 2e+02;
RESULT 491
ID AAS31923 standard; DNA; 28588 BP.
DE Human liver associated genomic DNA #97.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 5; Length 28588;
Pred. No. 2e+02;
RESULT 492
ID ABN90278 standard; DNA; 28588 BP.
DE Human liver antigen HLDRI94 genomic sequence, SEQ ID NO: 399.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 11.0%; Score 30; DB 6; Length 28588;
Pred. No. 2e+02;
RESULT 493
ID ADJ15191 standard; DNA; 28588 BP.
DE Human liver-related genomic DNA - SEQ ID 399.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 11; Length 28588;
Pred. No. 2e+02;
RESULT 494
ID AAF54018 standard; DNA; 38059 BP.
DE Human factor IX (hFIX) gene, SEQ ID NO: 4.
PN WO200075279-A2.
PD 14-DEC-2000.
PA (UNMI ) UNIV MICHIGAN.
Query Match
Best Local Similarity 11.0%; Score 30; DB 4; Length 38059;
Pred. No. 2.2e+02;
RESULT 495
ID ABN95627 standard; DNA; 38059 BP.
DE Gene #2125 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 6; Length 38059;
Pred. No. 2.2e+02;
RESULT 496
ID ADD71098 standard; DNA; 38059 BP.
DE Human coagulation factor IX gene SEQ ID NO: 102.
PN WO2003061564-A2.
PD 31-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
Query Match
Best Local Similarity 11.0%; Score 30; DB 10; Length 38059;
Pred. No. 2.2e+02;
RESULT 497
ID ADC85383 standard; DNA; 61457 BP.
DE Mouse Mcm3ap genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 11.0%; Score 30; DB 10; Length 61457;
Pred. No. 2.6e+02;
RESULT 498
ID ADA02903 standard; DNA; 67191 BP.
DE Mouse Mcm3ap carcinoma associated gene, SEQ ID NO: 1421.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 11.0%; Score 30; DB 9; Length 67191;
Pred. No. 2.7e+02;
RESULT 499
ID ADB72641 standard; DNA; 67191 BP.
DE Mouse Mcm3ap gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 11.0%; Score 30; DB 10; Length 67191;
Pred. No. 2.7e+02;
RESULT 500
ID ADL95495 standard; DNA; 67191 BP.
DE Murine MCM3AP genomic DNA.
PN US2003165878-A1.
PD 04-SEP-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match
Best Local Similarity 11.0%; Score 30; DB 11; Length 67191;
Pred. No. 2.7e+02;
RESULT 501
ID ADM74498 standard; DNA; 67191 BP.
DE Murine carcinoma associated (CA) nucleic acid #85.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match
Best Local Similarity 11.0%; Score 30; DB 12; Length 67191;
Pred. No. 2.7e+02;
RESULT 502
ID ADQ2606 standard; DNA; 195917 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 11.0%; Score 30; DB 12; Length 195917;
Pred. No. 3.9e+02;
RESULT 503
ID ACH22153 standard; cDNA; 498 BP.
DE Human adult ovary cDNA #533.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 10.9%; Score 29.8; DB 9; Length 498;
Pred. No. 53;
RESULT 505
ID ACA39303 standard; DNA; 614 BP.
DE Prokaryotic essential gene #20960.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 10.9%; Score 29.8; DB 8; Length 614;
Pred. No. 57;
RESULT 506
ID ACF68988 standard; DNA; 681 BP.
DE Photobacterium luminescens nucleotide sequence #7455.
PN WO200294867-A2.
PD 28-NOV-2002.
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PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match 10.9%; Score 29.8; DB 10; Length 681;
  Best Local Similarity 49.7%; Pred. No. 59;
RESULT 507
ID ADL03826 standard; DNA; 690 BP.
DE DNA encoding a M. catarrhalis protein #1512.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match 10.9%; Score 29.8; DB 12; Length 690;
  Best Local Similarity 63.0%; Pred. No. 59;
RESULT 508
ID ADK16096 standard; DNA; 1098 BP.
DE Nanocarphaem equitans cancer-associated (CA) gene #24.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
  Query Match 10.9%; Score 29.8; DB 12; Length 1098;
  Best Local Similarity 52.9%; Pred. No. 70;
RESULT 509
ID AAS77233 standard; cDNA; 2817 BP.
DE DNA encoding novel human diagnostic protein #13037.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 10.9%; Score 29.8; DB 5; Length 2817;
  Best Local Similarity 60.5%; Pred. No. 99;
RESULT 510
ID AAS78629 standard; cDNA; 2817 BP.
DE DNA encoding novel human diagnostic protein #14433.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 10.9%; Score 29.8; DB 5; Length 2817;
  Best Local Similarity 60.5%; Pred. No. 99;
RESULT 511
ID ADB62147 standard; cDNA; 3685 BP.
DE Human cDNA encoding clone BRSSN20001970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 10.9%; Score 29.8; DB 10; Length 3685;
  Best Local Similarity 49.1%; Pred. No. 1.1e+02;
RESULT 512
ID ABL26452 standard; DNA; 5646 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30829.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match 10.9%; Score 29.8; DB 4; Length 5646;
  Best Local Similarity 48.5%; Pred. No. 1.3e+02;
RESULT 513
ID AAS79134 standard; cDNA; 5962 BP.
DE DNA encoding novel human diagnostic protein #14938.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 10.9%; Score 29.8; DB 5; Length 5962;
  Best Local Similarity 60.5%; Pred. No. 1.3e+02;
RESULT 514
ID AAK66134 standard; DNA; 6295 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20946.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.9%; Score 29.8; DB 4; Length 6295;
  Best Local Similarity 51.9%; Pred. No. 1.3e+02;
RESULT 515
ID AAK66133 standard; DNA; 6303 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20945.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.9%; Score 29.8; DB 4; Length 6303;
  Best Local Similarity 51.9%; Pred. No. 1.3e+02;
RESULT 516
ID ABK31340 standard; DNA; 6352 BP.
DE Signal transduction associated gene modified DNA #92.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 10.9%; Score 29.8; DB 6; Length 6352;
  Best Local Similarity 58.4%; Pred. No. 1.3e+02;
RESULT 517
ID ABL70563 standard; DNA; 6352 BP.
DE Chemically treated cell signalling DNA sequence#227.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 10.9%; Score 29.8; DB 6; Length 6352;
  Best Local Similarity 58.4%; Pred. No. 1.3e+02;
RESULT 518
ID AAS61235 standard; DNA; 6352 BP.
DE Human gene regulation-associated gene oligonucleotide #190.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 10.9%; Score 29.8; DB 6; Length 6352;
  Best Local Similarity 58.4%; Pred. No. 1.3e+02;
RESULT 519
ID ABK28389 standard; DNA; 7589 BP.
DE DNA transcription associated genomic DNA #132.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 10.9%; Score 29.8; DB 6; Length 7589;
  Best Local Similarity 51.9%; Pred. No. 1.4e+02;
RESULT 520
ID AAL37081 standard; DNA; 13605 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3446.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.9%; Score 29.8; DB 4; Length 13605;
  Best Local Similarity 51.1%; Pred. No. 1.7e+02;
RESULT 521
ID ABX60069 standard; cDNA; 13605 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2413.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match 10.9%; Score 29.8; DB 8; Length 13605;
  Best Local Similarity 51.1%; Pred. No. 1.7e+02;
RESULT 522
ID ADJ30819 standard; DNA; 13605 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3446.
PN US2004009498-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.9%; Score 29.8; DB 12; Length 13605;
  Best Local Similarity 51.1%; Pred. No. 1.7e+02;
RESULT 523
ID ABL32619 standard; DNA; 16373 BP.
DE Human immune system associated gene SEQ ID NO: 592.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 10.9%; Score 29.8; DB 6; Length 16373;
  Best Local Similarity 51.9%; Pred. No. 1.9e+02;
RESULT 524
ID AAD28383 standard; DNA; 16373 BP.
DE Human chemically treated genomic DNA #24.
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PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.9%; Score 29.8; DB 6; Length 16373;
Best Local Similarity 51.9%; Pred. No. 1.9e+02;
RESULT 525
ID AAF28545 standard; DNA; 62909 BP.
DE Genomic fragment #32.
PN WO200078968-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.9%; Score 29.8; DB 4; Length 62909;
Best Local Similarity 63.0%; Pred. No. 3e+02;
RESULT 526
ID ADM97422 standard; DNA; 76341 BP.
DE Prostate and breast cancer associated human gene SRD5A2.
PN WO2004028346-A2.
PD 08-APR-2004.
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
Query Match 10.9%; Score 29.8; DB 12; Length 76341;
Best Local Similarity 60.5%; Pred. No. 3.3e+02;
RESULT 527
ID ABX16390 standard; DNA; 659158 BP.
DE Mouse high growth region.
PN US2002155564-A1.
PD 24-OCT-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 10.9%; Score 29.8; DB 8; Length 110000;
Best Local Similarity 51.1%; Pred. No. 3.7e+02;
RESULT 528
Query Match 10.9%; Score 29.8; DB 10; Length 110000;
Best Local Similarity 49.7%; Pred. No. 3.7e+02;
RESULT 529
ID ADK16049 standard; DNA; 490885 BP.
DE Nanoarchaeum equitans genome.
PN WO200303434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 10.9%; Score 29.8; DB 12; Length 110000;
Best Local Similarity 52.9%; Pred. No. 3.7e+02;
RESULT 530
ID ABR83574 standard; cDNA; 147419 BP.
DE Human cDNA differentially expressed in granulocytic cells #145.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.9%; Score 29.8; DB 6; Length 147419;
Best Local Similarity 51.1%; Pred. No. 4.1e+02;
RESULT 531
ID AB272040 standard; DNA; 207433 BP.
DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.
PN WO200178894-A2.
PD 25-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.9%; Score 29.8; DB 5; Length 207433;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 532
ID ABX74891 standard; DNA; 207433 BP.
DE BAC1098L22 DNA sequence.
PN WO200283077-A2.
PD 24-OCT-2002.
PA (SCHE) SCHERING CORP.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.9%; Score 29.8; DB 8; Length 207433;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 533
ID ADJ36614 standard; DNA; 207433 BP.
DE Bacterial artificial chromosome RPCI-11.
PN US2004002470-A1.
PD 01-JAN-2004.
PA (KEIT) KEITH T.
PA (LITT) LITTLE R. D.
PA (VER-) VAN BERDEWEGH P.

PA (DUPU/) DUPUIS J.
PA (DMAS/) DEL MASTRO R. G.
PA (SIMO/) SIMON J.
PA (ALLE/) ALLEN K.
PA (PAND/) PANDIT S.
Query Match 10.9%; Score 29.8; DB 12; Length 207433;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 534
ID ADL81193 standard; DNA; 207433 BP.
DE BAC1098L22 DNA sequence.
PN US2004023215-A1.
PD 05-FEB-2004.
PA (KEIT) KEITH T.
PA (LITT) LITTLE R. D.
PA (EERD/) EERDEWEGH P. V.
PA (DUPU/) DUPUIS J.
PA (DMAS/) DEL MASTRO R. G.
PA (SIMO/) SIMON J.
PA (ALLE/) ALLEN K.
PA (PAND/) PANDIT S.
Query Match 10.9%; Score 29.8; DB 12; Length 207433;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 535
ID ACF65380 standard; DNA; 210710 BP.
DE Photorhabdus luminescens nucleotide sequence #33.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.9%; Score 29.8; DB 10; Length 210710;
Best Local Similarity 49.7%; Pred. No. 4.7e+02;
RESULT 536
ID ABN64523 standard; cDNA; 352 BP.
DE Human cancer related polynucleotide SEQ ID NO 4490.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 29.6; DB 6; Length 352;
Best Local Similarity 51.5%; Pred. No. 54;
RESULT 537
ID ACH41552 standard; cDNA; 476 BP.
DE Human foetal brain cDNA #2919.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R. T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M. C.
PA (JONE/) JONES L. W.
Query Match 10.8%; Score 29.6; DB 9; Length 476;
Best Local Similarity 50.0%; Pred. No. 60;
RESULT 538
ID ABQ55617 standard; cDNA; 511 BP.
DE Human ovarian antigen HODHE36 cDNA, SEQ ID NO:1497.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 29.6; DB 6; Length 511;
Best Local Similarity 48.7%; Pred. No. 62;
RESULT 539
ID AAC59912 standard; cDNA; 1193 BP.
DE Human secreted protein cDNA sequence #6.
PN WO200055198-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 29.6; DB 3; Length 1193;
Best Local Similarity 54.6%; Pred. No. 84;
RESULT 540
ID ADL63683 standard; DNA; 1330 BP.
DE Human ovarian cancer DNA marker #21895.
PN WO200170979-A2.
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.8%; Score 29.6; DB 5; Length 1330;
Best Local Similarity 54.6%; Pred. No. 87;
RESULT 541
ID ABN91152 standard; DNA; 1404 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:615.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.8%; Score 29.6; DB 6; Length 1404;
Best Local Similarity 53.4%; Pred. No. 89;
RESULT 542
ID AAH52576 standard; DNA; 1599 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:545.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.8%; Score 29.6; DB 4; Length 1599;
Best Local Similarity 52.4%; Pred. No. 93;
RESULT 543
ID ABN90872 standard; DNA; 1692 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:335.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.8%; Score 29.6; DB 6; Length 1692;
Best Local Similarity 52.4%; Pred. No. 95;
RESULT 544
ID ACC62528 standard; cDNA; 1701 BP.
DE Human secreted protein #54 coding sequence SEQ ID 64.
PN WO200299066-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 29.6; DB 8; Length 1701;
Best Local Similarity 54.6%; Pred. No. 95;
RESULT 545
ID ADO35510 standard; DNA; 2712 BP.
DE Novel mouse gene sequence #183.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (PIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.8%; Score 29.6; DB 12; Length 2712;
Best Local Similarity 53.4%; Pred. No. 1.1e+02;
RESULT 546
ID ABQ67171 standard; DNA; 2864 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 201.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 6; Length 2864;
Best Local Similarity 54.6%; Pred. No. 1.1e+02;
RESULT 547
ID AAH55029 standard; DNA; 3398 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4393.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.8%; Score 29.6; DB 4; Length 3398;
Best Local Similarity 52.4%; Pred. No. 1.2e+02;
RESULT 548
ID AAH54572 standard; DNA; 3609 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3936.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.8%; Score 29.6; DB 4; Length 3609;
Best Local Similarity 52.4%; Pred. No. 1.2e+02;
RESULT 549
ID AAT96833 standard; DNA; 3865 BP.
DE Intron 3 of human pRb2/p130 tumour suppressor gene.
PN WO9738125-A1.
PD 16-OCT-1997.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 10.8%; Score 29.6; DB 2; Length 3865;
Best Local Similarity 54.6%; Pred. No. 1.3e+02;
RESULT 550
ID ACC69613 standard; cDNA; 4333 BP.
DE Human transductin-1 (TDC1) encoding cDNA SEQ ID NO:1.
PN WO2003025140-A2.
PD 27-MAR-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.8%; Score 29.6; DB 8; Length 4333;
Best Local Similarity 57.6%; Pred. No. 1.3e+02;
RESULT 551
ID ABQ69372 standard; DNA; 5982 BP.
DE Listeria innocua DNA sequence #811.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
Query Match 10.8%; Score 29.6; DB 6; Length 5982;
Best Local Similarity 53.4%; Pred. No. 1.5e+02;
RESULT 552
ID ABK33990 standard; DNA; 6074 BP.
DE Human DNA for staging of Astrocytomas #38.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 6; Length 6074;
Best Local Similarity 54.6%; Pred. No. 1.5e+02;
RESULT 553
ID ADA20378 standard; DNA; 6074 BP.
DE Prostate tumour related genomic DNA sample #22.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 8; Length 6074;
Best Local Similarity 54.6%; Pred. No. 1.5e+02;
RESULT 554
ID ADA84185 standard; DNA; 6074 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:43.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 8; Length 6074;
Best Local Similarity 54.6%; Pred. No. 1.5e+02;
RESULT 555
ID ABQ67050 standard; DNA; 6486 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 6; Length 6486;
Best Local Similarity 49.5%; Pred. No. 1.5e+02;
RESULT 556
ID ABL28044 standard; DNA; 14771 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35605.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 10.8%; Score 29.6; DB 4; Length 14771;
Best Local Similarity 56.0%; Pred. No. 2.1e+02;
RESULT 557
ID ABL33680 standard; DNA; 15951 BP.
DE Human immune system associated gene SEQ ID NO: 1653.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.6; DB 6; Length 15951;
Best Local Similarity 56.0%; Pred. No. 2.1e+02;
RESULT 558
ID ABL34580 standard; DNA; 15951 BP.
DE Human metastasis associated gene SEQ ID NO: 133.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match
Best Local Similarity 10.8%; Score 29.6; DB 6; Length 15951;
RESULT 559
ID ABL70373 standard; DNA; 15951 BP.
DE Chemically treated cell signalling DNA sequence#132.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 6; Length 15951;
RESULT 560
ID ABZ09891 standard; DNA; 19634 BP.
DE Human 5' and/or regulatory region of GPR37 DNA SEQ ID NO:31.
PN WO2002772-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 8; Length 19634;
RESULT 561
ID ABL28042 standard; DNA; 19674 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35599.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 4; Length 19674;
RESULT 562
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 6; Length 110000;
RESULT 563
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 6; Length 110000;
RESULT 564
ID ABQ67197 standard; DNA; 1163020 BP.
DE Listeria innocua contig DNA sequence #10.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 6; Length 110000;
RESULT 565
ID AAF22286 standard; DNA; 134499 BP.
DE BAC containing repeats from centromeres 1-4 #9.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UVCH-) UNIV CHICAGO.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 3; Length 134499;
RESULT 566
ID AAH51601 standard; DNA; 319608 BP.
DE Human chromosome 13q31-q33 genomic nucleotide sequence.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 3; Length 319608;
RESULT 567
ID AAS09301 standard; DNA; 319608 BP.
DE Human schizophrenia associated gene g35030 and biallelic markers Al-A71.
Query Match
Best Local Similarity 10.8%; Score 29.6; DB 5; Length 319608;
RESULT 568
ID AAS3224 standard; DNA; 1029 BP.
DE Haemophilus influenzae DNA for cellular proliferation protein #6.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 4; Length 1029;
RESULT 569
ID ACA34007 standard; DNA; 1029 BP.
DE Prokaryotic essential gene #15664.

PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 8; Length 1029;
RESULT 570
ID ABX17910 standard; cDNA; 1191 BP.
DE cDNA encoding human G-protein coupled receptor GCRC-64.
PN WO200279448-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 10; Length 1191;
RESULT 571
ID ADC86322 standard; DNA; 1342 BP.
DE Human GPCR gene SEQ ID NO:775.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 10; Length 1342;
RESULT 572
ID ABL25880 standard; DNA; 2555 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29113.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 4; Length 2555;
RESULT 573
ID ACH04305 standard; cDNA; 3095 BP.
DE Human cDNA differentially expressed in lung cancer #510.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 9; Length 3095;
RESULT 574
ID AAS45336 standard; DNA; 6167 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #21.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 4; Length 6167;
RESULT 575
ID ABL32642 standard; DNA; 6167 BP.
DE Human immune system associated gene SEQ ID NO: 615.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 6; Length 6167;
RESULT 576
ID ABL70193 standard; DNA; 6167 BP.
DE Chemically treated cell signalling DNA sequence#42.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 6; Length 6167;
RESULT 577
ID ABX28171 standard; DNA; 6167 BP.
DE DNA transcription associated genomic DNA #23.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 10.8%; Score 29.4; DB 6; Length 6167;
RESULT 578
ID AAS61151 standard; DNA; 6167 BP.
DE Human gene regulation-associated gene oligonucleotide #106.

PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.4; DB 6; Length 6167;
Best Local Similarity 52.0%; Pred. No. 1.8e+02;
RESULT 579
ID ABL04824 standard; cDNA; 6904 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8954.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 29.4; DB 4; Length 6904;
Best Local Similarity 51.1%; Pred. No. 1.8e+02;
RESULT 580
ID ABN80067 standard; DNA; 7041 BP.
DE Human chemically modified disease associated gene SEQ ID NO 84.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 10.8%; Score 29.4; DB 6; Length 7041;
Best Local Similarity 47.1%; Pred. No. 1.8e+02;
RESULT 581
ID ABL25924 standard; DNA; 7131 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2945.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 29.4; DB 4; Length 7131;
Best Local Similarity 51.1%; Pred. No. 1.8e+02;
RESULT 582
ID ABL19434 standard; DNA; 17073 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9775.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 29.4; DB 4; Length 17073;
Best Local Similarity 54.1%; Pred. No. 2.5e+02;
RESULT 583
ID RAD42098 standard; DNA; 29793 BP.
DE Poly adenosine diphosphate-ribose glycohydrolase (PARG) gene.
PN US6395543-B1.
PD 28-MAY-2002.
PA (KENT) UNIV KENTUCKY RES FOUND.
Query Match 10.8%; Score 29.4; DB 6; Length 29793;
Best Local Similarity 55.3%; Pred. No. 3.1e+02;
RESULT 584
ID ABK14948 standard; DNA; 29793 BP.
DE Worm poly(ADP-ribose) glycohydrolase (PARG) sequence from cosmid F20C5.
PN US6337202-B1.
PD 08-JAN-2002.
PA (KENT) UNIV KENTUCKY RES FOUND.
Query Match 10.8%; Score 29.4; DB 6; Length 29793;
Best Local Similarity 55.3%; Pred. No. 3.1e+02;
RESULT 585
ID ABK14930 standard; DNA; 29793 BP.
DE Worm poly(ADP-ribose) glycohydrolase (PARG) sequence from cosmid F20C5.
PN US6333148-B1.
PD 25-DEC-2001.
PA (KENT) UNIV KENTUCKY RES FOUND.
Query Match 10.8%; Score 29.4; DB 6; Length 29793;
Best Local Similarity 55.3%; Pred. No. 3.1e+02;
RESULT 586
ID ABX14494 standard; DNA; 29793 BP.
DE Cosmid F20C5 containing C. elegans PARG genomic DNA.
PN US2002132328-A1.
PD 19-SEP-2002.
PA (JACO/) JACOBSON M K.
PA (JACO/) JACOBSON E L.
PA (AMEJ/) AME J.
PA (LINW/) LIN W.
Query Match 10.8%; Score 29.4; DB 8; Length 29793;
Best Local Similarity 55.3%; Pred. No. 3.1e+02;
RESULT 587

ID ABL20870 standard; DNA; 42979 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14083.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 29.4; DB 4; Length 42979;
Best Local Similarity 49.7%; Pred. No. 3.5e+02;
RESULT 588
ID ABN89533 standard; DNA; 48436 BP.
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
PN US2002061562-A1.
PD 23-MAY-2002.
PA (FUKU/) FUKUDA M N.
PA (AKAM/) AKAMA T O.
Query Match 10.8%; Score 29.4; DB 6; Length 48436;
Best Local Similarity 51.1%; Pred. No. 3.7e+02;
RESULT 589
ID AAT42063 standard; DNA; 1830121 BP.
DE Haemophilus influenzae complete genome sequence.
PN WO9633276-A1.
PD 24-OCT-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 10.8%; Score 29.4; DB 2; Length 110000;
Best Local Similarity 48.0%; Pred. No. 4.9e+02;
RESULT 590
ID ABQ83210 standard; DNA; 397658 BP.
DE Human transporter protein genomic DNA SEQ ID NO:3.
PN WO2001050133-A1.
PD 19-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.8%; Score 29.4; DB 8; Length 110000;
Best Local Similarity 55.3%; Pred. No. 4.9e+02;
RESULT 591
ID AAT4365 standard; DNA; 113000 BP.
DE Partial genomic sequence of human oestrogen receptor beta DNA.
PN WO2001050133-A1.
PD 19-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.8%; Score 29.4; DB 9; Length 113000;
Best Local Similarity 49.7%; Pred. No. 5e+02;
RESULT 593
ID AAS43104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 29.4; DB 4; Length 325791;
Best Local Similarity 49.7%; Pred. No. 7.2e+02;
RESULT 594
ID ABZ23479 standard; DNA; 245 BP.
DE Nucleotide sequence of a fragment of Salmon fish DNA.
PN WO2002101090-A2.
PD 19-DEC-2002.
PA (CNRS) CENT NAT RECH SCI.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (ECOL-) ECOLE NORMALE SUPERIEURE DE LYON.
Query Match 10.7%; Score 29.2; DB 8; Length 245;
Best Local Similarity 13.8%; Pred. No. 63;
RESULT 595
ID ADB50217 standard; DNA; 588 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:759.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.7%; Score 29.2; DB 10; Length 588;
Best Local Similarity 52.5%; Pred. No. 87;
RESULT 596
ID AAD07868 standard; cDNA; 820 BP.
DE Human secreted protein-encoding gene 13 cDNA clone HIBEB47, SEQ ID NO:70.
PN WO200132675-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.7%; Score 29.2; DB 4; Length 820;
Best Local Similarity 62.2%; Pred. No. 98;
RESULT 597
ID ABK50746 standard; DNA; 895 BP.
DE Pyrus plant microsatellite DNA sequence #27.
PN JP2002034562-A.
PD 05-FEB-2002.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGVO SEIBUTSU SH.
Query Match 10.7%; Score 29.2; DB 6; Length 895;
Best Local Similarity 56.1%; Pred. No. 1e+02;
RESULT 598
ID ACA33964 standard; DNA; 1137 BP.
DE Prokaryotic essential gene #15621.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.7%; Score 29.2; DB 8; Length 1137;
Best Local Similarity 65.2%; Pred. No. 1.1e+02;
RESULT 599
ID ADC91483 standard; DNA; 1161 BP.
DE E. faecium DNA sequence SEQ ID 1110.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.7%; Score 29.2; DB 10; Length 1161;
Best Local Similarity 65.2%; Pred. No. 1.1e+02;
RESULT 600
ID ABNG6956 standard; DNA; 1767 BP.
DE Streptococcus polynucleotide SEQ ID NO 6025.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 10.7%; Score 29.2; DB 6; Length 1767;
Best Local Similarity 53.5%; Pred. No. 1.3e+02;
RESULT 601
ID ABN96789 standard; DNA; 2123 BP.
DE Gene #3287 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.7%; Score 29.2; DB 6; Length 2123;
Best Local Similarity 54.7%; Pred. No. 1.4e+02;
RESULT 602
ID AAD07821 standard; cDNA; 2529 BP.
DE Human secreted protein-encoding gene 13 cDNA clone HIBEB47, SEQ ID NO:23.
PN WO200132675-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 29.2; DB 4; Length 2529;
Best Local Similarity 62.2%; Pred. No. 1.5e+02;
RESULT 603
ID ABN81677 standard; DNA; 4220 BP.
DE Human CDK4 double bisulphite-converted genomic DNA SEQ ID NO 2.
PN WO200236814-A2.
PD 10-MAY-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 4220;
Best Local Similarity 48.8%; Pred. No. 1.8e+02;
RESULT 604
ID ABN81676 standard; DNA; 4220 BP.
DE Human CDK4 bisulphite-converted genomic DNA SEQ ID NO 1.
PN WO200236814-A2.
PD 10-MAY-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 4220;
Best Local Similarity 48.8%; Pred. No. 1.8e+02;
RESULT 605
ID ABL92255 standard; DNA; 5501 BP.
DE Chemically treated DNA repair gene fragment complementary to#32.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 10.7%; Score 29.2; DB 6; Length 5501;
Best Local Similarity 54.7%; Pred. No. 1.9e+02;
RESULT 606
ID AAS61244 standard; DNA; 5501 BP.
DE Human gene regulation-associated gene oligonucleotide #199.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 5501;
Best Local Similarity 54.7%; Pred. No. 1.9e+02;
RESULT 607
ID ABL49338 standard; DNA; 5501 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 38.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 5501;
Best Local Similarity 54.7%; Pred. No. 1.9e+02;
RESULT 608
ID ABL34542 standard; DNA; 5937 BP.
DE Human metastasis associated gene SEQ ID NO: 95.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 5937;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 609
ID ABN80150 standard; DNA; 5937 BP.
DE Human chemically modified disease associated gene SEQ ID NO 167.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 5937;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 610
ID ABL34428 standard; DNA; 9110 BP.
DE Human immune system associated gene SEQ ID NO: 2401.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 9110;
Best Local Similarity 54.7%; Pred. No. 2.3e+02;
RESULT 611
ID ADN02611 standard; DNA; 9227 BP.
DE S. dysenteriae serotype 8 O-antigen biosynthetic gene cluster (partial).
PN CN1429833-A.
PD 16-JUL-2003.
PA (UYNA-) UNIV NANKAI.
Query Match 10.7%; Score 29.2; DB 11; Length 9227;
Best Local Similarity 53.5%; Pred. No. 2.3e+02;
RESULT 612
ID AAV25594 standard; DNA; 10607 BP.
DE Human beta-casein genomic DNA.
PN US5739407-A.
PD 14-APR-1998.
PA (SYMB-) SYMBICOM AB.
Query Match 10.7%; Score 29.2; DB 2; Length 10607;
Best Local Similarity 65.2%; Pred. No. 2.5e+02;
RESULT 613
ID ABL34124 standard; DNA; 73334 BP.
DE Human immune system associated gene SEQ ID NO: 2097.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 73334;
Best Local Similarity 52.5%; Pred. No. 4.9e+02;
RESULT 614
ID ABL92318 standard; DNA; 73334 BP.
DE Chemically treated DNA repair gene fragment#64.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.7%; Score 29.2; DB 6; Length 73334;

Best Local Similarity 52.5%; Pred. No. 4.9e+02;
RESULT 615
ID AAK85261 standard; DNA; 75899 BP.
DE Human genomic DNA for protein phosphatase 1B, PTP1B.
PN US2002055479-A1.
PD 09-MAY-2002.
PA (COWS/) COWSERT L M.
PA (WYAT/) WYATT J. S.
PA (FREI/) FREIER S. M.
PA (MONI/) MONIA B P.
PA (BUTL/) BUTLER M M.
PA (MCKA/) MCKAY R.
Query Match 10.7%; Score 29.2; DB 6; Length 75899;
Best Local Similarity 50.7%; Pred. No. 5e+02;
RESULT 616
ID ADI13990 standard; DNA; 75899 BP.
DE Human protein phosphatase 1B (PTP1B) genomic DNA SeqID 243.
PN US2003220282-A1.
PD 27-NOV-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.7%; Score 29.2; DB 12; Length 75899;
Best Local Similarity 50.7%; Pred. No. 5e+02;
RESULT 617
ID ADP08388 standard; DNA; 95400 BP.
DE Human laminin alpha 4 (LAMA4) genomic DNA.
Query Match 10.7%; Score 29.2; DB 12; Length 95400;
Best Local Similarity 54.7%; Pred. No. 5.4e+02;
RESULT 618
Query Match 10.7%; Score 29.2; DB 6; Length 110000;
Best Local Similarity 53.5%; Pred. No. 5.7e+02;
RESULT 619
ID ADE11169 standard; DNA; 394191 BP.
DE Human transporter protein encoding gene SEQ ID NO:1.
Query Match 10.7%; Score 29.2; DB 10; Length 110000;
Best Local Similarity 54.7%; Pred. No. 5.7e+02;
RESULT 620
ID A262336 standard; cDNA; 257 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:21149.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 29; DB 6; Length 257;
Best Local Similarity 58.8%; Pred. No. 74;
RESULT 621
ID ABV03823 standard; cDNA; 356 BP.
DE Human prostate expression marker cDNA 3814.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.6%; Score 29; DB 5; Length 356;
Best Local Similarity 43.0%; Pred. No. 83;
RESULT 622
ID AAI80935 standard; cDNA; 408 BP.
DE Human polynucleotide SEQ ID NO 995.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 29; DB 4; Length 408;
Best Local Similarity 51.1%; Pred. No. 88;
RESULT 623
ID ABZ54199 standard; cDNA; 553 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 3312.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Query Match 10.6%; Score 29; DB 8; Length 553;
Best Local Similarity 57.0%; Pred. No. 98;
RESULT 624
ID AAT36042 standard; cDNA; 694 BP.
DE Murine Ink4c-p18 cDNA clone.
PN WO9624603-A1.
PD 15-AUG-1996.
PA (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 10.6%; Score 29; DB 2; Length 694;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
RESULT 625
ID AAX80476 standard; cDNA; 694 BP.
DE Mouse INK-4 protein p18 encoding cDNA.
PN US919997-A.
PD 06-JUL-1999.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 10.6%; Score 29; DB 2; Length 694;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
RESULT 626
ID ADA72899 standard; DNA; 855 BP.
DE Rice gene, SEQ ID 6225.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.6%; Score 29; DB 8; Length 855;
Best Local Similarity 54.1%; Pred. No. 1.1e+02;
RESULT 627
ID ACF70507 standard; DNA; 1029 BP.
DE Photorhabdus luminescens nucleotide sequence #8974.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.6%; Score 29; DB 10; Length 1029;
Best Local Similarity 54.1%; Pred. No. 1.2e+02;
RESULT 628
ID ABQ54841 standard; cDNA; 1205 BP.
DE Human ovarian antigen HE6CR19 cDNA, SEQ ID NO:721.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 29; DB 6; Length 1205;
Best Local Similarity 49.0%; Pred. No. 1.3e+02;
RESULT 629
ID AAC74396 standard; cDNA; 1424 BP.
DE Human secreted protein gene 1 SEQ ID NO:11.
PN WO200058496-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.8%; Score 29; DB 3; Length 1424;
Best Local Similarity 49.0%; Pred. No. 1.4e+02;
RESULT 630
ID ADM19639 standard; cDNA; 1502 BP.
DE Novel human channel/transporter gene #192 clone 2.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 29; DB 5; Length 1502;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
RESULT 631
ID ABZ16971 standard; DNA; 1573 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4776.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.6%; Score 29; DB 6; Length 1573;
Best Local Similarity 48.0%; Pred. No. 1.4e+02;
RESULT 632
ID ADO21878 standard; cDNA; 2655 BP.
DE Malaria parasite cyclic nucleotide phosphodiesterase PfPDE1 cDNA.
PN WO2004044192-A2.
PD 27-MAY-2004.
PA (TANA) TANABE SEIYAKU CO.
Query Match 10.6%; Score 29; DB 12; Length 2655;
Best Local Similarity 49.0%; Pred. No. 1.7e+02;
RESULT 633
ID ABX09864 standard; DNA; 2814 BP.

DE N. lactamica DNA encoding a vaccine antigen #16.
PN WO200277648-A2.
PD 03-OCT-2002.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 10.6%; Score 29; DB 8; Length 2814;
Best Local Similarity 52.0%; Pred. No. 1.8e+02;
RESULT 634
ID AD963201 standard; cDNA; 3125 BP.
DE Human cDNA encoding clone SPLEN20136700.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.6%; Score 29; DB 10; Length 3125;
Best Local Similarity 50.4%; Pred. No. 1.8e+02;
RESULT 635
ID AAD05229 standard; cDNA; 3143 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HHEPJ23, SEQ ID NO:20.
PN WO200134629-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 29; DB 4; Length 3143;
Best Local Similarity 50.4%; Pred. No. 1.8e+02;
RESULT 636
ID ADF59725 standard; cDNA; 3572 BP.
DE Human contig polynucleotide sequence SEQ ID NO:2092.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HVSE-) HVSE INC.
Query Match 10.6%; Score 29; DB 10; Length 3572;
Best Local Similarity 52.0%; Pred. No. 1.9e+02;
RESULT 637
ID AAH48716 standard; DNA; 5046 BP.
DE T. thermophila triterpenoid cyclase DNA.
PN EP1130103-A2.
PD 05-SEP-2001.
PA (CELA-) CELANESE VENTURES GMBH.
Query Match 10.6%; Score 29; DB 5; Length 5046;
Best Local Similarity 52.0%; Pred. No. 2.2e+02;
RESULT 638
ID ADF67944 standard; DNA; 5046 BP.
DE T. thermophila triterpenoid cyclase DNA #2.
PN DE19957889-A1.
PD 21-JUN-2001.
PA (AXIV-) AXIVA GMBH.
Query Match 10.6%; Score 29; DB 5; Length 5046;
Best Local Similarity 52.0%; Pred. No. 2.2e+02;
RESULT 639
ID ABLO7648 standard; cDNA; 5970 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17426.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.6%; Score 29; DB 4; Length 5970;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
RESULT 640
ID AA207666 standard; DNA; 11721 BP.
DE A. thaliana APETALA2 (AP2) complete genomic sequence.
PN WO9441974-A1.
PD 26-AUG-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 10.6%; Score 29; DB 2; Length 11721;
Best Local Similarity 48.7%; Pred. No. 2.9e+02;
RESULT 641
ID ABJ23263 standard; DNA; 15674 BP.
DE Human immune system associated gene SEQ ID NO: 336.
PN WO20000928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.6%; Score 29; DB 6; Length 15674;
Best Local Similarity 55.4%; Pred. No. 3.3e+02;
RESULT 642
ID ABL34477 standard; DNA; 15674 BP.
DE Human metastasis associated gene SEQ ID NO: 30.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.6%; Score 29; DB 6; Length 15674;
Best Local Similarity 55.4%; Pred. No. 3.3e+02;
RESULT 643
ID ABL70514 standard; DNA; 15674 BP.
DE Chemically treated cell signalling DNA sequence complementary to #202.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.6%; Score 29; DB 6; Length 15674;
Best Local Similarity 55.4%; Pred. No. 3.3e+02;
RESULT 644
ID ACF65374 standard; DNA; 69727 BP.
DE Photorhabdus luminescens nucleotide sequence #27.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.6%; Score 29; DB 10; Length 69727;
Best Local Similarity 54.1%; Pred. No. 5.6e+02;
RESULT 645
ID ADL13649 standard; DNA; 127098 BP.
DE Osteoarthritis-associated polymorphic nucleotide #181.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.6%; Score 29; DB 10; Length 127098;
Best Local Similarity 61.0%; Pred. No. 6.9e+02;
RESULT 646
ID ADC86642 standard; DNA; 349881 BP.
DE Human GPCR gene SEQ ID NO:1095.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.6%; Score 29; DB 10; Length 349881;
Best Local Similarity 77.8%; Pred. No. 9.7e+02;
RESULT 649
ID ABK76543 standard; DNA; 318 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #3834.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Query Match 10.5%; Score 28.8; DB 6; Length 318;
Best Local Similarity 50.7%; Pred. No. 93;
RESULT 650
ID ABV94448 standard; cDNA; 396 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:439.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 10.5%; Score 28.8; DB 6; Length 396;
Best Local Similarity 61.8%; Pred. No. 1e+02;
RESULT 651
ID AAK87618 standard; DNA; 706 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42430.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.8; DB 4; Length 706;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 652

Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 661
ID AAK87616 standard; DNA; 717 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42428.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.8; DB 4; Length 717;
Best Local Similarity 51.6%; Pred. No. 1.2e+02;
RESULT 653
ID ABQ75352 standard; cDNA; 993 BP.
DE Human lung specific nucleic acid sequence SEQ ID NO:91.
PN WO200264788-A2.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 10.5%; Score 28.8; DB 6; Length 993;
Best Local Similarity 54.8%; Pred. No. 1.4e+02;
RESULT 654
ID ABK82130 standard; cDNA; 1095 BP.
DE DNA encoding novel floral meristem identity protein LpWADS4-2.
PN WO200233091-A1.
PD 25-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 10.5%; Score 28.8; DB 6; Length 1095;
Best Local Similarity 48.8%; Pred. No. 1.4e+02;
RESULT 655
ID ADH84062 standard; DNA; 1296 BP.
DE Enterococcus faecalis polynucleotide #1947.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC-) DOUCETTE-STAMM L A.
PA (BUSH-) BUSH D.
Query Match 10.5%; Score 28.8; DB 10; Length 1296;
Best Local Similarity 49.3%; Pred. No. 1.5e+02;
RESULT 656
ID ABL28530 standard; DNA; 2414 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37063.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.5%; Score 28.8; DB 4; Length 2414;
Best Local Similarity 50.7%; Pred. No. 1.9e+02;
RESULT 657
ID AAQ68937 standard; DNA; 2849 BP.
DE Fowlpox virus (FPV) genomic EcoRI fragment on vector 443-88.14.
PN WO9419014-A1.
PD 01-SEP-1994.
PA (SYTR-) SYNTRO CORP.
PA (JAPG-) NIPPON ZEON KK.
Query Match 10.5%; Score 28.8; DB 2; Length 2849;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 658
ID AAQ70573 standard; DNA; 2849 BP.
DE Homology vector 443-88.14 contg. fowlpox virus genomic fragment.
PN WO9419015-A1.
PD 01-SEP-1994.
PA (SYTR-) SYNTRO CORP.
Query Match 10.5%; Score 28.8; DB 2; Length 2849;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 659
ID AAT48512 standard; DNA; 2849 BP.
DE Homology vector 443-88.14.
PN WO9640880-A1.
PD 19-DEC-1996.
PA (SYTR-) SYNTRO CORP.
Query Match 10.5%; Score 28.8; DB 2; Length 2849;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 660
ID AAX81142 standard; DNA; 2849 BP.
DE Homology vector 443-88.14 containing FPV genomic fragment.
PN US9525358-A.
PD 20-JUL-1999.
PA (SYTR-) SYNTRO CORP.
Query Match 10.5%; Score 28.8; DB 2; Length 2849;

Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 661
ID AAZ49290 standard; DNA; 2849 BP.
DE Homology vector 443-88.14 2.8 kb FPV genomic sequence, SEQ ID 4.
PN US6001369-A.
PD 14-DEC-1999.
PA (SYTR-) SYNTRO CORP.
Query Match 10.5%; Score 28.8; DB 3; Length 2849;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 662
ID AAC67857 standard; DNA; 2849 BP.
DE FPV homology vector 749-75.82 fragment 1.
PN US6136318-A.
PD 24-OCT-2000.
PA (JUNK-) JUNKER D E.
PA (COCH-) COCHRAN M D.
Query Match 10.5%; Score 28.8; DB 3; Length 2849;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 663
ID AAS87447 standard; cDNA; 2856 BP.
DE DNA encoding novel human diagnostic protein #23251.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.5%; Score 28.8; DB 5; Length 2856;
Best Local Similarity 56.2%; Pred. No. 2e+02;
RESULT 664
ID ADQ25278 standard; DNA; 5127 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8098.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.5%; Score 28.8; DB 12; Length 5127;
Best Local Similarity 48.8%; Pred. No. 2.5e+02;
RESULT 665
ID AAS45499 standard; DNA; 5476 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #102.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 4; Length 5476;
Best Local Similarity 53.6%; Pred. No. 2.6e+02;
RESULT 666
ID ABL34114 standard; DNA; 5476 BP.
DE Human immune system associated gene SEQ ID NO: 2087.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 5476;
Best Local Similarity 53.6%; Pred. No. 2.6e+02;
RESULT 667
ID ABL49381 standard; DNA; 5476 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 81.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 5476;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
RESULT 668
ID ABL33749 standard; DNA; 11805 BP.
DE Human immune system associated gene SEQ ID NO: 1722.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 11805;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
RESULT 669
ID ASN80238 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 255.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 15121;

Best Local Similarity 56.2%; Pred. No. 3.7e+02;
RESULT 670
ID ABL32727 standard; DNA; 16602 BP.
DE Human immune system associated gene SEQ ID NO: 700.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 16602;
Best Local Similarity 52.5%; Pred. No. 3.9e+02;
RESULT 671
ID ABR80069 standard; DNA; 16602 BP.
DE Human chemically modified disease associated gene SEQ ID NO 86.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 16602;
Best Local Similarity 52.5%; Pred. No. 3.9e+02;
RESULT 672
ID ABQ67084 standard; DNA; 18357 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 114.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.8; DB 6; Length 18357;
Best Local Similarity 52.5%; Pred. No. 4e+02;
RESULT 673
ID AAK71622 standard; DNA; 27062 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26434.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.8; DB 4; Length 27062;
Best Local Similarity 54.8%; Pred. No. 4.6e+02;
RESULT 674
ID AAL05346 standard; DNA; 27062 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8034.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.8; DB 4; Length 27062;
Best Local Similarity 54.8%; Pred. No. 4.6e+02;
RESULT 675
ID ABU98215 standard; DNA; 27062 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2867.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.8; DB 4; Length 27062;
Best Local Similarity 54.8%; Pred. No. 4.6e+02;
RESULT 676
ID ADC86182 standard; DNA; 29221 BP.
DE Human GPCR gene SEQ ID NO:635.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.5%; Score 28.8; DB 10; Length 29221;
Best Local Similarity 48.8%; Pred. No. 4.7e+02;
RESULT 677
ID ADQ18153 standard; DNA; 112604 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 970.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.5%; Score 28.8; DB 12; Length 112604;
Best Local Similarity 62.5%; Pred. No. 7.6e+02;
RESULT 678
ID ADN95229 standard; DNA; 128361 BP.
DE Human BEC/LEC-related gene sequence SeqID151.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

Query Match 10.5%; Score 28.8; DB 11; Length 128361;
Best Local Similarity 56.2%; Pred. No. 8e+02;
RESULT 679
ID AAL57272 standard; DNA; 177851 BP.
DE BA438B23-1 'human modifier of p53 pathway' DNA.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.5%; Score 28.8; DB 8; Length 177851;
Best Local Similarity 51.6%; Pred. No. 9e+02;
RESULT 680
ID AAH41223 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #2.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 10.5%; Score 28.8; DB 5; Length 349980;
Best Local Similarity 54.8%; Pred. No. 1.1e+03;
RESULT 681
ID ABK62981 standard; cDNA; 426 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #888.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.5%; Score 28.6; DB 6; Length 426;
Best Local Similarity 67.8%; Pred. No. 1.2e+02;
RESULT 682
ID ABN92575 standard; DNA; 450 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2038.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.5%; Score 28.6; DB 6; Length 450;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;
RESULT 683
ID ABS64610 standard; cDNA; 454 BP.
DE Human cDNA probe selectively hybridising to foetal cell mRNA #25.
PN WO200255985-A2.
PD 18-JUL-2002.
PA (HOFF) ROCHE DIAGNOSTICS CORP.
Query Match 10.5%; Score 28.6; DB 6; Length 454;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;
RESULT 684
ID ABN63352 standard; cDNA; 518 BP.
DE Human cancer related polynucleotide SEQ ID NO 3319.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 10.5%; Score 28.6; DB 6; Length 518;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 685
ID ABQ56789 standard; cDNA; 648 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:484.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 10.5%; Score 28.6; DB 6; Length 648;
Best Local Similarity 47.5%; Pred. No. 1.4e+02;
RESULT 686
ID ABQ98890 standard; DNA; 651 BP.
DE Human ORF697 coding sequence.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 10.5%; Score 28.6; DB 6; Length 651;
Best Local Similarity 51.1%; Pred. No. 1.4e+02;
RESULT 687

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ID ABH34681 standard; cDNA; 736 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1763.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.5%; Score 28.6; DB 4; Length 736;
  Best Local Similarity 54.5%; Pred. No. 1.4e+02;
RESULT 688
ID AAL25096 standard; cDNA; 773 BP.
DE Human breast cancer expressed polynucleotide 17553.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 10.5%; Score 28.6; DB 4; Length 773;
  Best Local Similarity 57.1%; Pred. No. 1.5e+02;
RESULT 689
ID AAA01909 standard; cDNA; 831 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1900.
PN WO958675-A2.
PD 18-NOV-1999.
PA (CHIR-) CHIRON CORP.
  Query Match 10.5%; Score 28.6; DB 3; Length 831;
  Best Local Similarity 53.9%; Pred. No. 1.5e+02;
RESULT 690
ID ABZ16462 standard; DNA; 855 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4267.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI-) SCRIPPS RES INST.
  Query Match 10.5%; Score 28.6; DB 6; Length 855;
  Best Local Similarity 57.1%; Pred. No. 1.5e+02;
RESULT 691
ID ADA69101 standard; DNA; 855 BP.
DE Arabidopsis thaliana gene, SEQ ID 2424.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
  Query Match 10.5%; Score 28.6; DB 8; Length 855;
  Best Local Similarity 57.1%; Pred. No. 1.5e+02;
RESULT 692
ID AAH05511 standard; cDNA; 859 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:2346.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 10.5%; Score 28.6; DB 4; Length 859;
  Best Local Similarity 51.1%; Pred. No. 1.5e+02;
RESULT 693
ID ADQ22637 standard; DNA; 1367 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5457.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match 10.5%; Score 28.6; DB 12; Length 1367;
  Best Local Similarity 52.0%; Pred. No. 1.8e+02;
RESULT 694
ID AAC77532 standard; cDNA; 1483 BP.
DE Human ORFX ORF3087 polynucleotide sequence SEQ ID NO:6173.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
  Query Match 10.5%; Score 28.6; DB 3; Length 1483;
  Best Local Similarity 51.1%; Pred. No. 1.9e+02;
RESULT 695
ID AAC98149 standard; cDNA; 1509 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:159.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 10.5%; Score 28.6; DB 3; Length 1509;
  Best Local Similarity 51.1%; Pred. No. 1.9e+02;
RESULT 696
ID ADQ22201 standard; DNA; 1552 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5021.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match 10.5%; Score 28.6; DB 12; Length 1552;
  Best Local Similarity 52.6%; Pred. No. 1.9e+02;
RESULT 697
ID ACA21813 standard; DNA; 1650 BP.
DE Prokaryotic essential gene #3470.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 10.5%; Score 28.6; DB 8; Length 1650;
  Best Local Similarity 59.0%; Pred. No. 1.9e+02;
RESULT 698
ID ABX05432 standard; cDNA; 1765 BP.
DE Human novel polynucleotide #447.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 10.5%; Score 28.6; DB 8; Length 1765;
  Best Local Similarity 51.1%; Pred. No. 2e+02;
RESULT 699
ID AAH99127 standard; cDNA; 1813 BP.
DE Human EST-derived coding sequence SEQ ID NO: 984.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 10.5%; Score 28.6; DB 4; Length 1813;
  Best Local Similarity 55.6%; Pred. No. 2e+02;
RESULT 700
ID ABX05431 standard; cDNA; 1819 BP.
DE Human novel polynucleotide #446.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 10.5%; Score 28.6; DB 8; Length 1819;
  Best Local Similarity 51.1%; Pred. No. 2e+02;
RESULT 701
ID ADJ40941 standard; cDNA; 2000 BP.
DE Plant cDNA #1941.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW-) BUDWORTH P.
PA (MOUG-) MOUGHAMER T.
PA (BRIG-) BRIGGS S P.
PA (COOP-) COOPER B.
PA (GLAZ-) GLAZEBROOK J.
PA (GOFF-) GOFF S A.
PA (KATA-) KATAGIRI F.
PA (KREP-) KREPS J.
PA (PROV-) PROVART N.
PA (RICK-) RICHE D.
PA (ZHUT-) ZHU T.
  Query Match 10.5%; Score 28.6; DB 12; Length 2000;
  Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 702
ID AAH15917 standard; cDNA; 2037 BP.
DE Human cDNA sequence SEQ ID NO:14479.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 10.5%; Score 28.6; DB 4; Length 2037;
  Best Local Similarity 51.1%; Pred. No. 2.1e+02;
RESULT 703
ID AAH29931 standard; DNA; 2243 BP.
DE C albicans apoptosis associated coding sequence #75.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC-) JANSSEN PHARM NV.
  Query Match 10.5%; Score 28.6; DB 4; Length 2243;
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Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 704
ID ADL12643 standard; cDNA; 2735 BP.
DE Human steroid-induced C3A liver cell cDNA #372.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 28.6; DB 12; Length 2735;
Best Local Similarity 49.0%; Pred. No. 2.3e+02;
RESULT 705
ID ADF77010 standard; cDNA; 2743 BP.
DE Novel human secreted and transmembrane protein cDNA seqID 685.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match 10.5%; Score 28.6; DB 10; Length 2743;
Best Local Similarity 49.0%; Pred. No. 2.3e+02;
RESULT 706
ID AAF18334 standard; DNA; 3013 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 353.
PN WO200505180-A2.
PD 21-SEP-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 10.5%; Score 28.6; DB 3; Length 3013;
Best Local Similarity 49.0%; Pred. No. 2.4e+02;
RESULT 707
ID AAH54843 standard; DNA; 3054 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4207.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.5%; Score 28.6; DB 4; Length 3054;
Best Local Similarity 49.0%; Pred. No. 2.4e+02;
RESULT 708
ID AAH54548 standard; DNA; 3126 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3912.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.5%; Score 28.6; DB 4; Length 3126;
Best Local Similarity 49.0%; Pred. No. 2.4e+02;
RESULT 709
ID AAD12567 standard; cDNA; 3323 BP.
DE Human protein having hydrophobic domain encoding cDNA clone HP03700.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
Query Match 10.5%; Score 28.6; DB 4; Length 3323;
Best Local Similarity 51.1%; Pred. No. 2.5e+02;
RESULT 710
ID ABS64611 standard; cDNA; 3661 BP.
DE Human cDNA probe selectively hybridising to foetal cell mRNA #26.
PN WO200255985-A2.
PD 18-JUL-2002.
PA (HOPF) ROCHE DIAGNOSTICS CORP.
Query Match 10.5%; Score 28.6; DB 6; Length 3661;
Best Local Similarity 49.0%; Pred. No. 2.6e+02;
RESULT 711
ID ABZ32319 standard; DNA; 4263 BP.
DE Candida albicans essential gene SEQ ID NO 6606.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.5%; Score 28.6; DB 6; Length 4263;
Best Local Similarity 67.8%; Pred. No. 2.7e+02;
RESULT 712
ID ADE62655 standard; DNA; 4711 BP.
DE Human gene XM.042066, SEQ ID NO 8587.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Query Match 10.5%; Score 28.6; DB 10; Length 4711;
Best Local Similarity 54.2%; Pred. No. 2.8e+02;
RESULT 713
ID ADE62659 standard; DNA; 4711 BP.
DE Human gene XM.042066, SEQ ID NO 8591.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.5%; Score 28.6; DB 10; Length 4711;
Best Local Similarity 54.2%; Pred. No. 2.8e+02;
RESULT 714
ID ABLJ5182 standard; cDNA; 4750 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40028.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.5%; Score 28.6; DB 4; Length 4750;
Best Local Similarity 53.0%; Pred. No. 2.8e+02;
RESULT 715
ID ABLJ2350 standard; DNA; 5236 BP.
DE Human immune system associated gene SEQ ID NO: 323.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 5236;
Best Local Similarity 61.3%; Pred. No. 2.9e+02;
RESULT 716
ID ADB85532 standard; DNA; 5313 BP.
DE Human MNB modulator of the SRBP pathway DYRK1A gene sequence.
PN WO2003066811-A2.
PD 14-AUG-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.5%; Score 28.6; DB 10; Length 5313;
Best Local Similarity 51.1%; Pred. No. 3e+02;
RESULT 717
ID ABL33017 standard; DNA; 6246 BP.
DE Human immune system associated gene SEQ ID NO: 990.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 6246;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
RESULT 718
ID ABK33966 standard; DNA; 6246 BP.
DE Human DNA for staging of Astrocytomas, complement, #25.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 6246;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
RESULT 719
ID ADA20363 standard; DNA; 6246 BP.
DE Prostate tumour related genomic DNA complement sample #14.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 8; Length 6246;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
RESULT 720
ID ADA84170 standard; DNA; 6246 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:28.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 8; Length 6246;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
RESULT 721
ID ABN80208 standard; DNA; 7323 BP.
DE Human chemically modified disease associated gene SEQ ID NO 225.
PN WO200200927-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 7323;
Best Local Similarity 45.7%; Pred. No. 3.3e+02;
RESULT 722
ID ABK61452 standard; cDNA; 7560 BP.
DE Human cDNA encoding protein NOV2.
PN WO200216599-A2.
PD 28-FEB-2002.
PA (CURA-) CURAGEN CORP.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 10.5%; Score 28.6; DB 6; Length 7560;
Best Local Similarity 54.2%; Pred. No. 3.4e+02;
RESULT 723
ID ABK40048 standard; DNA; 7746 BP.
DE Human chemically pretreated gene sequence #65 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 7746;
Best Local Similarity 48.0%; Pred. No. 3.4e+02;
RESULT 724
ID ABL33857 standard; DNA; 7746 BP.
DE Human immune system associated gene SEQ ID NO: 1830.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.5%; Score 28.6; DB 6; Length 7746;
Best Local Similarity 48.0%; Pred. No. 3.4e+02;
RESULT 725
ID AAA88864 standard; DNA; 8201 BP.
DE Human dentin sialophosphoprotein gene.
PN WO200062065-A1.
PD 19-OCT-2000.
PA (TUSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.5%; Score 28.6; DB 3; Length 8201;
Best Local Similarity 51.1%; Pred. No. 3.5e+02;
RESULT 726
ID ABQ73537 standard; DNA; 8201 BP.
DE Human dentin sialophosphoprotein precursor (DSPP) gene SEQ ID NO:1.
PN WO200258722-A1.
PD 01-AUG-2002.
PA (SHAN-) SHANGHAI RES CENT BIOTECHNOLOGY.
Query Match 10.5%; Score 28.6; DB 6; Length 8201;
Best Local Similarity 51.1%; Pred. No. 3.5e+02;
RESULT 727
ID AAK90312 standard; DNA; 10766 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3888.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.6; DB 4; Length 10766;
Best Local Similarity 51.1%; Pred. No. 3.8e+02;
RESULT 728
ID AAS39895 standard; DNA; 10766 BP.
DE Genomic sequence #314 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.6; DB 5; Length 10766;
Best Local Similarity 51.1%; Pred. No. 3.8e+02;
RESULT 729
ID ABE32855 standard; DNA; 10766 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 792.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.5%; Score 28.6; DB 9; Length 10766;
Best Local Similarity 51.1%; Pred. No. 3.8e+02;
RESULT 730
ID ADO34038 standard; DNA; 35586 BP.
DE Human CLA2 gene, SEQ ID 1.

PN BP1426442-A1.
PD 09-JUN-2004.
PA (MTM-) MTM LAB AG.
Query Match 10.5%; Score 28.6; DB 12; Length 35586;
Best Local Similarity 54.2%; Pred. No. 5.9e+02;
RESULT 731
ID AAD56159 standard; DNA; 38045 BP.
DE Human salvador genomic DNA.
PN WO2003035845-A2.
PD 01-MAY-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 10.5%; Score 28.6; DB 9; Length 38045;
Best Local Similarity 48.0%; Pred. No. 6e+02;
RESULT 732
ID AAK82012 standard; DNA; 49561 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36824.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 28.6; DB 4; Length 49561;
Best Local Similarity 51.1%; Pred. No. 6.6e+02;
RESULT 733
Query Match 10.5%; Score 28.6; DB 2; Length 64976;
Best Local Similarity 48.0%; Pred. No. 7.3e+02;
RESULT 734
Query Match 10.5%; Score 28.6; DB 2; Length 110000;
Best Local Similarity 57.1%; Pred. No. 8.8e+02;
RESULT 735
ID ABA92787 standard; DNA; 640681 BP.
DE Buchnera sp. genomic DNA SEQ ID NO:1.
PN JP2001292771-A.
PD 23-OCT-2001.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 10.5%; Score 28.6; DB 6; Length 110000;
Best Local Similarity 54.2%; Pred. No. 8.8e+02;
RESULT 736
Query Match 10.5%; Score 28.6; DB 10; Length 110000;
Best Local Similarity 55.6%; Pred. No. 8.8e+02;
RESULT 737
Query Match 10.5%; Score 28.6; DB 10; Length 110000;
Best Local Similarity 57.1%; Pred. No. 8.8e+02;
RESULT 738
Query Match 10.5%; Score 28.6; DB 10; Length 110000;
Best Local Similarity 57.1%; Pred. No. 8.8e+02;
RESULT 739
Query Match 10.5%; Score 28.6; DB 10; Length 110000;
Best Local Similarity 57.1%; Pred. No. 8.8e+02;
RESULT 740
ID ABV56465 standard; cDNA; 261 BP.
DE Human prostate expression marker cDNA 56456.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.4%; Score 28.4; DB 5; Length 261;
Best Local Similarity 54.9%; Pred. No. 1.2e+02;
RESULT 741
ID AAL23194 standard; cDNA; 371 BP.
DE Human breast cancer expressed polynucleotide 15651.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.4%; Score 28.4; DB 4; Length 371;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 742
ID ACH49514 standard; cDNA; 416 BP.
DE Human leukocyte cDNA #1108.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.

Query Match
Best Local Similarity 10.4%; Score 28.4; DB 9; Length 416;
RESULT 743
ID AAZ34255 standard; DNA; 457 BP.
DE Human EST DNAL5846.
PN W09946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 2; Length 457;
RESULT 744
ID AAC78565 standard; cDNA; 457 BP.
DE Human EST DNAL5846 nucleotide sequence SEQ ID NO:432.
PN W020053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 3; Length 457;
RESULT 745
ID ACA63823 standard; cDNA; 457 BP.
DE Novel human secreted and transmembrane protein DNAL5846.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 8; Length 457;
RESULT 746
ID ACA71987 standard; DNA; 457 BP.
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 432.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 8; Length 457;
RESULT 747
ID ABX92627 standard; cDNA; 457 BP.
DE Human PRO218 EST polynucleotide sequence #2.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 8; Length 457;
RESULT 748
ID ACA66368 standard; cDNA; 457 BP.
DE Human secreted/transmembrane protein EST DNAL5846.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 8; Length 457;
RESULT 749
ID ADA24971 standard; cDNA; 457 BP.
DE Novel human secreted and transmembrane protein EST DNAL5846.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 9; Length 457;
RESULT 750
ID AC29969 standard; cDNA; 457 BP.
DE Novel human secreted and transmembrane protein EST DNAL5846.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 9; Length 457;
RESULT 751
ID ADA12632 standard; cDNA; 457 BP.
DE Human secreted/transmembrane polypeptide PRO218 EST #2.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 9; Length 457;
RESULT 752
ID ACD29384 standard; cDNA; 457 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #108.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 9; Length 457;
RESULT 753
ID ADB73938 standard; cDNA; 457 BP.
DE Human PRO polynucleotide sequence #108.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 754
ID ADB76654 standard; cDNA; 457 BP.
DE Human PRO polynucleotide sequence #108.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 755
ID ADC44080 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 756
ID ADC61840 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 757
ID ADC63804 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 758
ID ADC66904 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 759
ID ADC69028 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 760
ID ADC63088 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.4%; Score 28.4; DB 10; Length 457;
RESULT 761

ID ADC68153 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 762
ID ADC41473 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 763
ID ADC67528 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 764
ID ADC62464 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 765
ID ADC42097 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 766
ID ADE49466 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 767
ID ADE35520 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 768
ID ADE16634 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 769
ID ADD73249 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 770
ID ADD72607 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 771
ID ADE17258 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 772
ID ADF47272 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 773
ID ADG53029 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 774
ID ADG60349 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 775
ID ACD42788 standard; cDNA; 457 BP.
DE Novel human secreted and transmembrane protein EST DNA15846.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 10; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 776
ID ADE48766 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 777
ID ADE89867 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FILV/) FERRARA N.
PA (FONG/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.

PA (GURNEY/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 778
ID ADF61507 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 779
ID ADF40199 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 780
ID ADF45995 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 781
ID ADF24391 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 782
ID ADF40823 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 783
ID ADF23767 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 784
ID ADF33750 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 785
ID ADF27217 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 786
ID ADF27853 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 787
ID ADF41447 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 788
ID ADF33126 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 789
ID ADF25492 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 790
ID ADF26593 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 791
ID ADF34382 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 792
ID ADF46619 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 793
ID ADF50605 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 794
ID ADG49981 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.

PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 795
ID ADG51853 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 796
ID ADG49357 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 797
ID ADG48733 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 798
ID ADG51229 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 799
ID ADG59173 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 800
ID ADG62629 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 801
ID ADH25654 standard; cDNA; 457 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:432.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 802
ID ADM17431 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 803
ID ADL7265 standard; cDNA; 457 BP.
DE Human EST from secreted/transmembrane protein, PRO218 #2.
PN US2004063921-A1.

PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.4%; Score 28.4; DB 12; Length 457;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 804
ID ABOQ69334 standard; DNA; 651 BP.
DE Listeria innocua DNA sequence #773.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.4%; Score 28.4; DB 6; Length 651;
Best Local Similarity 51.6%; Pred. No. 1.6e+02;
RESULT 805
ID ABOQ67667 standard; DNA; 705 BP.
DE Listeria innocua DNA sequence #469.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.4%; Score 28.4; DB 6; Length 705;
Best Local Similarity 51.6%; Pred. No. 1.6e+02;
RESULT 806
ID AAL15342 standard; cDNA; 732 BP.
DE Human breast cancer expressed polynucleotide 7799.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.4%; Score 28.4; DB 4; Length 732;
Best Local Similarity 52.5%; Pred. No. 1.7e+02;
RESULT 807
ID AAL24188 standard; cDNA; 746 BP.
DE Human breast cancer expressed polynucleotide 16645.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.4%; Score 28.4; DB 4; Length 746;
Best Local Similarity 52.5%; Pred. No. 1.7e+02;
RESULT 808
ID ACC61006 standard; DNA; 771 BP.
DE Gene sequence #SEQ ID 794.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.
Query Match 10.4%; Score 28.4; DB 10; Length 771;
Best Local Similarity 56.4%; Pred. No. 1.7e+02;
RESULT 809
ID ADK62643 standard; DNA; 771 BP.
DE Disease treating protein complex-derived gene #447.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZONE AG.
Query Match 10.4%; Score 28.4; DB 10; Length 771;
Best Local Similarity 56.4%; Pred. No. 1.7e+02;
RESULT 810
ID ABL34333 standard; DNA; 907 BP.
DE Human immune system associated gene SEQ ID NO: 2306.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 907;
Best Local Similarity 51.6%; Pred. No. 1.8e+02;
RESULT 811
ID AAC59217 standard; cDNA; 1032 BP.
DE Human secreted protein cDNA sequence #3.
PN WO200055199-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 3; Length 1032;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
RESULT 812
ID AAX20003 standard; DNA; 1069 BP.
DE Enterococcus faecalis EF002 gene fragment.

PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 813
ID ABN97988 standard; DNA; 1069 BP.
DE E faecalis EF002 gene fragment.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 6; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 814
ID ACA87952 standard; DNA; 1069 BP.
DE E. faecalis novel gene #4.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 815
ID ABX61558 standard; DNA; 1069 BP.
DE Enterococcus faecalis EF040 polynucleotide #4.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 816
ID AA20002 standard; DNA; 1161 BP.
DE Enterococcus faecalis gene EF002.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 817
ID ARN97987 standard; DNA; 1161 BP.
DE E faecalis EF002 gene.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 6; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 818
ID ACA87951 standard; DNA; 1161 BP.
DE E. faecalis novel gene #3.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 819
ID ABX61557 standard; DNA; 1161 BP.
DE Enterococcus faecalis EF040 polynucleotide #3.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 820
ID ADH85017 standard; DNA; 1296 BP.
DE Enterococcus faecalis polynucleotide #2902.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 10.4%; Score 28.4; DB 10; Length 1296;
Best Local Similarity 62.9%; Pred. No. 2.1e+02;
RESULT 821
ID ADC85568 standard; DNA; 1324 BP.
DE Human GPCR gene SEQ ID NO:21.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 813
ID ABN97988 standard; DNA; 1069 BP.
DE E faecalis EF002 gene fragment.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 6; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 814
ID ACA87952 standard; DNA; 1069 BP.
DE E. faecalis novel gene #4.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 815
ID ABX61558 standard; DNA; 1069 BP.
DE Enterococcus faecalis EF040 polynucleotide #4.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 816
ID AA20002 standard; DNA; 1161 BP.
DE Enterococcus faecalis gene EF002.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 817
ID ARN97987 standard; DNA; 1161 BP.
DE E faecalis EF002 gene.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 6; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 818
ID ACA87951 standard; DNA; 1161 BP.
DE E. faecalis novel gene #3.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 819
ID ABX61557 standard; DNA; 1161 BP.
DE Enterococcus faecalis EF040 polynucleotide #3.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 8; Length 1161;
Best Local Similarity 62.9%; Pred. No. 2e+02;
RESULT 820
ID ADH85017 standard; DNA; 1296 BP.
DE Enterococcus faecalis polynucleotide #2902.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 10.4%; Score 28.4; DB 10; Length 1296;
Best Local Similarity 62.9%; Pred. No. 2.1e+02;
RESULT 821
ID ADC85568 standard; DNA; 1324 BP.
DE Human GPCR gene SEQ ID NO:21.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 1069;
Best Local Similarity 62.9%; Pred. No. 1.9e+02;
RESULT 822
ID AAP88594 standard; cDNA; 1451 BP.
DE Human GCRBC-15 cDNA INCYTE ID 7475271CD1 SEQ ID 63.
PN WO200263004-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 28.4; DB 6; Length 1451;
Best Local Similarity 51.6%; Pred. No. 2.1e+02;
RESULT 823
ID ADO57300 standard; cDNA; 2074 BP.
DE DNA encoding kidney development associated protein seqid 67.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 10.4%; Score 28.4; DB 12; Length 2074;
Best Local Similarity 60.3%; Pred. No. 2.4e+02;
RESULT 824
ID AAV74265 standard; cDNA; 2268 BP.
DE Human heart muscle specific cDNA #3.
PN WO9856907-A1.
PD 17-DEC-1998.
PA (MEDI-) MEDIGENE AG.
Query Match 10.4%; Score 28.4; DB 2; Length 2268;
Best Local Similarity 46.1%; Pred. No. 2.5e+02;
RESULT 825
ID ABJ99755 standard; cDNA; 2280 BP.
DE Human secretory polynucleotide (sptm) 10.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 28.4; DB 6; Length 2280;
Best Local Similarity 46.1%; Pred. No. 2.5e+02;
RESULT 826
ID AAS31144 standard; cDNA; 2281 BP.
DE Human diagnostic and therapeutic polynucleotide (DITHP) #159.
PN WO200162927-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 28.4; DB 4; Length 2281;
Best Local Similarity 46.1%; Pred. No. 2.5e+02;
RESULT 827
ID ABS70446 standard; cDNA; 2281 BP.
DE Human bone remodelling gene #103.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 28.4; DB 6; Length 2281;
Best Local Similarity 46.1%; Pred. No. 2.5e+02;
RESULT 828
ID ABX34524 standard; cDNA; 2311 BP.
DE Human mddt cDNA SEQ ID 85.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 28.4; DB 8; Length 2311;
Best Local Similarity 46.1%; Pred. No. 2.5e+02;
RESULT 829
ID AAH18720 standard; cDNA; 2750 BP.
DE Human cDNA sequence SEQ ID NO:18992.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.4%; Score 28.4; DB 4; Length 2750;
Best Local Similarity 60.3%; Pred. No. 2.7e+02;

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RESULT 830
ID ADG33048 standard; DNA; 2750 BP.
DE Human DNA differentially expressed in patients with SLE SeqID372.
PN WO2003090694-A2.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 10.4%; Score 28.4; DB 10; Length 2750;
Best Local Similarity 60.3%; Pred. No. 2.7e+02;
RESULT 831
ID ABL25494 standard; DNA; 3371 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27955.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.4%; Score 28.4; DB 4; Length 3371;
Best Local Similarity 45.0%; Pred. No. 2.9e+02;
RESULT 832
ID AAQ44392 standard; cDNA to mRNA; 3712 BP.
DE Sequence of human OSP-4-1 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH-) HOECHST JAPAN LTD.
Query Match 10.4%; Score 28.4; DB 2; Length 3712;
Best Local Similarity 54.9%; Pred. No. 3e+02;
RESULT 833
ID ABL25028 standard; DNA; 3815 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 26557.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.4%; Score 28.4; DB 4; Length 3815;
Best Local Similarity 53.8%; Pred. No. 3e+02;
RESULT 834
ID ABL33286 standard; DNA; 5962 BP.
DE Human immune system associated gene SEQ ID NO: 1259.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 5962;
Best Local Similarity 47.7%; Pred. No. 3.6e+02;
RESULT 835
ID ABL33657 standard; DNA; 6640 BP.
DE Human immune system associated gene SEQ ID NO: 1630.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 6640;
Best Local Similarity 49.3%; Pred. No. 3.7e+02;
RESULT 836
ID AAI58487 standard; cDNA; 7393 BP.
DE Human polynucleotide SEQ ID NO 690.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 28.4; DB 4; Length 7393;
Best Local Similarity 52.5%; Pred. No. 3.8e+02;
RESULT 837
ID ADQ98702 standard; cDNA; 7393 BP.
DE DNA encoding human GPCR-like protein seqid 372.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 28.4; DB 5; Length 7393;
Best Local Similarity 52.5%; Pred. No. 3.8e+02;
RESULT 838
ID ADB48462 standard; cDNA; 7393 BP.
DE Novel human cDNA SEQ ID NO 372.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 10.4%; Score 28.4; DB 9; Length 7393;
Best Local Similarity 52.5%; Pred. No. 3.8e+02;
RESULT 839
ID AAX13089 standard; DNA; 7574 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:152.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 2; Length 7574;
Best Local Similarity 62.9%; Pred. No. 3.9e+02;
RESULT 840
ID ABS98884 standard; DNA; 7574 BP.
DE Enterococcus faecalis contig sequence #152.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 10.4%; Score 28.4; DB 6; Length 7574;
Best Local Similarity 62.9%; Pred. No. 3.9e+02;
RESULT 841
ID ABZ09978 standard; DNA; 7809 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #118.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 8; Length 7809;
Best Local Similarity 48.7%; Pred. No. 3.9e+02;
RESULT 842
ID ABL06638 standard; cDNA; 10318 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14396.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.4%; Score 28.4; DB 4; Length 10318;
Best Local Similarity 49.3%; Pred. No. 4.3e+02;
RESULT 843
ID ABL32319 standard; DNA; 10696 BP.
DE Human immune system associated gene SEQ ID NO: 292.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 10696;
Best Local Similarity 48.7%; Pred. No. 4.4e+02;
RESULT 844
ID ABL54340 standard; DNA; 10696 BP.
DE Chemically treated apoptosis gene complementary to gene #20.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 10696;
Best Local Similarity 48.7%; Pred. No. 4.4e+02;
RESULT 845
ID ABL92304 standard; DNA; 13919 BP.
DE Chemically treated DNA repair gene fragment#57.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 13919;
Best Local Similarity 53.6%; Pred. No. 4.8e+02;
RESULT 846
ID AAK83881 standard; DNA; 17310 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38693.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 17310;
Best Local Similarity 47.7%; Pred. No. 5.2e+02;
RESULT 847
ID ABK39952 standard; DNA; 17703 BP.
DE Human chemically pretreated gene sequence #17 strand 1.
PN WO200202806-A2.
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PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.4%; Score 28.4; DB 6; Length 17703;
Best Local Similarity 47.3%; Pred. No. 5.3e+02;
RESULT 848
ID AALJ37510 standard; DNA; 31314 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3875.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 31314;
Best Local Similarity 53.6%; Pred. No. 6.5e+02;
RESULT 849
ID AEX60498 standard; cDNA; 31314 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2842.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.4%; Score 28.4; DB 8; Length 31314;
Best Local Similarity 53.6%; Pred. No. 6.5e+02;
RESULT 850
ID ADJ31248 standard; DNA; 31314 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3875.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 12; Length 31314;
Best Local Similarity 53.6%; Pred. No. 6.5e+02;
RESULT 851
ID AAL05410 standard; DNA; 31949 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8098.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 31949;
Best Local Similarity 52.5%; Pred. No. 6.5e+02;
RESULT 852
ID ABU98269 standard; DNA; 31949 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2921.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 31949;
Best Local Similarity 52.5%; Pred. No. 6.5e+02;
RESULT 853
ID AAL05411 standard; DNA; 32186 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8099.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 32186;
Best Local Similarity 52.5%; Pred. No. 6.5e+02;
RESULT 854
ID ABU98270 standard; DNA; 32186 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2922.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 28.4; DB 4; Length 32186;
Best Local Similarity 52.5%; Pred. No. 6.5e+02;
RESULT 855
ID ABQ99652 standard; DNA; 38736 BP.
DE Human membrane spanning 4-domain family, subfamily A genomic sequence.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 10.4%; Score 28.4; DB 6; Length 38736;
Best Local Similarity 49.3%; Pred. No. 7e+02;
RESULT 856
ID ABU11838 standard; cDNA; 49380 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29996.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 10.4%; Score 28.4; DB 4; Length 49380;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
RESULT 857
ID ADP45592 standard; DNA; 76500 BP.
DE Human MAP kinase MAPK10 (JNK3) gDNA.
PN WO2004047623-A2.
PD 10-JUN-2004.
Query Match 10.4%; Score 28.4; DB 12; Length 76500;
Best Local Similarity 52.5%; Pred. No. 8.9e+02;
RESULT 858
Query Match 10.4%; Score 28.4; DB 6; Length 95269;
Best Local Similarity 50.7%; Pred. No. 9.6e+02;
RESULT 859
ID ADA02747 standard; DNA; 96599 BP.
DE Mouse lrf2 carcinoma associated gene, SEQ ID NO:1265.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.4%; Score 28.4; DB 9; Length 96599;
Best Local Similarity 60.3%; Pred. No. 9.7e+02;
RESULT 860
ID ADB72485 standard; DNA; 96599 BP.
DE Mouse lrf2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.4%; Score 28.4; DB 10; Length 96599;
Best Local Similarity 60.3%; Pred. No. 9.7e+02;
RESULT 861
ID ADC85227 standard; DNA; 96599 BP.
DE Mouse lrf2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.4%; Score 28.4; DB 10; Length 96599;
Best Local Similarity 60.3%; Pred. No. 9.7e+02;
RESULT 862
ID ADM74342 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #7.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 10.4%; Score 28.4; DB 12; Length 96599;
Best Local Similarity 60.3%; Pred. No. 9.7e+02;
RESULT 863
Query Match 10.4%; Score 28.4; DB 2; Length 110000;
Best Local Similarity 76.1%; Pred. No. 1e+03;
RESULT 864
Query Match 10.4%; Score 28.4; DB 6; Length 110000;
Best Local Similarity 51.6%; Pred. No. 1e+03;
RESULT 865
Query Match 10.4%; Score 28.4; DB 6; Length 110000;
Best Local Similarity 51.6%; Pred. No. 1e+03;
RESULT 866
ID ABQ69245 standard; DNA; 3011208 BP.
DE Listeria innocua DNA sequence #684.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.4%; Score 28.4; DB 6; Length 110000;
Best Local Similarity 51.6%; Pred. No. 1e+03;
RESULT 867
Query Match 10.4%; Score 28.4; DB 6; Length 110000;
Best Local Similarity 50.7%; Pred. No. 1e+03;
RESULT 868
Query Match 10.4%; Score 28.4; DB 6; Length 110000;
Best Local Similarity 51.6%; Pred. No. 1e+03;
RESULT 869

Query Match 10.4%; Score 28.4; DB 8; Length 110000;
Best Local Similarity 51.6%; Pred. No. 1e+03;
RESULT 870
Query Match 10.4%; Score 28.4; DB 8; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1e+03;
RESULT 871
Query Match 10.4%; Score 28.4; DB 10; Length 110000;
Best Local Similarity 51.1%; Pred. No. 1e+03;
RESULT 872
Query Match 10.4%; Score 28.4; DB 10; Length 110000;
Best Local Similarity 56.4%; Pred. No. 1e+03;
RESULT 873
Query Match 10.4%; Score 28.4; DB 10; Length 110000;
Best Local Similarity 56.4%; Pred. No. 1e+03;
RESULT 874
ID AAH44801 standard; DNA; 112190 BP.
DE Human GPCR protein KAT06734L DNA containing exons 3 to 9 SEQ ID NO:16.
PN JP2001245666-A.
PD 11-SEP-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 10.4%; Score 28.4; DB 4; Length 112190;
Best Local Similarity 52.5%; Pred. No. 1e+03;
RESULT 875
ID ADP84158 standard; DNA; 129017 BP.
DE Human AST-1 locus DNA representing part of the GPRA gene SeqID 1.
Query Match 10.4%; Score 28.4; DB 12; Length 129017;
Best Local Similarity 52.5%; Pred. No. 1.1e+03;
RESULT 876
ID ADP65634 standard; DNA; 137908 BP.
DE Human sequence from clone 914P14 on chromosome Xq23 Contains DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.4%; Score 28.4; DB 11; Length 137908;
Best Local Similarity 50.7%; Pred. No. 1.1e+03;
RESULT 877
ID ABT11173 standard; DNA; 168174 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.4%; Score 28.4; DB 6; Length 168174;
Best Local Similarity 56.4%; Pred. No. 1.2e+03;
RESULT 878
ID ABT11114 standard; DNA; 168273 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.4%; Score 28.4; DB 6; Length 168273;
Best Local Similarity 56.4%; Pred. No. 1.2e+03;
RESULT 879
ID ACF62736 standard; DNA; 183610 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 10.4%; Score 28.4; DB 8; Length 183610;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 880
ID ADB20851 standard; DNA; 183610 BP.
DE Wppl based cancer related nucleic acid SEQ ID NO:664.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 10.4%; Score 28.4; DB 8; Length 183610;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 881
ID ADB87940 standard; DNA; 183610 BP.
DE Human UGR1A1 gene sequence SEQ ID NO:664.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

Query Match 10.4%; Score 28.4; DB 10; Length 183610;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 882
ID ADB96923 standard; DNA; 183610 BP.
DE Human MDRI related DNA sequence SEQ ID NO:664.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 10.4%; Score 28.4; DB 10; Length 183610;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 883
ID ADB92114 standard; DNA; 183610 BP.
DE Human MDRI related DNA sequence SEQ ID NO:664.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 10.4%; Score 28.4; DB 10; Length 183610;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 884
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine serine kinase.
Query Match 10.4%; Score 28.4; DB 6; Length 326014;
Best Local Similarity 53.6%; Pred. No. 1.4e+03;
RESULT 885
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine serine kinase.
Query Match 10.4%; Score 28.4; DB 6; Length 326014;
Best Local Similarity 51.6%; Pred. No. 1.4e+03;
RESULT 886
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Query Match 10.4%; Score 28.4; DB 12; Length 326014;
Best Local Similarity 53.8%; Pred. No. 1.4e+03;
RESULT 887
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Query Match 10.4%; Score 28.4; DB 12; Length 326014;
Best Local Similarity 51.6%; Pred. No. 1.4e+03;
RESULT 888
ID AAT75253 standard; DNA; 233 BP.
DE Nucleotide sequence encoding human RAD50 intron 6.
PN WO9727284-A2.
PD 31-JUL-1997.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 10.3%; Score 28.2; DB 2; Length 233;
Best Local Similarity 53.1%; Pred. No. 1.3e+02;
RESULT 889
ID ADH31868 standard; DNA; 291 BP.
DE Yeast small open reading frame smORF326, SEQ ID NO:326.
PN WO200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 28.2; DB 6; Length 291;
Best Local Similarity 54.3%; Pred. No. 1.4e+02;
RESULT 890
ID AAC16587 standard; cDNA; 304 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 20662.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 10.3%; Score 28.2; DB 3; Length 304;
Best Local Similarity 52.1%; Pred. No. 1.4e+02;
RESULT 891
ID ABX88534 standard; cDNA; 304 BP.
DE Corn ear-derived polynucleotide (cpd) #6994.
PN US6476212-B1.
PD 05-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.3%; Score 28.2; DB 10; Length 304;
Best Local Similarity 55.7%; Pred. No. 1.4e+02;
RESULT 892
ID AAC09513 standard; cDNA; 380 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 13588.

PN EPI033401-A2.
PD 06-SEP-2000.
PA (GEST.) GENSET.
Query Match 10.3%; Score 28.2; DB 3; Length 380;
Best Local Similarity 51.2%; Pred. No. 1.5e+02;
RESULT 893
ID ABN94868 standard; DNA; 392 BP.
DE Gene #1366 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28.2; DB 6; Length 392;
Best Local Similarity 53.1%; Pred. No. 1.5e+02;
RESULT 894
ID ABV46766 standard; cDNA; 496 BP.
DE Human prostate expression marker cDNA 46757.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28.2; DB 5; Length 496;
Best Local Similarity 59.3%; Pred. No. 1.7e+02;
RESULT 895
ID ABV77972 standard; DNA; 516 BP.
DE Hypoxia-repressed protein coding sequence #40.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 10.3%; Score 28.2; DB 6; Length 516;
Best Local Similarity 52.1%; Pred. No. 1.7e+02;
RESULT 896
ID AAH33609 standard; cDNA; 631 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:665.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28.2; DB 4; Length 631;
Best Local Similarity 51.2%; Pred. No. 1.8e+02;
RESULT 897
ID ABQ38867 standard; DNA; 679 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 25458.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 679;
Best Local Similarity 52.6%; Pred. No. 1.9e+02;
RESULT 898
ID ABQ38866 standard; DNA; 679 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 25457.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 679;
Best Local Similarity 52.6%; Pred. No. 1.9e+02;
RESULT 899
ID AAH92502 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1202a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match 10.3%; Score 28.2; DB 4; Length 700;
Best Local Similarity 53.1%; Pred. No. 1.9e+02;
RESULT 900
ID ABQ65637 standard; DNA; 709 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 214.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
Query Match 10.3%; Score 28.2; DB 4; Length 1442;
Best Local Similarity 59.3%; Pred. No. 2.5e+02;
Query Match 10.3%; Score 28.2; DB 6; Length 709;
Best Local Similarity 53.1%; Pred. No. 1.9e+02;
RESULT 901
ID ABN98945 standard; DNA; 856 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 10.3%; Score 28.2; DB 6; Length 709;
Best Local Similarity 53.1%; Pred. No. 1.9e+02;
RESULT 902
ID ACR39552 standard; DNA; 996 BP.
DE Prokaryotic essential gene #21209.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28.2; DB 8; Length 996;
Best Local Similarity 61.6%; Pred. No. 2.2e+02;
RESULT 903
ID ACR28354 standard; DNA; 1191 BP.
DE Prokaryotic essential gene #10011.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28.2; DB 8; Length 1191;
Best Local Similarity 47.0%; Pred. No. 2.3e+02;
RESULT 904
ID ABK49115 standard; cDNA; 1409 BP.
DE Human cDNA encoding transcription factor LCR-F19.02.
PN WO2002020583-A1.
PD 14-MAR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 10.3%; Score 28.2; DB 6; Length 1409;
Best Local Similarity 53.1%; Pred. No. 2.4e+02;
RESULT 905
ID AAH99669 standard; cDNA; 1442 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:504.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28.2; DB 4; Length 1442;
Best Local Similarity 59.3%; Pred. No. 2.5e+02;

RESULT 906
ID AAS68406 standard; cDNA; 1465 BP.
DE DNA encoding novel human diagnostic protein #4210.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28.2; DB 5; Length 1465;
Best Local Similarity 59.3%; Pred. No. 2.5e+02;
RESULT 907
ID ADI30894 standard; cDNA; 1799 BP.
DE Human cDNA #220.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 10.3%; Score 28.2; DB 11; Length 1799;
Best Local Similarity 51.2%; Pred. No. 2.7e+02;
RESULT 908
ID AAC43185 standard; DNA; 1863 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38339.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.3%; Score 28.2; DB 3; Length 1863;
Best Local Similarity 54.3%; Pred. No. 2.7e+02;
RESULT 909
ID ABZ16408 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4213.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 2000;
Best Local Similarity 61.6%; Pred. No. 2.8e+02;
RESULT 910
ID AAC49336 standard; DNA; 2250 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 60775.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.3%; Score 28.2; DB 3; Length 2250;
Best Local Similarity 54.3%; Pred. No. 2.9e+02;
RESULT 911
ID AAZ231609 standard; cDNA; 2442 BP.
DE Human labyrinthin cDNA.
PN WO9947683-A1.
PD 23-SEP-1999.
PA (RADO/) RADOSEVICH J A.
Query Match 10.3%; Score 28.2; DB 2; Length 2442;
Best Local Similarity 54.3%; Pred. No. 3e+02;
RESULT 912
ID ABK39743 standard; cDNA; 2442 BP.
DE cDNA encoding clone #48005 (L979P) of lung tumour protein version #2.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.3%; Score 28.2; DB 6; Length 2442;
Best Local Similarity 54.3%; Pred. No. 3e+02;
RESULT 913
ID ACA12072 standard; cDNA; 2442 BP.
DE Human lung cancer-associated cDNA L979P extended sequence.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 10.3%; Score 28.2; DB 8; Length 2442;
Best Local Similarity 54.3%; Pred. No. 3e+02;
RESULT 914
ID ACA03258 standard; cDNA; 2442 BP.
DE Lung cancer therapyand diagnosis associated cDNA #1745.
PN US2002172952-A1.
PD 17-JUL-2003.
RESULT 915
ID ADH47310 standard; cDNA; 2442 BP.
DE Human lung tumour cDNA clone, SEQ ID NO 1791.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.3%; Score 28.2; DB 10; Length 2442;
Best Local Similarity 54.3%; Pred. No. 3e+02;
RESULT 916
ID ACA52736 standard; DNA; 2949 BP.
DE Prokaryotic essential gene #34393.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28.2; DB 8; Length 2949;
Best Local Similarity 47.0%; Pred. No. 3.2e+02;
RESULT 917
ID ADI82490 standard; DNA; 3038 BP.
DE Human modifier of p21 (MP21) gene sequence SeqID56.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 10.3%; Score 28.2; DB 12; Length 3038;
Best Local Similarity 59.3%; Pred. No. 3.2e+02;
RESULT 918
ID ADN04785 standard; cDNA; 3038 BP.
DE Antipsoriatic cDNA sequence #607.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 28.2; DB 12; Length 3038;
Best Local Similarity 59.3%; Pred. No. 3.2e+02;
RESULT 919
ID ABO79518 standard; cDNA; 3145 BP.
DE cDNA encoding a protein similar to human sorting nexin.
PN WO200262839-A2.
PD 15-AUG-2002.
PA (UYMA-) UNIV MAASTRICHT.
Query Match 10.3%; Score 28.2; DB 6; Length 3145;
Best Local Similarity 59.3%; Pred. No. 3.3e+02;
RESULT 920
ID AAV05551 standard; cDNA; 3218 BP.
DE Human TRAP-2 kinase gene.
PN WO9801541-A1.
PD 15-JAN-1998.
PA (TULA-) TULARIK INC.
Query Match 10.3%; Score 28.2; DB 2; Length 3218;
Best Local Similarity 50.4%; Pred. No. 3.3e+02;
RESULT 921
ID ABL10930 standard; cDNA; 3365 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27272.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.3%; Score 28.2; DB 4; Length 3365;
Best Local Similarity 53.1%; Pred. No. 3.3e+02;
RESULT 922
ID ABA08779 standard; cDNA; 3497 BP.
DE Human RING-H2 homologue-encoding cDNA, SEQ ID NO:555.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28.2; DB 4; Length 3497;
Best Local Similarity 51.2%; Pred. No. 3.4e+02;
RESULT 923
ID ADD29717 standard; mRNA; 3507 BP.
DE Mouse tumour suppressor mRNA SEQ ID NO:173.
PN WO2003058201-A2.
PD 17-JUL-2003.

PA (QUAR-) QUARK BIOTECH INC.
PA (CLEV-) CLEVELAND CLINIC FOUND.
Query Match 10.3%; Score 28.2; DB 10; Length 3507;
Best Local Similarity 51.2%; Pred. No. 3.4e+02;
RESULT 924
ID AAV61482 standard; cDNA; 3527 BP.
DE Human secreted protein cw775_1 cDNA.
PN WO9841539-A2.
PD 24-SEP-1998.
PA (GEMX) GENETICS INST INC.
Query Match 10.3%; Score 28.2; DB 2; Length 3527;
Best Local Similarity 51.2%; Pred. No. 3.4e+02;
RESULT 925
ID ABQ92009 standard; cDNA; 3527 BP.
DE Human polynucleotide SEQ ID NO 6.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO) JACOBS K.
PA (MCCO) MCCOY J M.
PA (LAVA) LAVALLIE E R.
PA (COLL) COLLINS-RACIE L A.
PA (EVAN) EVANS C.
PA (MERB) MERBERG D.
PA (TREB) TREACY M.
PA (SPAU) SPAULDING V.
Query Match 10.3%; Score 28.2; DB 6; Length 3527;
Best Local Similarity 51.2%; Pred. No. 3.4e+02;
RESULT 926
ID ADAL19288 standard; cDNA; 3598 BP.
DE Human insulin resistance marker IRM148 (ring finger protein 3) cDNA.
PN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 10.3%; Score 28.2; DB 10; Length 3598;
Best Local Similarity 51.2%; Pred. No. 3.4e+02;
RESULT 927
ID ADH8380 standard; DNA; 3921 BP.
DE Enterococcus faecalis polynucleotide #3265.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
PA (BUSH) BUSH D.
Query Match 10.3%; Score 28.2; DB 10; Length 3921;
Best Local Similarity 50.4%; Pred. No. 3.5e+02;
RESULT 928
ID AAK08941 standard; DNA; 5563 BP.
DE GATA-1 promoter region.
PN WO9856902-A2.
PD 17-DEC-1998.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 10.3%; Score 28.2; DB 2; Length 5563;
Best Local Similarity 64.6%; Pred. No. 4e+02;
RESULT 929
ID ABL33746 standard; DNA; 6351 BP.
DE Human immune system associated gene SEQ ID NO: 1719.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 6351;
Best Local Similarity 52.1%; Pred. No. 4.2e+02;
RESULT 930
ID ABL33553 standard; DNA; 7065 BP.
DE Human immune system associated gene SEQ ID NO: 1526.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 7065;
Best Local Similarity 73.5%; Pred. No. 4.4e+02;
RESULT 931
ID ADM47730 standard; DNA; 7858 BP.
DE Polynucleotide sequence #148 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.

PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 10.3%; Score 28.2; DB 12; Length 7858;
Best Local Similarity 54.3%; Pred. No. 4.5e+02;
RESULT 932
ID ABN80225 standard; DNA; 8067 BP.
DE Human chemically modified disease associated gene SEQ ID NO 242.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 8067;
Best Local Similarity 53.1%; Pred. No. 4.6e+02;
RESULT 933
ID ABL13258 standard; cDNA; 9936 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34256.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.3%; Score 28.2; DB 4; Length 9936;
Best Local Similarity 61.6%; Pred. No. 4.9e+02;
RESULT 934
ID ABX39936 standard; DNA; 11422 BP.
DE Human chemically pretreated gene sequence #9 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 11422;
Best Local Similarity 49.7%; Pred. No. 5.2e+02;
RESULT 935
ID ABL32218 standard; DNA; 11422 BP.
DE Human immune system associated gene SEQ ID NO: 191.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 11422;
Best Local Similarity 49.7%; Pred. No. 5.2e+02;
RESULT 936
ID ABX94628 standard; DNA; 11863 BP.
DE C. elegans ses-3 DNA.
PN WO2003000717-A2.
PD 03-JAN-2003.
PA (ELEG-) ELEGENE AG.
Query Match 10.3%; Score 28.2; DB 8; Length 11863;
Best Local Similarity 49.0%; Pred. No. 5.3e+02;
RESULT 937
ID ABL34070 standard; DNA; 13503 BP.
DE Human immune system associated gene SEQ ID NO: 2043.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 13503;
Best Local Similarity 50.4%; Pred. No. 5.5e+02;
RESULT 938
ID ABK40062 standard; DNA; 13784 BP.
DE Human chemically pretreated gene sequence #72 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28.2; DB 6; Length 13784;
Best Local Similarity 47.9%; Pred. No. 5.6e+02;
RESULT 939
ID AAK72936 standard; DNA; 14169 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27748.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28.2; DB 4; Length 14169;
Best Local Similarity 46.6%; Pred. No. 5.6e+02;
RESULT 940
ID ADH19017 standard; DNA; 15657 BP.
DE Human heparin cofactor II (HCF2) gDNA.
PN WO2003091453-A1.

PD 06-NOV-2003.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 10.3%; Score 28.2; DB 10; Length 15657;
Best Local Similarity 45.9%; Pred. No. 5.8e+02;
RESULT 941
ID AAZ32190 standard; DNA; 15848 BP.
DE Human heparin cofactor II exon 1 to 5 nucleotide sequence.
PN WO950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 10.3%; Score 28.2; DB 2; Length 15848;
Best Local Similarity 45.9%; Pred. No. 5.9e+02;
RESULT 942
ID ABN95864 standard; DNA; 15849 BP.
DE Gene #2362 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28.2; DB 6; Length 15849;
Best Local Similarity 45.9%; Pred. No. 5.9e+02;
RESULT 943
ID AAS18543 standard; DNA; 18887 BP.
DE DNA encoding UDP glycosyltransferase 1 (UGT1A1).
PN WO200179230-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 10.3%; Score 28.2; DB 6; Length 18887;
Best Local Similarity 49.7%; Pred. No. 6.2e+02;
RESULT 944
ID AAX13292 standard; DNA; 20860 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:355.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28.2; DB 2; Length 20860;
Best Local Similarity 50.4%; Pred. No. 6.5e+02;
RESULT 945
ID ABS99087 standard; DNA; 20860 BP.
DE Enterococcus faecalis contig sequence #355.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS-) KUNSCH C A.
PA (DILL-) DILLON P J.
PA (BARA-) BARASH S.
Query Match 10.3%; Score 28.2; DB 6; Length 20860;
Best Local Similarity 50.4%; Pred. No. 6.5e+02;
RESULT 946
ID ADO22771 standard; DNA; 24001 BP.
DE DNA encoding human interleukin 22 receptor.
PN US2004097447-A1.
PD 20-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.3%; Score 28.2; DB 12; Length 24001;
Best Local Similarity 50.4%; Pred. No. 6.8e+02;
RESULT 947
Query Match 10.3%; Score 28.2; DB 2; Length 80073;
Best Local Similarity 61.6%; Pred. No. 1e+03;
RESULT 948
ID ADF11646 standard; DNA; 94752 BP.
DE Human chromosome 17 clone HPRC905N1 nucleic acid.
PN WO2003087763-A2.
PD 23-OCT-2003.
PA (CELL-) CELLTech R & D INC.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
Query Match 10.3%; Score 28.2; DB 10; Length 94752;
Best Local Similarity 47.9%; Pred. No. 1.1e+03;
RESULT 949
ID ADA02981 standard; DNA; 96599 BP.
DE Mouse Map2k5 carcinoma associated gene, SEQ ID NO:1499.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28.2; DB 9; Length 96599;
Best Local Similarity 51.2%; Pred. No. 1.1e+03;
RESULT 950
ID ADB72719 standard; DNA; 96599 BP.
DE Mouse Map2k5 gene.
PN WO2003008593-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28.2; DB 10; Length 96599;
Best Local Similarity 51.2%; Pred. No. 1.1e+03;
RESULT 951
ID ADC85461 standard; DNA; 96599 BP.
DE Mouse Map2k5 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28.2; DB 10; Length 96599;
Best Local Similarity 51.2%; Pred. No. 1.1e+03;
RESULT 952
ID ADM74576 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #124.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
PA (ENGEL-) ENGELHARD E K.
Query Match 10.3%; Score 28.2; DB 12; Length 96599;
Best Local Similarity 51.2%; Pred. No. 1.1e+03;
RESULT 953
Query Match 10.3%; Score 28.2; DB 2; Length 110000;
Best Local Similarity 53.1%; Pred. No. 1.2e+03;
RESULT 954
Query Match 10.3%; Score 28.2; DB 2; Length 110000;
Best Local Similarity 50.4%; Pred. No. 1.2e+03;
RESULT 955
Query Match 10.3%; Score 28.2; DB 2; Length 110000;
Best Local Similarity 50.4%; Pred. No. 1.2e+03;
RESULT 956
Query Match 10.3%; Score 28.2; DB 6; Length 110000;
Best Local Similarity 54.3%; Pred. No. 1.2e+03;
RESULT 957
ID ADG89426 standard; DNA; 137870 BP.
DE Human matrilin-3 gene SEQ ID NO:1.
Query Match 10.3%; Score 28.2; DB 10; Length 137870;
Best Local Similarity 59.3%; Pred. No. 1.3e+03;
RESULT 958
ID AAH41224 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #3.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 10.3%; Score 28.2; DB 5; Length 349980;
Best Local Similarity 47.9%; Pred. No. 1.7e+03;
RESULT 959
ID AAH41225 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #4.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 10.3%; Score 28.2; DB 5; Length 349980;
Best Local Similarity 47.9%; Pred. No. 1.7e+03;
RESULT 960
ID AAS50893 standard; DNA; 247 BP.
DE Staphylococcus aureus cellular proliferation inhibitory sequence #2117.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 4; Length 247;
Best Local Similarity 50.8%; Pred. No. 1.5e+02;
RESULT 961
ID ACA18160 standard; DNA; 247 BP.
DE Prokaryotic essential gene antisense oligonucleotide #6030.
PN WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 8; Length 247;
Best Local Similarity 50.8%; Pred. No. 1.5e+02;
RESULT 962
ID ABU86380 standard; cDNA; 268 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:9358.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.3%; Score 28; DB 6; Length 268;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
RESULT 963
ID ABK91741 standard; DNA; 327 BP.
DE DNA encoding murine glucose transport-related polypeptide #9.
PN WO200233046-A2.
PD 25-APR-2002.
PA (UNWA-) UNIV MASSACHUSETTS.
Query Match 10.3%; Score 28; DB 6; Length 327;
Best Local Similarity 50.8%; Pred. No. 1.7e+02;
RESULT 964
ID ABX65177 standard; cDNA; 369 BP.
DE Human gene trapped sequence (GTS) cDNA SEQ ID NO 784.
PN US2002110809-A1.
PD 15-AUG-2002.
PA (NEHL/) NEHLS M C.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 10.3%; Score 28; DB 8; Length 369;
Best Local Similarity 53.2%; Pred. No. 1.7e+02;
RESULT 965
ID AAC28678 standard; cDNA; 373 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 32753.
PN EF1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 10.3%; Score 28; DB 3; Length 373;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
RESULT 966
ID ABQ56033 standard; cDNA; 387 BP.
DE Human ovarian antigen HPDV136 cDNA, SEQ ID NO:1913.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 6; Length 387;
Best Local Similarity 58.2%; Pred. No. 1.8e+02;
RESULT 967
ID ABV16971 standard; cDNA; 418 BP.
DE Human prostate expression marker cDNA 16962.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 418;
Best Local Similarity 60.5%; Pred. No. 1.8e+02;
RESULT 968
ID AA551903 standard; DNA; 438 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #320.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 4; Length 438;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 969
ID ACF75022 standard; DNA; 438 BP.
DE Staphylococcus aureus DNA #2702.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 10.3%; Score 28; DB 8; Length 438;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 970
ID AA555091 standard; DNA; 441 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1403.
PN WO200218632-A2.

PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 4; Length 441;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 971
ID AAS55314 standard; DNA; 441 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1626.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 4; Length 441;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 972
ID AAS54490 standard; DNA; 441 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #802.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 4; Length 441;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 973
ID ACA20022 standard; DNA; 441 BP.
DE Prokaryotic essential gene #1679.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 8; Length 441;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
RESULT 974
ID ABV36408 standard; cDNA; 528 BP.
DE Human prostate expression marker cDNA 36399.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 528;
Best Local Similarity 50.0%; Pred. No. 2e+02;
RESULT 975
ID ABV45430 standard; cDNA; 528 BP.
DE Human prostate expression marker cDNA 45421.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 528;
Best Local Similarity 50.0%; Pred. No. 2e+02;
RESULT 976
ID ABQ33824 standard; DNA; 573 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20415.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 573;
Best Local Similarity 52.6%; Pred. No. 2e+02;
RESULT 977
ID ABQ33825 standard; DNA; 573 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20416.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 573;
Best Local Similarity 52.6%; Pred. No. 2e+02;
RESULT 978
ID ABO35515 standard; DNA; 573 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22106.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 573;
Best Local Similarity 52.6%; Pred. No. 2e+02;
RESULT 979
ID ABO35514 standard; DNA; 573 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22105.
PN WO200218632-A2.

PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 573;
Best Local Similarity 52.6%; Pred. No. 2e+02;
RESULT 980
ID ABQ57311 standard; cDNA; 582 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:1006.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 10.3%; Score 28; DB 6; Length 582;
Best Local Similarity 59.0%; Pred. No. 2.1e+02;
RESULT 981
ID ACH69966 standard; DNA; 599 BP.
DE Human genome derived single exon probe #3161.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 10.3%; Score 28; DB 12; Length 599;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
RESULT 982
ID ABK63310 standard; cDNA; 603 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1217.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28; DB 6; Length 603;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
RESULT 983
ID ADB57606 standard; DNA; 603 BP.
DE Toxicity-related gene, SEQ ID 2632.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28; DB 10; Length 603;
Best Local Similarity 52.8%; Pred. No. 2.1e+02;
RESULT 984
ID ADB52126 standard; DNA; 603 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2669.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28; DB 10; Length 603;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
RESULT 985
ID ARAH45574 standard; DNA; 665 BP.
DE Porcine DNA encoding interleukin-18 (IL-18).
PN JP2001103967-A.
PD 17-APR-2001.
PA (NORQ) NORINSUISANSHO KACHIKU EISEI.
PA (MUNE/) MUNETA Y.
PA (MORI/) MORI Y.
PA (SHIM/) SHIMOCHI Y.
PA (ARAI/) ARAI K.
Query Match 10.3%; Score 28; DB 4; Length 665;
Best Local Similarity 77.3%; Pred. No. 2.2e+02;
RESULT 986
ID AAL66519 standard; DNA; 665 BP.
DE Pig coding sequence.
PN JP2001169785-A.
PD 26-JUN-2001.
PA (NORQ) NORINSUISANSHO KACHIKU EISEI.
PA (MUNE/) MUNETA Y.
PA (MORI/) MORI Y.
PA (SHIM/) SHIMOCHI Y.
PA (ARAI/) ARAI K.
Query Match 10.3%; Score 28; DB 5; Length 665;
Best Local Similarity 77.3%; Pred. No. 2.2e+02;
RESULT 987
ID AAL22994 standard; cDNA; 756 BP.
DE Human breast cancer expressed polynucleotide 15451.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 4; Length 756;
Best Local Similarity 50.8%; Pred. No. 2.3e+02;
RESULT 988
ID ABV29998 standard; cDNA; 764 BP.
DE Human prostate expression marker cDNA 29989.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 764;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 989
ID ABV24119 standard; cDNA; 764 BP.
DE Human prostate expression marker cDNA 24110.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 764;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 990
ID ACH95737 standard; DNA; 783 BP.
DE Klebsiella pneumoniae polynucleotide seqid 1532.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 28; DB 11; Length 783;
Best Local Similarity 56.5%; Pred. No. 2.3e+02;
RESULT 991
ID AAL23837 standard; cDNA; 788 BP.
DE Human breast cancer expressed polynucleotide 16294.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 4; Length 788;
Best Local Similarity 47.4%; Pred. No. 2.3e+02;
RESULT 992
ID ADA29583 standard; DNA; 819 BP.
DE DNA encoding Acinetobacter baumannii protein #870.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 28; DB 9; Length 819;
Best Local Similarity 52.8%; Pred. No. 2.3e+02;
RESULT 993
ID ADO43421 standard; cDNA; 826 BP.
DE Lutzomyia longipalpis (sand fly) salivary protein LJM114 cDNA.
PN WO2004039958-A2.
PD 13-MAY-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (PESQ-) CENT PESQUISAS GONCALO MONIZ.
Query Match 10.3%; Score 28; DB 12; Length 826;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
RESULT 994
ID ABV15622 standard; cDNA; 895 BP.
DE Human prostate expression marker cDNA 15613.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.3%; Score 28; DB 5; Length 895;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
RESULT 995
ID ACA44725 standard; DNA; 1002 BP.
DE Prokaryotic essential gene #26382.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITFA PHARM INC.
Query Match 10.3%; Score 28; DB 8; Length 1002;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
RESULT 996
ID ADF02733 standard; DNA; 1062 BP.
DE Bacterial polynucleotide #3018.

PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.3%; Score 28; DB 10; Length 1062;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
RESULT 997
ID AAS82371 standard; cDNA; 1431 BP.
DE DNA encoding novel human diagnostic protein #18175.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28; DB 5; Length 1431;
Best Local Similarity 56.5%; Pred. No. 2.8e+02;
RESULT 998
ID AAS94239 standard; cDNA; 1431 BP.
DE DNA encoding novel human diagnostic protein #30043.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28; DB 5; Length 1431;
Best Local Similarity 56.5%; Pred. No. 2.8e+02;
RESULT 999
ID AAS82055 standard; cDNA; 1431 BP.
DE DNA encoding novel human diagnostic protein #17859.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28; DB 5; Length 1431;
Best Local Similarity 56.5%; Pred. No. 2.8e+02;
RESULT 1000
ID AAS93034 standard; cDNA; 1431 BP.
DE DNA encoding novel human diagnostic protein #28838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 28; DB 5; Length 1431;
Best Local Similarity 56.5%; Pred. No. 2.8e+02;
RESULT 1001
ID AAC59077 standard; cDNA; 2114 BP.
DE Human secreted protein coding sequence SEQ ID NO: 39.
PN WO20005171-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 3; Length 2114;
Best Local Similarity 49.3%; Pred. No. 3.3e+02;
RESULT 1002
ID AAC93380 standard; cDNA; 2158 BP.
DE Human secreted protein gene 17 SEQ ID NO:27.
PN WO200061620-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 3; Length 2158;
Best Local Similarity 49.3%; Pred. No. 3.3e+02;
RESULT 1003
ID ACA52823 standard; DNA; 2304 BP.
DE Prokaryotic essential gene #34480.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 8; Length 2304;
Best Local Similarity 55.0%; Pred. No. 3.4e+02;
RESULT 1004
ID AAK94255 standard; cDNA; 2563 BP.
DE Human full-length cDNA, SEQ ID NO: 2868.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.3%; Score 28; DB 4; Length 2563;
Best Local Similarity 50.8%; Pred. No. 3.5e+02;
RESULT 1005
ID ADL30835 standard; cDNA; 2563 BP.
DE Full length human cDNA clone SeqID 2868.

PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.3%; Score 28; DB 12; Length 2563;
Best Local Similarity 50.8%; Pred. No. 3.5e+02;
RESULT 1006
ID ACA30395 standard; DNA; 2841 BP.
DE Prokaryotic essential gene #12052.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.3%; Score 28; DB 8; Length 2841;
Best Local Similarity 51.6%; Pred. No. 3.6e+02;
RESULT 1007
ID ABV94250 standard; cDNA; 2871 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:241.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 10.3%; Score 28; DB 6; Length 2871;
Best Local Similarity 50.8%; Pred. No. 3.7e+02;
RESULT 1008
ID ADP65006 standard; DNA; 2871 BP.
DE Human thrombospondin 3 (THBS3) DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.3%; Score 28; DB 11; Length 2871;
Best Local Similarity 50.8%; Pred. No. 3.7e+02;
RESULT 1009
ID ADP65489 standard; DNA; 3127 BP.
DE Human thrombospondin 3 (THBS3) mRNA, complete cds DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.3%; Score 28; DB 11; Length 3127;
Best Local Similarity 50.8%; Pred. No. 3.8e+02;
RESULT 1010
ID ADQ19407 standard; DNA; 3127 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2226.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 28; DB 12; Length 3127;
Best Local Similarity 50.8%; Pred. No. 3.8e+02;
RESULT 1011
ID ADQ23637 standard; DNA; 3224 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6457.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 28; DB 12; Length 3224;
Best Local Similarity 50.8%; Pred. No. 3.8e+02;
RESULT 1012
ID AAF75866 standard; DNA; 3708 BP.
DE Histidine protein kinase coding sequence #3.
PN WO200116332-A1.
PD 08-MAR-2001.
PA (SUNR) SUNTORY LTD.
Query Match 10.3%; Score 28; DB 4; Length 3708;
Best Local Similarity 52.6%; Pred. No. 4e+02;
RESULT 1013
ID AAX83478 standard; cDNA to mRNA; 3960 BP.
DE A.thaliana potassium channel KAT2 gene.
PN WO9931259-A1.
PD 24-JUN-1999.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 10.3%; Score 28; DB 2; Length 3960;
Best Local Similarity 55.0%; Pred. No. 4.1e+02;
RESULT 1014
ID AAH14686 standard; cDNA; 4281 BP.
DE Human cDNA sequence SEQ ID NO:12384.

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PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 4281;
  Pred. No. 4.2e+02;
RESULT 1015
ID ADU75040 standard; DNA; 4281 BP.
DE Marker gene SEQ ID NO:292.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 12; Length 4281;
  Pred. No. 4.2e+02;
RESULT 1016
ID AAF75865 standard; DNA; 4679 BP.
DE Histidine protein kinase coding sequence #2.
PN WO200116332-A1.
PD 08-MAR-2001.
PA (SUNR) SUNTORY LTD.
PA (SAOK) NIPPON PAPER IND CO LTD.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 4679;
  Pred. No. 4.4e+02;
RESULT 1017
ID ABQ60834 standard; cDNA; 4769 BP.
DE FLJ10898 fis clone NT2RP5003492 encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 6; Length 4769;
  Pred. No. 4.4e+02;
RESULT 1018
ID ADL46078 standard; DNA; 4911 BP.
DE Human ovarian cancer DNA marker #19968.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 5; Length 4911;
  Pred. No. 4.4e+02;
RESULT 1019
ID AAK85933 standard; DNA; 5742 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40745.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 5742;
  Pred. No. 4.7e+02;
RESULT 1020
ID ADF90748 standard; DNA; 5886 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 210.
PN JF2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 10; Length 5886;
  Pred. No. 4.7e+02;
RESULT 1021
ID AAD21947 standard; DNA; 6176 BP.
DE Zea mays alanine amino transferase (aat1) intron 9.
PN WO200175071-A1.
PD 11-OCT-2001.
PA (REGC) UNIV CALIFORNIA.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 6; Length 6176;
  Pred. No. 4.8e+02;
RESULT 1022
ID ABL26736 standard; DNA; 6883 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31681.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 6883;
  Pred. No. 5e+02;
RESULT 1023
ID AAS30639 standard; DNA; 7461 BP.
DE DNA encoding novel lung cancer antigen, Seq ID No 91.
PN WO200155300-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 7461;
  Pred. No. 5.2e+02;
RESULT 1024
ID AAS28701 standard; DNA; 7461 BP.
DE Genomic sequence #541 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 4; Length 7461;
  Pred. No. 5.2e+02;
RESULT 1025
ID ACA03402 standard; DNA; 7461 BP.
DE DNA encoding human lung cancer antigen HIPAA05.
PN US2002173454-A1.
PD 21-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 8; Length 7461;
  Pred. No. 5.2e+02;
RESULT 1026
ID ADB96750 standard; DNA; 7461 BP.
DE Novel lung cancer antigen genomic DNA #21.
PN US2003049703-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 9; Length 7461;
  Pred. No. 5.2e+02;
RESULT 1027
ID ADG41897 standard; DNA; 7461 BP.
DE Human respiratory system associated genomic DNA seq id 1135.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 10; Length 7461;
  Pred. No. 5.2e+02;
RESULT 1028
ID ADC36595 standard; DNA; 8602 BP.
DE DNA sequence of the invention #11.
PN WO2003027141-A1.
PD 03-APR-2003.
PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
PA (STAN/) STANLEY D.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 10; Length 8602;
  Pred. No. 5.4e+02;
RESULT 1029
ID ABA21227 standard; DNA; 9042 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13558.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 5; Length 9042;
  Pred. No. 5.5e+02;
RESULT 1030
ID AET42539 standard; DNA; 9137 BP.
DE Human nucleic acid-associated protein (NAAP) coding sequence #20.
PN WO2003010329-A2.
PD 06-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 8; Length 9137;
  Pred. No. 5.5e+02;
RESULT 1031
ID ABL32294 standard; DNA; 9415 BP.
DE Human immune system associated gene SEQ ID NO: 267.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match
  Best Local Similarity 10.3%; Score 28; DB 6; Length 9415;
  Pred. No. 5.6e+02;
RESULT 1032
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ID ABL322335 standard; DNA; 10528 BP.
DE Human immune system associated gene SEQ ID NO: 308.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 10528;
Best Local Similarity 48.2%; Pred. No. 5.8e+02;
RESULT 1033
ID AAS46594 standard; DNA; 13469 BP.
DE Tumour suppressor gene derived chemically modified sequence #316.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 4; Length 13469;
Best Local Similarity 56.5%; Pred. No. 6.4e+02;
RESULT 1034
ID AAV74516 standard; DNA; 16397 BP.
DE Staphylococcus aureus contig SEQ ID #205.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 2; Length 16397;
Best Local Similarity 50.8%; Pred. No. 6.9e+02;
RESULT 1035
ID ADC01147 standard; DNA; 16943 BP.
DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 1191.
PN JF200235074-A.
PD 10-DEC-2002.
PA (UVTS-) UNIV TSUKUBA.
Query Match 10.3%; Score 28; DB 10; Length 16943;
Best Local Similarity 49.3%; Pred. No. 6.9e+02;
RESULT 1036
ID ACD19153 standard; DNA; 16950 BP.
DE E. coli 0157 unique DNA sequence OZID_166.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BIAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Query Match 10.3%; Score 28; DB 9; Length 16950;
Best Local Similarity 49.3%; Pred. No. 6.9e+02;
RESULT 1037
ID ADB54177 standard; DNA; 17897 BP.
DE Pretreated genomic DNA region 101.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 10; Length 17897;
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
RESULT 1038
ID ADB54305 standard; DNA; 17897 BP.
DE Pretreated genomic DNA region 229.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 10; Length 17897;
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
RESULT 1039
ID ABL08688 standard; cDNA; 21509 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20546.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.3%; Score 28; DB 4; Length 21509;
Best Local Similarity 53.7%; Pred. No. 7.6e+02;
RESULT 1040
ID ABL34622 standard; DNA; 23683 BP.
DE Human metastasis associated gene SEQ ID NO: 175.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 10.3%; Score 28; DB 6; Length 23683;
Best Local Similarity 63.2%; Pred. No. 7.8e+02;
RESULT 1041
ID ABL70481 standard; DNA; 23683 BP.
DE Chemically treated cell signalling DNA sequence#186.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.3%; Score 28; DB 6; Length 23683;
Best Local Similarity 63.2%; Pred. No. 7.8e+02;
RESULT 1042
ID ADG98369 standard; DNA; 28313 BP.
DE Human cholesteryl ester transfer protein (CETP) gene.
Query Match 10.3%; Score 28; DB 10; Length 28313;
Best Local Similarity 60.5%; Pred. No. 8.3e+02;
RESULT 1043
ID ADF74520 standard; DNA; 28320 BP.
DE Human genomic DNA encoding the cholesteryl ester transfer protein (CETP).
PN WO2003091698-A2.
PD 06-NOV-2003.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 10.3%; Score 28; DB 10; Length 28320;
Best Local Similarity 60.5%; Pred. No. 8.3e+02;
RESULT 1044
ID AAG30638 standard; DNA; 32174 BP.
DE DNA encoding novel lung cancer antigen, Seq ID No 90.
PN WO200155300-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1045
ID AAI62606 standard; DNA; 32174 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 256.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1046
ID AAL36280 standard; DNA; 32174 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2645.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1047
ID AAL07447 standard; DNA; 32174 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10135.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1048
ID AAL03792 standard; DNA; 32174 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6480.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1049
ID AAL07491 standard; DNA; 32174 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10179.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1050
ID AAS28700 standard; DNA; 32174 BP.

DE Genomic sequence #540 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1051
ID AAS32655 standard; DNA; 32174 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 509.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1052
ID AAI62904 standard; DNA; 32174 BP.
DE Human genomic DNA SEQ ID NO 232.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1053
ID ABK72131 standard; DNA; 32174 BP.
DE Human ovarian antigen #47 genomic sequence #1.
PN WO200155329-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1054
ID ABA15665 standard; DNA; 32174 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7996.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1055
ID ABA21505 standard; DNA; 32174 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13836.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1056
ID ABA19477 standard; DNA; 32174 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11808.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1057
ID ABA20359 standard; DNA; 32174 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12690.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1058
ID AAS34394 standard; DNA; 32174 BP.
DE Human DNA for a novel foetal antigen, SEQ ID NO 1818.
PN WO200155312-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 5; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1059
ID ABK91723 standard; DNA; 32174 BP.
DE Novel ovarian related polynucleotide #32.

PN US2002045230-A1.
PD 18-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBI/) RUBIN S M.
PA (BARA/) BARASH S C.
Query Match 10.3%; Score 28; DB 6; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1060
ID ACA03401 standard; DNA; 32174 BP.
DE DNA encoding novel lung cancer antigen HIPAA05.
PN US2002173454-A1.
PD 21-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBI/) RUBIN S M.
PA (BARA/) BARASH S C.
Query Match 10.3%; Score 28; DB 8; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1061
ID ABX59268 standard; cDNA; 32174 BP.
DE CDNA encoding novel human musculoskeletal system antigen #1612.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBI/) RUBIN S M.
PA (BARA/) BARASH S C.
Query Match 10.3%; Score 28; DB 8; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1062
ID ADG41896 standard; DNA; 32174 BP.
DE Human respiratory system associated genomic DNA seq id 1134.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 9; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1063
ID ADG41896 standard; DNA; 32174 BP.
DE Human respiratory system associated genomic DNA seq id 1134.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 10; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1064
ID ADJ30018 standard; DNA; 32174 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2645.
PN US2004009489-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 12; Length 32174;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
RESULT 1065
ID AAK68883 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23695.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1066
ID AAK72925 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27737.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1067
ID AAK75870 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30682.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1068
ID AAK71499 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26311.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1069
ID AAK83538 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38350.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1070
ID AAK69604 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24416.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1071
ID AAK80325 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35137.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1072
ID AAK66361 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21173.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 4; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1073
ID AB274370 standard; DNA; 38771 BP.
DE Secreted protein gene 264 genomic fragment HPMCJ84, SEQ ID NO:1517.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 8; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1074
ID AB274036 standard; DNA; 38771 BP.
DE Secreted protein gene 165 genomic fragment HKACI79, SEQ ID NO:1183.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 8; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1075
ID AB274376 standard; DNA; 38771 BP.
DE Secreted protein gene 265 genomic fragment HPMCV30, SEQ ID NO:1523.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 8; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1076
ID ADA44358 standard; DNA; 38771 BP.
DE Human secreted protein DNA SEQ ID 551.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 8; Length 38771;

Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1077
ID ADC20853 standard; DNA; 38771 BP.
DE Human secreted protein-related DNA sequence #271.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 10; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1078
ID AB267623 standard; DNA; 38771 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1146.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 10; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1079
ID AB267941 standard; DNA; 38771 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1464.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 10; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1080
ID AB267947 standard; DNA; 38771 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1470.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 28; DB 10; Length 38771;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 1081
ID AAX83007 standard; DNA; 51259 BP.
DE Partial mouse WRN genomic sequence #3.
PN WO9724435-A1.
PD 10-JUL-1997.
PA (DARW-) DARWIN MOLECULAR CORP.
Query Match 10.3%; Score 28; DB 2; Length 51259;
Best Local Similarity 58.3%; Pred. No. 1e+03;
RESULT 1082
ID ABL61995 standard; DNA; 89328 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:332.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.3%; Score 28; DB 6; Length 89328;
Best Local Similarity 47.7%; Pred. No. 1.3e+03;
RESULT 1083
ID ADA02885 standard; DNA; 96593 BP.
DE Mouse B1m carcinoma associated gene, SEQ ID NO:1403.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28; DB 9; Length 96593;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1084
ID ADB72623 standard; DNA; 96593 BP.
DE Mouse B1m gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28; DB 10; Length 96593;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1085
ID ADM74480 standard; DNA; 96593 BP.
DE Murine carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 10.3%; Score 28; DB 12; Length 96593;

Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1086
ID ADC85364 standard; DNA; 96594 BP.
DE Human Pap coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.3%; Score 28; DB 10; Length 96594;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1087
ID AAV52850 standard; DNA; 116624 BP.
DE Human eval gene contig 4405-9480.
PN WO9832849-A2.
PD 30-JUL-1998.
PA (INSP) INST PASTEUR.
Query Match 10.3%; Score 28; DB 2; Length 116624;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
RESULT 1090
ID ADC8530 standard; DNA; 141912 BP.
DE Human GPCR gene SEQ ID NO:983.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.3%; Score 28; DB 10; Length 141912;
Best Local Similarity 45.5%; Pred. No. 1.5e+03;
RESULT 1091
ID ADP45593 standard; DNA; 147300 BP.
DE Human Rho family guanine-nucleotide exchange factor KIAA0861 gDNA.
PN WO2004047623-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.3%; Score 28; DB 12; Length 147300;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1092
ID ADQ19901 standard; DNA; 158811 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2720.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 28; DB 12; Length 158811;
Best Local Similarity 48.2%; Pred. No. 1.5e+03;
RESULT 1093
ID ASK84349 standard; cDNA; 222930 BP.
DE Human cDNA differentially expressed in granulocytic cells #920.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.3%; Score 28; DB 6; Length 222930;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1094
ID ABL87180 standard; cDNA; 311 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10158.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.2%; Score 27.8; DB 6; Length 311;
Best Local Similarity 54.4%; Pred. No. 1.9e+02;
RESULT 1095
ID ABL85170 standard; cDNA; 354 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:8148.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.2%; Score 27.8; DB 6; Length 354;
Best Local Similarity 49.7%; Pred. No. 2e+02;
RESULT 1096

ID ACH16903 standard; cDNA; 388 BP.
DE Human adult heart cDNA #1217.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.2%; Score 27.8; DB 9; Length 388;
Best Local Similarity 49.0%; Pred. No. 2e+02;
RESULT 1097
ID AA191396 standard; cDNA; 396 BP.
DE Human polynucleotide SEQ ID NO 11456.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 27.8; DB 4; Length 396;
Best Local Similarity 59.5%; Pred. No. 2.1e+02;
RESULT 1098
ID ABX36295 standard; cDNA; 411 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1460.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 10.2%; Score 27.8; DB 8; Length 411;
Best Local Similarity 51.2%; Pred. No. 2.1e+02;
RESULT 1099
ID ABX42784 standard; cDNA; 412 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7949.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 10.2%; Score 27.8; DB 8; Length 412;
Best Local Similarity 51.2%; Pred. No. 2.1e+02;
RESULT 1100
ID AA110180 standard; DNA; 467 BP.
DE Probe #113 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1101
ID ABA51813 standard; DNA; 467 BP.
DE Human foetal liver single exon nucleic acid probe #118.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1102
ID AA131430 standard; DNA; 467 BP.
DE Probe #116 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1103
ID ABA21642 standard; DNA; 467 BP.
DE Probe #108 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;

RESULT 1104
ID AAK25556 standard; DNA; 467 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 113.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1105
ID AAK00120 standard; DNA; 467 BP.
DE Human brain expressed single exon probe SEQ ID NO: 111.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1106
ID ABS25127 standard; DNA; 467 BP.
DE Human liver single exon probe, SEQ ID No 117.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1107
ID AAI00122 standard; DNA; 467 BP.
DE Probe #113 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 5; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1108
ID ABS00126 standard; DNA; 467 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 117.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 6; Length 467;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1109
ID AAI10645 standard; DNA; 478 BP.
DE Probe #578 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1110
ID ABA52292 standard; DNA; 478 BP.
DE Human foetal liver single exon nucleic acid probe #597.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1111
ID AAI31899 standard; DNA; 478 BP.
DE Probe #585 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1112
ID ABA22093 standard; DNA; 478 BP.
DE Probe #559 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1113

ID AAK26016 standard; DNA; 478 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 573.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1114
ID AAK00567 standard; DNA; 478 BP.
DE Human brain expressed single exon probe SEQ ID NO: 558.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1115
ID ABS25603 standard; DNA; 478 BP.
DE Human liver single exon probe, SEQ ID No 593.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1116
ID AAI00575 standard; DNA; 478 BP.
DE Probe #566 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 5; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1117
ID ABS00597 standard; DNA; 478 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 598.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.2%; Score 27.8; DB 6; Length 478;
Best Local Similarity 69.1%; Pred. No. 2.2e+02;
RESULT 1118
ID ACH73507 standard; DNA; 520 BP.
DE Human genome derived single exon probe #6702.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 10.2%; Score 27.8; DB 12; Length 520;
Best Local Similarity 54.4%; Pred. No. 2.3e+02;
RESULT 1119
ID ADI71999 standard; DNA; 549 BP.
DE Human ovarian cancer DNA marker #4741.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.2%; Score 27.8; DB 5; Length 549;
Best Local Similarity 54.4%; Pred. No. 2.3e+02;
RESULT 1120
ID ADL37148 standard; DNA; 549 BP.
DE Human ovarian cancer DNA marker #11038.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.2%; Score 27.8; DB 5; Length 549;
Best Local Similarity 54.4%; Pred. No. 2.3e+02;
RESULT 1121
ID ADL43532 standard; DNA; 580 BP.
DE Human ovarian cancer DNA marker #17422.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.2%; Score 27.8; DB 5; Length 580;
Best Local Similarity 54.4%; Pred. No. 2.4e+02;

RESULT 1122
ID ABQ45590 standard; DNA; 602 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 32181.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 602;
Best Local Similarity 53.2%; Pred. No. 2.4e+02;
RESULT 1123
ID ABQ45591 standard; DNA; 602 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 32182.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 602;
Best Local Similarity 53.2%; Pred. No. 2.4e+02;
RESULT 1124
ID AAF76057 standard; DNA; 609 BP.
DE Enterococcus faecium vanXD gene, SEQ ID NO:39.
PN WO200112803-A2.
PD 22-FEB-2001.
PA (BETH-) BETH ISRAEL DRACONESS MEDICAL CENT.
Query Match 10.2%; Score 27.8; DB 4; Length 609;
Best Local Similarity 52.1%; Pred. No. 2.4e+02;
RESULT 1125
ID AAX20759 standard; DNA; 656 BP.
DE Polynucleotide sequence from the genome of Treponema pallidum.
PN WO9859034-A2.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.2%; Score 27.8; DB 2; Length 656;
Best Local Similarity 54.4%; Pred. No. 2.5e+02;
RESULT 1126
ID AAS69573 standard; cDNA; 682 BP.
DE DNA encoding novel human diagnostic protein #5377.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSSEQ INC.
Query Match 10.2%; Score 27.8; DB 5; Length 682;
Best Local Similarity 53.2%; Pred. No. 2.5e+02;
RESULT 1127
ID AAZ77517 standard; cDNA; 701 BP.
DE Human ovarian tumor cDNA library derived EST fragment 68.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.2%; Score 27.8; DB 2; Length 701;
Best Local Similarity 48.4%; Pred. No. 2.5e+02;
RESULT 1128
ID ABN67226 standard; DNA; 1029 BP.
DE Streptococcus polynucleotide SEQ ID NO 2365.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 10.2%; Score 27.8; DB 6; Length 1029;
Best Local Similarity 57.5%; Pred. No. 2.9e+02;
RESULT 1129
ID AAC67659 standard; cDNA; 1099 BP.
DE Human secreted protein cDNA sequence #29.
PN WO200058355-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.2%; Score 27.8; DB 3; Length 1099;
Best Local Similarity 50.4%; Pred. No. 3e+02;
RESULT 1130
ID ACA27997 standard; DNA; 1194 BP.
DE Prokaryotic essential gene #9654.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.2%; Score 27.8; DB 8; Length 1194;
Best Local Similarity 47.0%; Pred. No. 3.1e+02;

RESULT 1131
ID ABX17903 standard; cDNA; 1276 BP.
DE cDNA encoding human G-protein coupled receptor GCRC-57.
PN WO200279448-A2.
PD 10-OCT-2002.
PA (INGV-) INCYTE GENOMICS INC.
Query Match 10.2%; Score 27.8; DB 10; Length 1276;
Best Local Similarity 47.9%; Pred. No. 3.1e+02;
RESULT 1132
ID ADC86320 standard; DNA; 1342 BP.
DE Human GPCR gene SEQ ID NO:773.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 10.2%; Score 27.8; DB 10; Length 1342;
Best Local Similarity 47.9%; Pred. No. 3.2e+02;
RESULT 1133
ID ABX71384 standard; cDNA; 1613 BP.
DE Human testes-derived cDNA from clone DKF2phtes3_2g7.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 10.2%; Score 27.8; DB 5; Length 1613;
Best Local Similarity 53.2%; Pred. No. 3.4e+02;
RESULT 1134
ID AAQ25532 standard; DNA; 1648 BP.
DE Sequence of genomic clone contg. the entire Histidine-rich protein
DE (HISRP) gene.
PN US5116965-A.
PD 26-MAY-1992.
PA (SLOK) SLOAN KETTERING INST CANCER.
Query Match 10.2%; Score 27.8; DB 2; Length 1648;
Best Local Similarity 54.4%; Pred. No. 3.5e+02;
RESULT 1135
ID ADP04618 standard; cDNA; 1707 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 213.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 10.2%; Score 27.8; DB 12; Length 1707;
Best Local Similarity 51.2%; Pred. No. 3.5e+02;
RESULT 1136
ID ABQ67836 standard; DNA; 1716 BP.
DE Listeria innocua DNA sequence #638.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.2%; Score 27.8; DB 6; Length 1716;
Best Local Similarity 65.1%; Pred. No. 3.5e+02;
RESULT 1137
ID ADB63282 standard; cDNA; 1803 BP.
DE Human cDNA encoding clone TESTI2004990.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.2%; Score 27.8; DB 10; Length 1803;
Best Local Similarity 53.2%; Pred. No. 3.6e+02;
RESULT 1138
ID AAH28330 standard; DNA; 2370 BP.
DE Nucleotide sequence of a bacterial surface array protein (SAP).
PN WO200149823-A2.
PD 12-JUL-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
Query Match 10.2%; Score 27.8; DB 4; Length 2370;
Best Local Similarity 53.2%; Pred. No. 3.9e+02;
RESULT 1139
ID ABS76421 standard; cDNA; 2611 BP.
DE cDNA encoding human ovarian cancer marker M445.
PN WO200271928-A2.
PD 19-SEP-2002.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.2%; Score 27.8; DB 6; Length 2611;
Best Local Similarity 50.4%; Pred. No. 4.1e+02;
RESULT 1140
ID ABL29192 standard; DNA; 2660 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.2%; Score 27.8; DB 4; Length 2660;
Best Local Similarity 59.5%; Pred. No. 4.1e+02;
RESULT 1141
ID ABL92329 standard; DNA; 2872 BP.
DE Chemically treated DNA repair gene fragment complementary to #69.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 2872;
Best Local Similarity 59.5%; Pred. No. 4.2e+02;
RESULT 1142
ID ABL49392 standard; DNA; 2872 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 92.
PN WO20017377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 2872;
Best Local Similarity 59.5%; Pred. No. 4.2e+02;
RESULT 1143
ID ADD01140 standard; cDNA; 3190 BP.
DE Human signal transducer kinase 22.55 encoding cDNA #SEQ ID 1.
PN CN1381571-A.
PD 27-NOV-2002.
PA (BICOW-) BICOW WINDOW GENE DEV INC SHANGHAI.
Query Match 10.2%; Score 27.8; DB 10; Length 3190;
Best Local Similarity 53.2%; Pred. No. 4.4e+02;
RESULT 1144
ID ABL32171 standard; DNA; 3973 BP.
DE Human immune system associated gene SEQ ID NO: 144.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 3973;
Best Local Similarity 53.2%; Pred. No. 4.7e+02;
RESULT 1145
ID ADJ67448 standard; DNA; 4257 BP.
DE Human ovarian specific gene SEQ ID NO:162.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 10.2%; Score 27.8; DB 12; Length 4257;
Best Local Similarity 51.2%; Pred. No. 4.9e+02;
RESULT 1146
ID AAF85149 standard; DNA; 4790 BP.
DE DNA encoding a disvelled associated kinase (DAK) isoform DAKb.
PN WO200125408-A1.
PD 12-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 10.2%; Score 27.8; DB 4; Length 4790;
Best Local Similarity 50.4%; Pred. No. 5.1e+02;
RESULT 1147
ID ADD48702 standard; DNA; 4933 BP.
DE Rat gene M64793, SEQ ID NO 14411.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.2%; Score 27.8; DB 10; Length 4933;
Best Local Similarity 47.0%; Pred. No. 5.1e+02;
RESULT 1148
ID ADD47239 standard; DNA; 4933 BP.
DE Rat gene M64793, SEQ ID NO 12933.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.2%; Score 27.8; DB 10; Length 4933;
Best Local Similarity 47.0%; Pred. No. 5.1e+02;
RESULT 1149
ID AAF76022 standard; DNA; 5781 BP.
DE E. faecium VanD vancomycin resistance gene cluster, SEQ ID NO:4.
PN WO200112803-A2.
PD 22-FEB-2001.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match 10.2%; Score 27.8; DB 4; Length 5781;
Best Local Similarity 52.1%; Pred. No. 5.4e+02;
RESULT 1150
ID AB258670 standard; DNA; 5829 BP.
DE Human KCNMA gene related DNA (GenBank Identifier No. GI#7914977).
PN WO200299058-A2.
PD 12-DEC-2002.
PA (EXBL-) EXELIXIS INC.
Query Match 10.2%; Score 27.8; DB 9; Length 5829;
Best Local Similarity 57.5%; Pred. No. 5.4e+02;
RESULT 1151
ID ABL32757 standard; DNA; 5945 BP.
DE Human immune system associated gene SEQ ID NO: 730.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 5945;
Best Local Similarity 51.2%; Pred. No. 5.5e+02;
RESULT 1152
ID ADF90711 standard; DNA; 6115 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 173.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 10.2%; Score 27.8; DB 10; Length 6115;
Best Local Similarity 51.2%; Pred. No. 5.5e+02;
RESULT 1153
ID ABK31391 standard; DNA; 6226 BP.
DE Signal transduction associated gene modified complementary DNA #117.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 6226;
Best Local Similarity 62.0%; Pred. No. 5.6e+02;
RESULT 1154
ID ABL70338 standard; DNA; 6226 BP.
DE Chemically treated cell signalling DNA sequence complementary to #114.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 6226;
Best Local Similarity 62.0%; Pred. No. 5.6e+02;
RESULT 1155
ID AAS61293 standard; DNA; 6226 BP.
DE Human gene regulation-associated gene oligonucleotide #248.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 6226;
Best Local Similarity 62.0%; Pred. No. 5.6e+02;
RESULT 1156
ID AAS46618 standard; DNA; 6863 BP.
DE Tumour suppressor gene derived chemically modified sequence #340.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 4; Length 6863;
Best Local Similarity 50.4%; Pred. No. 5.8e+02;
RESULT 1157
ID AAS45367 standard; DNA; 8842 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #36.
PN WO200168911-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 4; Length 8842;
Best Local Similarity 55.8%; Pred. No. 6.3e+02;
RESULT 1158
ID ABK28204 standard; DNA; 8842 BP.
DE DNA transcription associated complementary genomic DNA #39.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 8842;
Best Local Similarity 55.8%; Pred. No. 6.3e+02;
RESULT 1159
ID AAS45377 standard; DNA; 9091 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #41.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 4; Length 9091;
Best Local Similarity 57.5%; Pred. No. 6.4e+02;
RESULT 1160
ID ABK28214 standard; DNA; 9091 BP.
DE DNA transcription associated complementary genomic DNA #44.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 9091;
Best Local Similarity 57.5%; Pred. No. 6.4e+02;
RESULT 1161
ID AAK69092 standard; DNA; 9454 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23904.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.2%; Score 27.8; DB 4; Length 9454;
Best Local Similarity 57.5%; Pred. No. 6.5e+02;
RESULT 1162
ID ABO67046 standard; DNA; 10254 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 76.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 10254;
Best Local Similarity 53.2%; Pred. No. 6.7e+02;
RESULT 1163
ID ABZ68481 standard; DNA; 11029 BP.
DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.
PN WO200281511-A1.
PD 17-OCT-2002.
PA (INSP) INST PASTEUR.
PA (KIMR-) KIMRON VETERINARY INST.
Query Match 10.2%; Score 27.8; DB 8; Length 11029;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1164
ID ABV74821 standard; DNA; 11029 BP.
DE West Nile virus strain NY99-flamingo 382-99 complete genome.
PN WO200281741-A2.
PD 17-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.2%; Score 27.8; DB 10; Length 11029;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1165
ID AAD63517 standard; DNA; 13894 BP.
DE Mycoplasma genitalium chaperone gene.
PN US2003138777-A1.
PD 24-JUL-2003.
PA (EVAN/) EVANS G A.
Query Match 10.2%; Score 27.8; DB 10; Length 13894;
Best Local Similarity 49.7%; Pred. No. 7.5e+02;
RESULT 1166
ID ACC69147 standard; DNA; 13894 BP.
DE M. genitalium polypeptide chaperone gene cassette DNA SEQ ID NO:15.
PN WO2003025145-A2.

PD 27-MAR-2003.
PA (EGEA-) EGEA BIOSCIENCES INC.
Query Match 10.2%; Score 27.8; DB 10; Length 13894;
Best Local Similarity 49.7%; Pred. No. 7.5e+02;
RESULT 1167
ID ADN48952 standard; DNA; 13894 BP.
DE Mycoplasma genitalium functional gene fragment #15.
PN US2004063097-A1.
PD 01-APR-2004.
PA (EVAN/) EVANS G A.
Query Match 10.2%; Score 27.8; DB 12; Length 13894;
Best Local Similarity 49.7%; Pred. No. 7.5e+02;
RESULT 1168
ID RAH48024 standard; DNA; 14041 BP.
DE Internal control B19c #1.
PN WO200146463-A2.
PD 28-JUN-2001.
PA (BAXT) BAXTER AG.
Query Match 10.2%; Score 27.8; DB 4; Length 14041;
Best Local Similarity 18.3%; Pred. No. 7.5e+02;
RESULT 1169
ID ABL33194 standard; DNA; 14861 BP.
DE Human immune system associated gene SEQ ID NO: 1167.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 14861;
Best Local Similarity 57.5%; Pred. No. 7.6e+02;
RESULT 1170
ID ABL70553 standard; DNA; 14861 BP.
DE Chemically treated cell signalling DNA sequence#222.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 14861;
Best Local Similarity 57.5%; Pred. No. 7.6e+02;
RESULT 1171
ID AAS61202 standard; DNA; 14861 BP.
DE Human gene regulation-associated gene oligonucleotide #157.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 14861;
Best Local Similarity 57.5%; Pred. No. 7.6e+02;
RESULT 1172
ID AAS45389 standard; DNA; 15732 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #47.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 4; Length 15732;
Best Local Similarity 57.5%; Pred. No. 7.8e+02;
RESULT 1173
ID ABK28234 standard; DNA; 15732 BP.
DE DNA transcription associated complementary genomic DNA #54.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.2%; Score 27.8; DB 6; Length 15732;
Best Local Similarity 57.5%; Pred. No. 7.8e+02;
RESULT 1174
ID AAK69093 standard; DNA; 16920 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23905.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.2%; Score 27.8; DB 4; Length 16920;
Best Local Similarity 57.5%; Pred. No. 8e+02;
RESULT 1175
ID AAX13065 standard; DNA; 32768 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:128.
PN WO9850555-A2.
PD 12-NOV-1998.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.2%; Score 27.8; DB 2; Length 32768;
Best Local Similarity 49.7%; Pred. No. 1e+03;
RESULT 1176
ID ABS98860 standard; DNA; 32768 BP.
DE Enterococcus faecalis contig sequence #128.
FN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 10.2%; Score 27.8; DB 6; Length 32768;
Best Local Similarity 49.7%; Pred. No. 1e+03;
RESULT 1177
ID ADC87687 standard; DNA; 50000 BP.
DE Human mammalian target of rapamycin genomic fragment #32.
FN WO2003048360-A1.
PD 12-JUN-2003.
PA (NFWI-) NEW IND RES ORG.
Best Local Similarity 62.0%; Pred. No. 1.2e+03;
RESULT 1178
ID ADA02753 standard; DNA; 54355 BP.
DE Mouse Morf carcinoma associated Gene, SEQ ID NO:1271.
FN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.2%; Score 27.8; DB 9; Length 54355;
Best Local Similarity 57.5%; Pred. No. 1.2e+03;
RESULT 1179
ID ADB72491 standard; DNA; 54355 BP.
DE Mouse Morf gene.
FN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.2%; Score 27.8; DB 10; Length 54355;
Best Local Similarity 57.5%; Pred. No. 1.2e+03;
RESULT 1180
ID ADC85233 standard; DNA; 54355 BP.
DE Mouse Morf genomic sequence.
FN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.2%; Score 27.8; DB 10; Length 54355;
Best Local Similarity 57.5%; Pred. No. 1.2e+03;
RESULT 1181
ID ADM74348 standard; DNA; 54355 BP.
DE Murine carcinoma associated (CA) nucleic acid #10.
FN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 10.2%; Score 27.8; DB 12; Length 54355;
Best Local Similarity 57.5%; Pred. No. 1.2e+03;
RESULT 1182
ID ABE87050 standard; cDNA; 66804 BP.
DE Human transporter protein genomic DNA.
Query Match 10.2%; Score 27.8; DB 6; Length 66804;
Best Local Similarity 54.4%; Pred. No. 1.3e+03;
RESULT 1183
ID ADG88330 standard; DNA; 66804 BP.
DE Human transporter protein genomic DNA.
Query Match 10.2%; Score 27.8; DB 10; Length 66804;
Best Local Similarity 54.4%; Pred. No. 1.3e+03;
RESULT 1184
ID ABG69244 standard; DNA; 81905 BP.
DE Listeria innocua DNA sequence #683.
FN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.2%; Score 27.8; DB 6; Length 81905;
Best Local Similarity 65.1%; Pred. No. 1.4e+03;
RESULT 1185
ID AB067198 standard; DNA; 82689 BP.
DE Listeria innocua plasmid DNA sequence.
FN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 10.2%; Score 27.8; DB 6; Length 82689;
Best Local Similarity 65.1%; Pred. No. 1.4e+03;
RESULT 1186
ID ADE82948 standard; DNA; 167163 BP.
DE Human PVT1 genomic DNA sequence.
FN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.2%; Score 27.8; DB 10; Length 167163;
Best Local Similarity 52.1%; Pred. No. 1.8e+03;
RESULT 1187
ID ADL13643 standard; DNA; 170170 BP.
DE Osteoarthritis-associated polymorphic nucleotide #175.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.2%; Score 27.8; DB 10; Length 170170;
Best Local Similarity 49.7%; Pred. No. 1.8e+03;
RESULT 1188
ID ADL13809 standard; DNA; 214019 BP.
DE Osteoarthritis-associated polymorphic nucleotide #341.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.2%; Score 27.8; DB 10; Length 214019;
Best Local Similarity 69.1%; Pred. No. 1.9e+03;
RESULT 1189
ID ADS9207 standard; DNA; 262090 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:44.
FN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 10.2%; Score 27.8; DB 12; Length 262090;
Best Local Similarity 51.2%; Pred. No. 2e+03;
RESULT 1190
ID ADP75188 standard; DNA; 276820 BP.
DE Human ADAMTS2 gene.
FN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.2%; Score 27.8; DB 11; Length 276820;
Best Local Similarity 50.4%; Pred. No. 2.1e+03;
RESULT 1191
ID ABV59670 standard; cDNA; 282 BP.
DE Human prostate expression marker cDNA 59661.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.1%; Score 27.6; DB 5; Length 282;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
RESULT 1192
ID ABV59998 standard; cDNA; 294 BP.
DE Human prostate expression marker cDNA 59989.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.1%; Score 27.6; DB 5; Length 294;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
RESULT 1193
ID ADE10825 standard; DNA; 417 BP.
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:4237.
FN WO2003048304-A2.
PD 12-JUN-2003.

PA (AMHP) WYETH HOLDINGS CORP.
Query Match 10.1%; Score 27.6; DB 9; Length 417;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
RESULT 1194
ID AAI13242 standard; DNA; 436 BP.
DE Probe #3175 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1195
ID ABA54939 standard; DNA; 436 BP.
DE Human foetal liver single exon nucleic acid probe #3244.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1196
ID AAI34594 standard; DNA; 436 BP.
DE Probe #3280 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1197
ID ABA44498 standard; DNA; 436 BP.
DE Human breast cell single exon nucleic acid probe #3193.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1198
ID ABA24706 standard; DNA; 436 BP.
DE Probe #3172 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1199
ID AAK28665 standard; DNA; 436 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 3222.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1200
ID AAK03212 standard; DNA; 436 BP.
DE Human brain expressed single exon probe SEQ ID NO: 3203.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1201
ID ABA28264 standard; DNA; 436 BP.
DE Human liver single exon probe, SEQ ID No 3254.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1202
ID AAI03145 standard; DNA; 436 BP.
DE Probe #3136 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 10.1%; Score 27.6; DB 5; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1203
ID ABS03176 standard; DNA; 436 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 3167.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 6; Length 436;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
RESULT 1204
ID AAI15582 standard; DNA; 448 BP.
DE Probe #5515 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1205
ID ABA57534 standard; DNA; 448 BP.
DE Human foetal liver single exon nucleic acid probe #5839.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1206
ID AAI37089 standard; DNA; 448 BP.
DE Probe #5775 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1207
ID ABA27005 standard; DNA; 448 BP.
DE Probe #5471 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1208
ID AAK31184 standard; DNA; 448 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 5741.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1209
ID AAK05581 standard; DNA; 448 BP.
DE Human brain expressed single exon probe SEQ ID NO: 5572.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1210
ID ABS30865 standard; DNA; 448 BP.
DE Human liver single exon probe, SEQ ID No 5855.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 448;
Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1211
ID ABS05936 standard; DNA; 448 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 5927.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.1%; Score 27.6; DB 6; Length 448;

Best Local Similarity 55.1%; Pred. No. 2.5e+02;
RESULT 1212
ID ACH28744 standard; cDNA; 472 BP.
DE Human adult ovary cDNA #7124.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.1%; Score 27.6; DB 9; Length 472;
Best Local Similarity 56.7%; Pred. No. 2.5e+02;
RESULT 1213
ID AB058582 standard; cDNA; 474 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:2277.
FN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 10.1%; Score 27.6; DB 6; Length 474;
Best Local Similarity 51.9%; Pred. No. 2.5e+02;
RESULT 1214
ID ADQ20676 standard; DNA; 481 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3496.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.1%; Score 27.6; DB 12; Length 481;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 1215
ID ABV56711 standard; cDNA; 516 BP.
DE Human prostate expression marker cDNA 56702.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.1%; Score 27.6; DB 5; Length 516;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
RESULT 1216
ID AD024652 standard; DNA; 584 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7472.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.1%; Score 27.6; DB 12; Length 584;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
RESULT 1217
ID AA505961 standard; cDNA; 801 BP.
DE Degenerate cDNA sequence for human UMLR variant #2.
FN WO200130850-A1.
PD 03-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 801;
Best Local Similarity 22.6%; Pred. No. 3.1e+02;
RESULT 1218
ID AAH53802 standard; DNA; 888 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2997.
FN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.1%; Score 27.6; DB 4; Length 888;
Best Local Similarity 50.8%; Pred. No. 3.2e+02;
RESULT 1219
ID AA505960 standard; cDNA; 891 BP.
DE Degenerate cDNA sequence for human UMLR variant #1.
FN WO200130850-A1.
PD 03-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.1%; Score 27.6; DB 4; Length 891;
Best Local Similarity 22.6%; Pred. No. 3.2e+02;
RESULT 1220
ID AAC64074 standard; cDNA; 972 BP.
DE Mouse ion channel protein KCNE3 (MiRP2) cDNA, SEQ ID NO:7.
FN WO200063434-A1.

PD 26-OCT-2000.
PA (UTAH) UNIV UTAH RES FOUND.
PA (UYIA) UNIV YALE.
Query Match 10.1%; Score 27.6; DB 3; Length 972;
Best Local Similarity 50.8%; Pred. No. 3.3e+02;
RESULT 1221
ID ABA77081 standard; DNA; 1014 BP.
DE Proliferative glomerular nephritis-associated gene sequence SEQ ID:88.
FN WO200173022-A1.
PD 04-OCT-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 10.1%; Score 27.6; DB 4; Length 1014;
Best Local Similarity 50.4%; Pred. No. 3.3e+02;
RESULT 1222
ID AAC74251 standard; cDNA; 1034 BP.
DE Human secreted protein gene 29 SEQ ID NO:39.
FN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 27.6; DB 3; Length 1034;
Best Local Similarity 51.6%; Pred. No. 3.4e+02;
RESULT 1223
ID ADJ92292 standard; cDNA; 1044 BP.
DE Mouse hair keratin-associated-protein encoding cDNA SEQ ID NO:151.
FN WO2003042387-A1.
PD 22-MAY-2003.
PA (UYKE-) UNIV KEIO.
PA (NIPR-) JAPAN SOC PROMOTION SCI.
Query Match 10.1%; Score 27.6; DB 10; Length 1044;
Best Local Similarity 51.6%; Pred. No. 3.4e+02;
RESULT 1224
ID AAS90615 standard; cDNA; 1192 BP.
DE DNA encoding novel human diagnostic protein #26419.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 27.6; DB 5; Length 1192;
Best Local Similarity 49.3%; Pred. No. 3.5e+02;
RESULT 1225
ID AA41312 standard; cDNA; 1315 BP.
DE Human normal ovarian tissue derived cDNA 91.
FN DE19816395-A1.
PD 07-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.1%; Score 27.6; DB 2; Length 1315;
Best Local Similarity 56.7%; Pred. No. 3.7e+02;
RESULT 1226
ID ADA29218 standard; DNA; 1338 BP.
DE DNA encoding Acinetobacter baumannii protein #505.
FN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.1%; Score 27.6; DB 9; Length 1338;
Best Local Similarity 56.7%; Pred. No. 3.7e+02;
RESULT 1227
ID AAL62038 standard; cDNA; 1531 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-26 cDNA.
FN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.1%; Score 27.6; DB 9; Length 1531;
Best Local Similarity 51.6%; Pred. No. 3.9e+02;
RESULT 1228
ID AAF71473 standard; DNA; 1575 BP.
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:227.
FN WO200100844-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 10.1%; Score 27.6; DB 4; Length 1575;
Best Local Similarity 56.7%; Pred. No. 3.9e+02;
RESULT 1229
ID AAA37673 standard; DNA; 1731 BP.
DE Human peptidase, HPEP-17 coding sequence.

PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCYTE-) INCYTE PHARM INC.
Query Match 10.1%; Score 27.6; DB 3; Length 1731;
Best Local Similarity 51.6%; Pred. No. 4.1e+02;
RESULT 1230
ID AAZ77455 standard; cDNA; 2809 BP.
DE Human ovarian tumor cDNA library derived EST fragment 6.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.1%; Score 27.6; DB 2; Length 2809;
Best Local Similarity 56.2%; Pred. No. 4.8e+02;
RESULT 1231
ID AAF21851 standard; DNA; 3039 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 238.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 27.6; DB 3; Length 3039;
Best Local Similarity 56.7%; Pred. No. 5e+02;
RESULT 1232
ID AAH54212 standard; DNA; 3043 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3576.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.1%; Score 27.6; DB 4; Length 3043;
Best Local Similarity 50.8%; Pred. No. 5e+02;
RESULT 1233
ID AAH54724 standard; DNA; 3214 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4088.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.1%; Score 27.6; DB 4; Length 3214;
Best Local Similarity 50.8%; Pred. No. 5.1e+02;
RESULT 1234
ID ABT13431 standard; DNA; 3361 BP.
DE Breast specific related polynucleotide SEQ ID No 146.
PN WO200277232-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 10.1%; Score 27.6; DB 8; Length 3361;
Best Local Similarity 52.8%; Pred. No. 5.2e+02;
RESULT 1235
ID AAH54954 standard; DNA; 3417 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4318.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.1%; Score 27.6; DB 4; Length 3417;
Best Local Similarity 50.8%; Pred. No. 5.2e+02;
RESULT 1236
ID ABA15591 standard; DNA; 3515 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7922.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 27.6; DB 5; Length 3515;
Best Local Similarity 53.8%; Pred. No. 5.2e+02;
RESULT 1237
ID AAH29796 standard; DNA; 4265 BP.
DE S. cerevisiae apoptosis associated coding sequence YJL190C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANGSEN PHARM NV.
Query Match 10.1%; Score 27.6; DB 4; Length 4265;
Best Local Similarity 72.0%; Pred. No. 5.6e+02;
RESULT 1238
ID ACF25352 standard; DNA; 4459 BP.
DE Human dihydropyrimidinase-related protein gene.
PN EP1284298-A2.

PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 10.1%; Score 27.6; DB 9; Length 4459;
Best Local Similarity 56.7%; Pred. No. 5.7e+02;
RESULT 1239
ID ADC66333 standard; DNA; 4459 BP.
DE Human collapsin response mediator protein 2 gene 3' UTR sequence.
PN WO2003040320-A2.
PD 15-MAY-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 10.1%; Score 27.6; DB 10; Length 4459;
Best Local Similarity 56.7%; Pred. No. 5.7e+02;
RESULT 1240
ID AAC75103 standard; cDNA; 5245 BP.
DE Human ORFX ORF58 polynucleotide sequence SEQ ID NO:1315.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 27.6; DB 3; Length 5245;
Best Local Similarity 49.3%; Pred. No. 6.1e+02;
RESULT 1241
ID ABL32151 standard; DNA; 5276 BP.
DE Human immune system associated gene SEQ ID NO: 124.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 5276;
Best Local Similarity 55.1%; Pred. No. 6.1e+02;
RESULT 1242
ID AAK51871 standard; cDNA; 5376 BP.
DE Human polynucleotide SEQ ID NO 416.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 27.6; DB 4; Length 5376;
Best Local Similarity 51.6%; Pred. No. 6.1e+02;
RESULT 1243
ID AAK52855 standard; cDNA; 5378 BP.
DE Human polynucleotide SEQ ID NO 2384.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 27.6; DB 4; Length 5378;
Best Local Similarity 51.6%; Pred. No. 6.1e+02;
RESULT 1244
ID AAI99536 standard; DNA; 5690 BP.
DE Human polynucleotide SEQ ID NO 54.
PN WO200155173-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 27.6; DB 4; Length 5690;
Best Local Similarity 63.6%; Pred. No. 6.2e+02;
RESULT 1245
ID ABL32182 standard; DNA; 5763 BP.
DE Human immune system associated gene SEQ ID NO: 155.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 5763;
Best Local Similarity 49.3%; Pred. No. 6.3e+02;
RESULT 1246
ID ABK31540 standard; DNA; 6045 BP.
DE Signal transduction associated gene modified DNA #192.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 6045;
Best Local Similarity 53.8%; Pred. No. 6.4e+02;
RESULT 1247
ID ABL70623 standard; DNA; 6045 BP.
DE Chemically treated cell signalling DNA sequence#257.
PN WO200202807-A2.
PD 10-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 6045;
Best Local Similarity 53.8%; Pred. No. 6.4e+02;
RESULT 1248
ID AB210205 standard; DNA; 6289 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #345.
PN WC200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 8; Length 6289;
Best Local Similarity 52.6%; Pred. No. 6.5e+02;
RESULT 1249
ID ADM79326 standard; cDNA; 6539 BP.
DE Mouse lymphoma associated, LA, contig #4.
PN US2003224460-A1.
PD 04-DEC-2003.
PA (PEDE/) PEDERSEN F S.
PA (SORE/) SORENSEN A B.
PA (HERN/) HERNANDEZ J M.
PA (NIEL/) NIELSEN A A.
PA (MOVI/) MOVING H.
Query Match 10.1%; Score 27.6; DB 12; Length 6539;
Best Local Similarity 56.7%; Pred. No. 6.6e+02;
RESULT 1250
ID ABK72272 standard; DNA; 6543 BP.
DE Lymphoma associated polynucleotide #131.
PN WC200224867-A2.
PD 28-MAR-2002.
PA (UYAA-) UNIV AARHUS.
Query Match 10.1%; Score 27.6; DB 6; Length 6543;
Best Local Similarity 56.7%; Pred. No. 6.6e+02;
RESULT 1251
ID ABL33764 standard; DNA; 6876 BP.
DE Human immune system associated gene SEQ ID NO: 1737.
PN WC200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 6876;
Best Local Similarity 55.1%; Pred. No. 6.7e+02;
RESULT 1252
ID ABL32982 standard; DNA; 7143 BP.
DE Human immune system associated gene SEQ ID NO: 955.
PN WC200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 7143;
Best Local Similarity 51.6%; Pred. No. 6.8e+02;
RESULT 1253
ID AAS45447 standard; DNA; 7934 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #76.
PN WC200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 4; Length 7934;
Best Local Similarity 58.5%; Pred. No. 7e+02;
RESULT 1254
ID ABK28296 standard; DNA; 7934 BP.
DE DNA transfection associated complementary genomic DNA #85.
PN WC200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 7934;
Best Local Similarity 58.5%; Pred. No. 7e+02;
RESULT 1255
ID AAS61344 standard; DNA; 7934 BP.
DE Human gene regulation-associated gene oligonucleotide #299.
PN WC200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 7934;
Best Local Similarity 58.5%; Pred. No. 7e+02;
RESULT 1256
ID ADB84197 standard; DNA; 9289 BP.

DE Human lymphoid cell proliferative disorder gene derived DNA #133.
PN WC2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 10; Length 9289;
Best Local Similarity 52.6%; Pred. No. 7.4e+02;
RESULT 1257
ID AAS1008 standard; DNA; 9465 BP.
DE Simian immunodeficiency virus SIVrcm.
PN WC200034529-A1.
PD 15-JUN-2000.
PA (UABR-) UAB RES FOUND.
Query Match 10.1%; Score 27.6; DB 3; Length 9465;
Best Local Similarity 46.4%; Pred. No. 7.5e+02;
RESULT 1258
ID AAZ49991 standard; DNA; 10594 BP.
DE Plasmid pGN205 for inhibition of unc-22 expression in C. elegans.
PN WC200001846-A2.
PD 13-JAN-2000.
PA (DEVG-) DEVGEN NV.
Query Match 10.1%; Score 27.6; DB 3; Length 10594;
Best Local Similarity 53.8%; Pred. No. 7.8e+02;
RESULT 1259
ID AAZ49992 standard; DNA; 10598 BP.
DE Plasmid pGN207 for inhibition of unc-22 expression in C. elegans.
PN WC200001846-A2.
PD 13-JAN-2000.
PA (DEVG-) DEVGEN NV.
Query Match 10.1%; Score 27.6; DB 3; Length 10598;
Best Local Similarity 53.8%; Pred. No. 7.8e+02;
RESULT 1260
ID AAK81507 standard; DNA; 11718 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36319.
PN WC200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 27.6; DB 4; Length 11718;
Best Local Similarity 52.6%; Pred. No. 8.1e+02;
RESULT 1261
ID AAZ49998 standard; DNA; 12494 BP.
DE Plasmid pGN110 for expression of T7 RNA polymerase in C. elegans.
PN WC200001846-A2.
PD 13-JAN-2000.
PA (DEVG-) DEVGEN NV.
Query Match 10.1%; Score 27.6; DB 3; Length 12494;
Best Local Similarity 53.8%; Pred. No. 8.3e+02;
RESULT 1262
ID ABL34141 standard; DNA; 15698 BP.
DE Human immune system associated gene SEQ ID NO: 2114.
PN WC200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 15698;
Best Local Similarity 50.0%; Pred. No. 9e+02;
RESULT 1263
ID ABL32261 standard; DNA; 15881 BP.
DE Human immune system associated gene SEQ ID NO: 234.
PN WC200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 15881;
Best Local Similarity 53.8%; Pred. No. 9e+02;
RESULT 1264
ID ABK31183 standard; DNA; 15881 BP.
DE Signal transduction associated gene modified complementary DNA #13.
PN WC200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 15881;
Best Local Similarity 53.8%; Pred. No. 9e+02;
RESULT 1265
ID ABL70144 standard; DNA; 15881 BP.
DE Chemically treated cell signalling DNA sequence complementary to #17.

PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 15881;
Best Local Similarity 53.8%; Pred. No. 9e+02;
RESULT 1266
ID AAS61070 standard; DNA; 15881 BP.
DE Human gene regulation-associated gene oligonucleotide #25.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 15881;
Best Local Similarity 53.8%; Pred. No. 9e+02;
RESULT 1267
ID ABL32767 standard; DNA; 19659 BP.
DE Human immune system associated gene SEQ ID NO: 740.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 19659;
Best Local Similarity 53.8%; Pred. No. 9.8e+02;
RESULT 1268
ID ABQ67073 standard; DNA; 20579 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 103.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.1%; Score 27.6; DB 6; Length 20579;
Best Local Similarity 51.6%; Pred. No. 9.9e+02;
RESULT 1269
ID ABO67191 standard; DNA; 33146 BP.
DE Listeria innocua contig DNA sequence #4.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
Query Match 10.1%; Score 27.6; DB 6; Length 33146;
Best Local Similarity 48.1%; Pred. No. 1.2e+03;
RESULT 1270
ID ADL27146 standard; DNA; 96593 BP.
DE Human genomic sequence for PPP3CC.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 10.1%; Score 27.6; DB 11; Length 96593;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1271
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 9; Length 96595;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1272
ID ADB72806 standard; DNA; 96595 BP.
DE Human PPP3CC gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 10; Length 96595;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1273
ID ADA66352 standard; DNA; 96596 BP.
DE Human PPP3CC gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 9; Length 96596;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1274
ID ABS54549 standard; DNA; 98472 BP.

DE Human multidrug resistance associated protein gene associated sequence.
PN WO200257410-A2.
PD 25-JUL-2002.
PA (DNAS-) DNA SCI LAB INC.
Query Match 10.1%; Score 27.6; DB 6; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1275
ID ACF62745 standard; DNA; 98472 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:673.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 27.6; DB 8; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1276
ID ADB20860 standard; DNA; 98472 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:673.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 27.6; DB 8; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1277
ID ADB87949 standard; DNA; 98472 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:673.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 27.6; DB 10; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1278
ID ADB96932 standard; DNA; 98472 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:673.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 27.6; DB 10; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1279
ID ADB92123 standard; DNA; 98472 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:673.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 10.1%; Score 27.6; DB 10; Length 98472;
Best Local Similarity 52.6%; Pred. No. 1.7e+03;
RESULT 1280
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 9; Length 96595;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1271
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 9; Length 96595;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1272
ID ADB72806 standard; DNA; 96595 BP.
DE Human PPP3CC gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 10; Length 96595;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1273
ID ADA66352 standard; DNA; 96596 BP.
DE Human PPP3CC gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 10.1%; Score 27.6; DB 9; Length 96596;
Best Local Similarity 46.8%; Pred. No. 1.7e+03;
RESULT 1274
ID ABS54549 standard; DNA; 98472 BP.

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RESULT 1289
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 55.1%; Pred. No. 1.8e+03;
RESULT 1290
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1291
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1292
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1293
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1294
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1295
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1296
Query Match          10.1%; Score 27.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
ID AC64845 standard; DNA; 115218 BP.
DE Human HNRNP GP43 DNA corresponding to AL034397.
FN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match          10.1%; Score 27.6; DB 8; Length 115218;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1297
ID ACF62749 standard; DNA; 128993 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:681.
FN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 8; Length 128993;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1298
ID ADB20868 standard; DNA; 128993 BP.
DE MRPI based cancer related nucleic acid SEQ ID NO:681.
FN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 8; Length 128993;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1299
ID ADB87957 standard; DNA; 128993 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:681.
FN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 10; Length 128993;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1300
ID ADB96940 standard; DNA; 128993 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:681.
FN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 10; Length 128993;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1301
ID ADB92131 standard; DNA; 128993 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:681.
FN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 10; Length 128993;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1302
ID AAF22296 standard; DNA; 129021 BP.
DE BAC containing repeats from centromeres 1-4 #19.
FN WO200055325-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match          10.1%; Score 27.6; DB 10; Length 129021;
Best Local Similarity 52.6%; Pred. No. 1.9e+03;
RESULT 1303
ID ADL13873 standard; DNA; 183178 BP.
DE Osteoarthritis-associated polymorphic nucleotide #405.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match          10.1%; Score 27.6; DB 10; Length 183178;
Best Local Similarity 51.6%; Pred. No. 2.1e+03;
RESULT 1304
ID ADC86940 standard; DNA; 349901 BP.
DE Human GPCR gene SEQ ID NO:1393.
FN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match          10.1%; Score 27.6; DB 10; Length 349901;
Best Local Similarity 53.8%; Pred. No. 2.5e+03;
RESULT 1305
ID ADC87621 standard; DNA; 349938 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2074.
FN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match          10.1%; Score 27.6; DB 10; Length 349938;
Best Local Similarity 53.8%; Pred. No. 2.5e+03;
RESULT 1306
ID AAH68333 standard; DNA; 349980 BP.
DE C glutamicum coding sequence fragment SEQ ID NO: 7068.
FN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match          10.1%; Score 27.6; DB 5; Length 349980;
Best Local Similarity 56.7%; Pred. No. 2.5e+03;
RESULT 1307
ID ADH84487 standard; DNA; 201 BP.
DE Enterococcus faecalis polynucleotide #2372.
FN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match          10.0%; Score 27.4; DB 10; Length 201;
Best Local Similarity 50.4%; Pred. No. 2.2e+02;
RESULT 1308
ID ADQ18444 standard; DNA; 424 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1263.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match          10.0%; Score 27.4; DB 12; Length 424;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
RESULT 1309
ID ADL37205 standard; DNA; 433 BP.
DE Human ovarian cancer DNA marker #11095.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match          10.0%; Score 27.4; DB 5; Length 433;
Best Local Similarity 43.7%; Pred. No. 2.8e+02;
RESULT 1310
ID ADI72056 standard; DNA; 433 BP.
DE Human ovarian cancer DNA marker #4798.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match          10.0%; Score 27.4; DB 5; Length 433;
Best Local Similarity 43.7%; Pred. No. 2.8e+02;
RESULT 1311
ID AAK62056 standard; cDNA; 457 BP.
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DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:7116.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 457;
Best Local Similarity 57.6%; Pred. No. 2.9e+02;
RESULT 1312
ID ACH18968 standard; cDNA; 462 BP.
DE Human adult heart cDNA #3282.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 10.0%; Score 27.4; DB 9; Length 462;
Best Local Similarity 62.3%; Pred. No. 2.9e+02;
RESULT 1313
ID ADQ22941 standard; DNA; 466 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5761.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 27.4; DB 12; Length 466;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
RESULT 1314
ID AAS21889 standard; DNA; 468 BP.
DE Human collagen gene COL9A1 intron 10.
PN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOO-) UNIV OULU.
Query Match 10.0%; Score 27.4; DB 5; Length 468;
Best Local Similarity 55.9%; Pred. No. 2.9e+02;
RESULT 1315
ID AAC93690 standard; cDNA; 498 BP.
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:185.
PN WO200061621-A2.
PD 19-OCT-2000.
PA (HESK-) HESKA CORP.
Query Match 10.0%; Score 27.4; DB 3; Length 498;
Best Local Similarity 65.6%; Pred. No. 3e+02;
RESULT 1316
ID ABZ08157 standard; cDNA; 530 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8148.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 10.0%; Score 27.4; DB 6; Length 530;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
RESULT 1317
ID AAC53727 standard; DNA; 559 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75494.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.0%; Score 27.4; DB 3; Length 559;
Best Local Similarity 57.6%; Pred. No. 3.1e+02;
RESULT 1318
ID ABQ41297 standard; DNA; 617 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27888.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 617;
Best Local Similarity 52.1%; Pred. No. 3.2e+02;
RESULT 1319
ID ABQ41296 standard; DNA; 617 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27887.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 10.0%; Score 27.4; DB 6; Length 617;
Best Local Similarity 52.1%; Pred. No. 3.2e+02;
RESULT 1320
ID ABT11573 standard; DNA; 634 BP.
DE Yeast selected interacting domain coding sequence SEQ ID NO: 645.
PN WO200266504-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 10.0%; Score 27.4; DB 6; Length 634;
Best Local Similarity 75.6%; Pred. No. 3.3e+02;
RESULT 1321
ID ABS62968 standard; DNA; 635 BP.
DE Selected Interacting Domain (SID) polynucleotide #165.
PN WO200259255-A2.
PD 01-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 10.0%; Score 27.4; DB 6; Length 635;
Best Local Similarity 75.6%; Pred. No. 3.3e+02;
RESULT 1322
ID ABK73027 standard; DNA; 650 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #318.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO ) NOVOZYMES BIOTECH INC.
Query Match 10.0%; Score 27.4; DB 6; Length 650;
Best Local Similarity 54.5%; Pred. No. 3.3e+02;
RESULT 1323
ID ADL4028 standard; cDNA; 935 BP.
DE Human cDNA encoding sarcoma-associated antigen NY-SAR-27.
PN US2004063101-A1.
PD 01-APR-2004.
PA (SCAN/) SCANLAN M J.
PA (LEES/) LEE S.
PA (OLDL/) OLD L J.
Query Match 10.0%; Score 27.4; DB 12; Length 935;
Best Local Similarity 55.9%; Pred. No. 3.8e+02;
RESULT 1324
ID ACA24780 standard; DNA; 990 BP.
DE Prokaryotic essential Gene #6437.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.0%; Score 27.4; DB 8; Length 990;
Best Local Similarity 52.1%; Pred. No. 3.8e+02;
RESULT 1325
ID AAL51357 standard; DNA; 1000 BP.
DE Haemophilus influenzae BASB229 gene-related DNA sequence.
PN WO2002100891-A2.
PD 19-DEC-2002.
PA (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.
Query Match 10.0%; Score 27.4; DB 10; Length 1000;
Best Local Similarity 49.6%; Pred. No. 3.8e+02;
RESULT 1326
ID AAS85335 standard; cDNA; 1002 BP.
DE DNA encoding novel human diagnostic protein #21139.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 27.4; DB 5; Length 1002;
Best Local Similarity 53.2%; Pred. No. 3.9e+02;
RESULT 1327
ID ADL02866 standard; DNA; 1080 BP.
DE DNA encoding a M. catarrhalis protein #552.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 27.4; DB 12; Length 1080;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1328
ID ABL63139 standard; DNA; 1086 BP.
DE Breast cancer related gene sequence SEQ ID NO:1476.
PN WO200194629-A2.
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PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 27.4; DB 6; Length 1086;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1329
ID ABK84302 standard; cDNA; 1086 BP.
DE Human cDNA differentially expressed in granulocytic cells #873.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 27.4; DB 6; Length 1086;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1330
ID AB232352 standard; cDNA; 1086 BP.
DE Nucleotide sequence GI4885400 related to holochochrome C synthase.
PN WO200299054-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 10.0%; Score 27.4; DB 8; Length 1086;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1331
ID AB223251 standard; cDNA; 1086 BP.
DE Nucleotide sequence GI1209634 related to holochochrome C synthase.
PN WO200299054-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 10.0%; Score 27.4; DB 8; Length 1086;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1332
ID ADQ19774 standard; DNA; 1086 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2593.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 27.4; DB 12; Length 1086;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1333
ID AAT68079 standard; DNA; 1200 BP.
DE H. pylori cytoplasmic protein ORF 11ep12011orf9.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR-) ASTRA AB.
Query Match 10.0%; Score 27.4; DB 2; Length 1200;
Best Local Similarity 48.4%; Pred. No. 4.1e+02;
RESULT 1334
ID AA199442 standard; DNA; 1521 BP.
DE Human excretory related polynucleotide SEQ ID NO 1206.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 1521;
Best Local Similarity 45.0%; Pred. No. 4.5e+02;
RESULT 1335
ID AA164087 standard; cDNA; 1521 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 120.
PN WO200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 1521;
Best Local Similarity 45.0%; Pred. No. 4.5e+02;
RESULT 1336
ID ADF71685 standard; DNA; 1521 BP.
DE Human bladder associated antigen #16 genomic DNA #1.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 12; Length 1521;
Best Local Similarity 45.0%; Pred. No. 4.5e+02;
RESULT 1337
ID AAC78091 standard; cDNA; 1566 BP.
DE Human cancer associated gene sequence SEQ ID NO:485.
PN WO200055350-A1.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 3; Length 1566;
Best Local Similarity 62.3%; Pred. No. 4.5e+02;
RESULT 1338
ID AAH33534 standard; cDNA; 1566 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:590.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 1566;
Best Local Similarity 62.3%; Pred. No. 4.5e+02;
RESULT 1339
ID AB210125 standard; DNA; 1630 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #265.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 8; Length 1630;
Best Local Similarity 59.7%; Pred. No. 4.6e+02;
RESULT 1340
ID ABS51362 standard; cDNA; 1759 BP.
DE cDNA encoding human secretory protein #60.
PN WO200257304-A2.
PD 25-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.4; DB 6; Length 1759;
Best Local Similarity 53.2%; Pred. No. 4.7e+02;
RESULT 1341
ID ADQ23910 standard; DNA; 1833 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6730.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 27.4; DB 12; Length 1833;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
RESULT 1342
ID ACC61838 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 2458.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 10.0%; Score 27.4; DB 10; Length 2000;
Best Local Similarity 59.7%; Pred. No. 4.9e+02;
RESULT 1343
ID ADK63771 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #1490.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 10.0%; Score 27.4; DB 10; Length 2000;
Best Local Similarity 59.7%; Pred. No. 4.9e+02;
RESULT 1344
ID AA233670 standard; cDNA; 2009 BP.
DE Human breast tumour-associated EST 60.
PN DE19813839-A1.
PD 23-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.0%; Score 27.4; DB 2; Length 2009;
Best Local Similarity 59.9%; Pred. No. 5e+02;
RESULT 1345
ID AAI59197 standard; cDNA; 2030 BP.
DE Human polynucleotide SEQ ID NO 1400.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 27.4; DB 4; Length 2030;
Best Local Similarity 55.9%; Pred. No. 5e+02;
RESULT 1346
ID ADO99420 standard; cDNA; 2030 BP.
DE DNA encoding human GPCR-like protein seqid 1090.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.

Query Match 10.0%; Score 27.4; DB 5; Length 2030;
Best Local Similarity 55.9%; Pred. No. 5e+02;
RESULT 1347
ID ADB49180 standard; cDNA; 2030 BP.
DE Novel human cDNA SEQ ID NO 1090.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 10.0%; Score 27.4; DB 9; Length 2030;
Best Local Similarity 55.9%; Pred. No. 5e+02;
RESULT 1348
ID ABS64932 standard; cDNA; 2065 BP.
DE Soybean ribonuclease D-like (RNaseD-like) cDNA #3.
PN US200208026-A1.
PD 04-JUL-2002.
PA (BUTL/) BUTLER K H.
PA (CAHO/) CAHOON R E.
PA (RAFA/) RAFALSKI J A.
PA (SAKA/) SAKAI H.
Query Match 10.0%; Score 27.4; DB 6; Length 2065;
Best Local Similarity 57.6%; Pred. No. 5e+02;
RESULT 1349
ID AAH15656 standard; cDNA; 2182 BP.
DE Human cDNA sequence SEQ ID NO:14003.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.4; DB 4; Length 2182;
Best Local Similarity 62.3%; Pred. No. 5.1e+02;
RESULT 1350
ID ADE56467 standard; DNA; 2358 BP.
DE Human gene D88674, SEQ ID NO 2320.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 27.4; DB 10; Length 2358;
Best Local Similarity 83.8%; Pred. No. 5.2e+02;
RESULT 1351
ID ADE60749 standard; DNA; 2358 BP.
DE Human gene D88674, SEQ ID NO 6661.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 27.4; DB 10; Length 2358;
Best Local Similarity 83.8%; Pred. No. 5.2e+02;
RESULT 1352
ID ADE60753 standard; DNA; 2358 BP.
DE Human gene D88674, SEQ ID NO 6665.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 27.4; DB 10; Length 2358;
Best Local Similarity 83.8%; Pred. No. 5.2e+02;
RESULT 1353
ID AAH18621 standard; cDNA; 2597 BP.
DE Human cDNA sequence SEQ ID NO:18837.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.4; DB 4; Length 2597;
Best Local Similarity 62.3%; Pred. No. 5.4e+02;
RESULT 1354
ID AAZ07171 standard; cDNA; 2790 BP.
DE Human lung tumour protein L86S-36 extended cDNA sequence.
PN WO938973-A2.
PD 05-AUG-1999.

PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.4; DB 2; Length 2790;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1355
ID AAC79095 standard; cDNA; 2790 BP.
DE Human lung tumour-specific cDNA #48.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.4; DB 3; Length 2790;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1356
ID AAD23170 standard; cDNA; 2790 BP.
DE Human lung tumour-specific protein L86S-36 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.4; DB 4; Length 2790;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1357
ID ADD66387 standard; cDNA; 2790 BP.
DE Human lung tumour-specific related cDNA, SEQ ID NO 79.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.4; DB 10; Length 2790;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1358
ID ADE87641 standard; cDNA; 2790 BP.
DE Human lung tumour antigen cDNA #48.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.4; DB 10; Length 2790;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1359
ID ADQ30691 standard; DNA; 2804 BP.
DE Human airway trypsin-like protease HAT coding sequence.
PN WO2004053496-A1.
PD 24-JUN-2004.
PA (HINZ/) HINZMANN B.
PA (HEID/) HEIDEN E.
PA (HERM/) HERMANN K.
PA (ROSE/) ROSENTHAL A.
Query Match 10.0%; Score 27.4; DB 12; Length 2804;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
RESULT 1360
ID AAC76844 standard; cDNA; 2848 BP.
DE Human ORFX ORF2399 polynucleotide sequence SEQ ID NO:4797.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 27.4; DB 3; Length 2848;
Best Local Similarity 55.9%; Pred. No. 5.6e+02;
RESULT 1361
ID AAH14011 standard; cDNA; 3239 BP.
DE Human cDNA sequence SEQ ID NO:11103.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.4; DB 4; Length 3239;
Best Local Similarity 55.9%; Pred. No. 5.9e+02;
RESULT 1362
ID ADG31188 standard; DNA; 3418 BP.
DE Novel mouse gene #13.
PN WO2003089644-A1.
PD 30-OCT-2003.
PA (RIKE) RIKEN KK.
PA (DNAP-) DNAPFORM KK.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 10.0%; Score 27.4; DB 12; Length 3418;
Best Local Similarity 50.4%; Pred. No. 6e+02;
RESULT 1363

ID ADG10483 standard; cDNA; 3427 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:73.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 10.0%; Score 27.4; DB 10; Length 3427;
Best Local Similarity 55.9%; Pred. No. 6e+02;
RESULT 1364
ID ADI26064 standard; cDNA; 3430 BP.
DE Human cDNA encoding protein that promotes STAT6 activation #15.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 10.0%; Score 27.4; DB 12; Length 3430;
Best Local Similarity 55.9%; Pred. No. 6e+02;
RESULT 1365
ID ABL10838 standard; cDNA; 3583 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26996.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.4; DB 4; Length 3583;
Best Local Similarity 52.1%; Pred. No. 6.1e+02;
RESULT 1366
ID AHI17677 standard; cDNA; 3614 BP.
DE Human cDNA sequence SEQ ID NO:17248.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.4; DB 4; Length 3614;
Best Local Similarity 45.0%; Pred. No. 6.1e+02;
RESULT 1367
ID AA199443 standard; DNA; 3615 BP.
DE Human excretory related polynucleotide SEQ ID NO 1207.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 3615;
Best Local Similarity 45.0%; Pred. No. 6.1e+02;
RESULT 1368
ID AA164088 standard; cDNA; 3615 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 121.
PN WO200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 3615;
Best Local Similarity 45.0%; Pred. No. 6.1e+02;
RESULT 1369
ID ADF71686 standard; DNA; 3615 BP.
DE Human bladder associated antigen #16 genomic DNA #2.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 12; Length 3615;
Best Local Similarity 45.0%; Pred. No. 6.1e+02;
RESULT 1370
ID ADG31189 standard; DNA; 3617 BP.
DE Novel mouse gene #14.
PN WO2003089644-A1.
PD 30-OCT-2003.
PA (RIKE) RIKEN KK.
PA (DNAF-) DNAFORM KK.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 10.0%; Score 27.4; DB 12; Length 3617;
Best Local Similarity 50.4%; Pred. No. 6.1e+02;
RESULT 1371
ID ADG31187 standard; DNA; 3646 BP.
DE Novel mouse gene #12.
PN WO2003089644-A1.
PD 30-OCT-2003.
PA (RIKE) RIKEN KK.
PA (DNAF-) DNAFORM KK.
PA (MITU) MITSUBISHI CHEM CORP.

Query Match 10.0%; Score 27.4; DB 12; Length 3646;
Best Local Similarity 50.4%; Pred. No. 6.1e+02;
RESULT 1372
ID AAH54209 standard; DNA; 4041 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3573.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.4; DB 4; Length 4041;
Best Local Similarity 49.6%; Pred. No. 6.4e+02;
RESULT 1373
ID ADO36310 standard; DNA; 4178 BP.
DE Intracellular antibody isolation-related KAN gene #82.
PN WO2004046192-A2.
PD 03-JUN-2004.
PA (LAYL-) LAY LINE GENOMICS SPA.
Query Match 10.0%; Score 27.4; DB 12; Length 4178;
Best Local Similarity 59.7%; Pred. No. 6.4e+02;
RESULT 1374
ID AAH54625 standard; DNA; 4342 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3989.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.4; DB 4; Length 4342;
Best Local Similarity 49.6%; Pred. No. 6.5e+02;
RESULT 1375
ID ABL30304 standard; DNA; 4472 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42385.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.4; DB 4; Length 4472;
Best Local Similarity 46.6%; Pred. No. 6.6e+02;
RESULT 1376
ID AA199444 standard; DNA; 4507 BP.
DE Human excretory related polynucleotide SEQ ID NO 1208.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 4507;
Best Local Similarity 45.0%; Pred. No. 6.6e+02;
RESULT 1377
ID AA164089 standard; cDNA; 4507 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 122.
PN WO200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 4507;
Best Local Similarity 45.0%; Pred. No. 6.6e+02;
RESULT 1378
ID ADF71687 standard; DNA; 4507 BP.
DE Human bladder associated antigen #16 genomic DNA #3.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 12; Length 4507;
Best Local Similarity 45.0%; Pred. No. 6.6e+02;
RESULT 1379
ID ABL26568 standard; DNA; 5516 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31177.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.4; DB 4; Length 5516;
Best Local Similarity 52.1%; Pred. No. 7.1e+02;
RESULT 1380
ID ADN95328 standard; DNA; 5572 BP.
DE Human BEC/LEC-related gene sequence SeqID250.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

Query Match
Best Local Similarity 10.0%; Score 27.4; DB 11; Length 5572;
RESULT 1381
ID ABL32288 standard; DNA; 5875 BP.
DE Human immune system associated gene SEQ ID NO: 261.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 5875;
Best Local Similarity 65.6%; Pred. No. 7.3e+02;
RESULT 1382
ID ADB54002 standard; DNA; 5952 BP.
DE PCNA genomic DNA region.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 10; Length 5952;
Best Local Similarity 55.9%; Pred. No. 7.3e+02;
RESULT 1383
ID AAS45338 standard; DNA; 6025 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #22.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 4; Length 6025;
Best Local Similarity 48.4%; Pred. No. 7.4e+02;
RESULT 1384
ID ABL32622 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 595.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 6161;
Best Local Similarity 47.4%; Pred. No. 7.4e+02;
RESULT 1385
ID AAS46584 standard; DNA; 6167 BP.
DE Tumour suppressor gene derived chemically modified sequence #306.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 4; Length 6167;
Best Local Similarity 49.6%; Pred. No. 7.4e+02;
RESULT 1386
ID ABL33839 standard; DNA; 6167 BP.
DE Human immune system associated gene SEQ ID NO: 1812.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 6167;
Best Local Similarity 49.6%; Pred. No. 7.4e+02;
RESULT 1387
ID AAZ45239 standard; DNA; 6463 BP.
DE DNA encoding angiogenesis-associated protein which binds plasminogen.
PN WO966038-A1.
PD 23-DEC-1999.
PA (PHAA) PHARMACIA & UPJOHN AB.
Query Match 10.0%; Score 27.4; DB 3; Length 6463;
Best Local Similarity 62.3%; Pred. No. 7.5e+02;
RESULT 1388
ID ABL32907 standard; DNA; 6685 BP.
DE Human immune system associated gene SEQ ID NO: 880.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 6685;
Best Local Similarity 69.8%; Pred. No. 7.6e+02;
RESULT 1389
ID RAD28386 standard; DNA; 7434 BP.
DE Human chemically treated genomic DNA #27.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 7434;

Best Local Similarity 50.4%; Pred. No. 7.9e+02;
RESULT 1390
ID AAD57227 standard; cDNA; 8043 BP.
DE Human CGDD-7 cDNA.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.4; DB 9; Length 8043;
Best Local Similarity 62.3%; Pred. No. 8.2e+02;
RESULT 1391
ID AAZ29606 standard; DNA; 8126 BP.
DE Basic fragmentation vector, pDVO DNA.
PN WO966059-A1.
PD 23-DEC-1999.
PA (VLAAR-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 10.0%; Score 27.4; DB 3; Length 8126;
Best Local Similarity 59.7%; Pred. No. 8.2e+02;
RESULT 1392
ID ABL33274 standard; DNA; 13038 BP.
DE Human immune system associated gene SEQ ID NO: 1247.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 13038;
Best Local Similarity 59.7%; Pred. No. 9.7e+02;
RESULT 1393
ID ABL17489 standard; DNA; 14254 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9820.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 5; Length 14254;
Best Local Similarity 62.3%; Pred. No. 1e+03;
RESULT 1394
ID AAV74355 standard; DNA; 15109 BP.
DE Staphylococcus aureus contig SEQ ID #44.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 2; Length 15109;
Best Local Similarity 53.2%; Pred. No. 1e+03;
RESULT 1395
ID ABL34140 standard; DNA; 15698 BP.
DE Human immune system associated gene SEQ ID NO: 2113.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 15698;
Best Local Similarity 53.2%; Pred. No. 1e+03;
RESULT 1396
ID AAL37254 standard; DNA; 17908 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3619.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 17908;
Best Local Similarity 50.4%; Pred. No. 1.1e+03;
RESULT 1397
ID AAL03779 standard; DNA; 17908 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6467.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 4; Length 17908;
Best Local Similarity 50.4%; Pred. No. 1.1e+03;
RESULT 1398
ID ABX60242 standard; cDNA; 17908 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2586.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match 10.0%; Score 27.4; DB 8; Length 17908;
Best Local Similarity 50.4%; Pred. No. 1.1e+03;
RESULT 1399
ID ADJ30992 standard; DNA; 17908 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3619.
FN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 12; Length 17908;
Best Local Similarity 50.4%; Pred. No. 1.1e+03;
RESULT 1400
ID AAS12088 standard; DNA; 18636 BP.
DE Human tumour necrosis factor receptor-like genomic polynucleotide #1.
FN WO200155440-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 5; Length 18636;
Best Local Similarity 55.9%; Pred. No. 1.1e+03;
RESULT 1401
ID AB079004 standard; DNA; 18636 BP.
DE Human tumour necrosis factor gene from clone HEOQR40 #1.
FN US2002086820-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 10.0%; Score 27.4; DB 6; Length 18636;
Best Local Similarity 55.9%; Pred. No. 1.1e+03;
RESULT 1402
ID ADC35307 standard; DNA; 18636 BP.
DE Human TNFR-like gene 2 genomic sequence #1.
FN US2003077703-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.4; DB 10; Length 18636;
Best Local Similarity 55.9%; Pred. No. 1.1e+03;
RESULT 1403
ID AAS44505 standard; DNA; 22509 BP.
DE Human LEKTI DNA clone CIT978SKB_94F21 contig 11, SPINK5 exons 1-4.
FN WO200164747-A1.
PD 07-SEP-2001.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 10.0%; Score 27.4; DB 4; Length 22509;
Best Local Similarity 53.2%; Pred. No. 1.2e+03;
RESULT 1404
ID ABJ34622 standard; DNA; 23683 BP.
DE Human metastasis associated gene SEQ ID NO: 175.
FN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 23683;
Best Local Similarity 57.6%; Pred. No. 1.2e+03;
RESULT 1405
ID ABU70481 standard; DNA; 23683 BP.
DE Chemically treated cell signalling DNA sequence#186.
FN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 23683;
Best Local Similarity 57.6%; Pred. No. 1.2e+03;
RESULT 1406
ID AAS21771 standard; DNA; 24183 BP.
DE Human gene for collagen COL9A1.
FN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
Query Match 10.0%; Score 27.4; DB 5; Length 24183;
Best Local Similarity 55.9%; Pred. No. 1.2e+03;
RESULT 1407
ID AAS44506 standard; DNA; 31529 BP.
DE Human LEKTI DNA clone CIT978SKB_94F21 contig 8, SPINK5 exon 5.

FN WO200164747-A1.
PD 07-SEP-2001.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 10.0%; Score 27.4; DB 4; Length 31529;
Best Local Similarity 53.2%; Pred. No. 1.3e+03;
RESULT 1408
ID ABL34197 standard; DNA; 37973 BP.
DE Human immune system associated gene SEQ ID NO: 2170.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 6; Length 37973;
Best Local Similarity 55.9%; Pred. No. 1.4e+03;
RESULT 1409
ID AAF28535 standard; DNA; 45613 BP.
DE Genomic fragment #22.
FN WO200078968-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.4; DB 4; Length 45613;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
RESULT 1410
ID ABS5699 standard; DNA; 54842 BP.
DE Bovine Claudin-16 deficiency associated polynucleotide sequence #2.
FN JP2002238570-A.
PD 27-AUG-2002.
PA (CHIK-) CHIKUSAN GIJUTSU KYOKAI SH.
PA (KACH-) KACHIKU KAIRYO JIGYODAN SH.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KACHIKU KAIRYO CE.
Query Match 10.0%; Score 27.4; DB 6; Length 54842;
Best Local Similarity 59.7%; Pred. No. 1.6e+03;
RESULT 1411
ID AAS46787 standard; DNA; 61020 BP.
DE Tumour suppressor gene derived chemically modified sequence #513.
FN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.4; DB 4; Length 61020;
Best Local Similarity 59.7%; Pred. No. 1.7e+03;
RESULT 1412
Query Match 10.0%; Score 27.4; DB 6; Length 65589;
Best Local Similarity 53.2%; Pred. No. 1.7e+03;
RESULT 1413
ID ABV72623 standard; DNA; 82938 BP.
DE Human transporter protein encoding gene.
Query Match 10.0%; Score 27.4; DB 6; Length 82938;
Best Local Similarity 75.6%; Pred. No. 1.9e+03;
RESULT 1414
ID ABS52816 standard; DNA; 100543 BP.
DE Genomic DNA encoding human secreted protein #4.
FN WO200264626-A2.
PD 22-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.4; DB 6; Length 100543;
Best Local Similarity 52.1%; Pred. No. 2e+03;
RESULT 1415
ID ADA13316 standard; DNA; 108359 BP.
DE Human fringe-like secreted protein gene, SEQ ID NO:3.
Query Match 10.0%; Score 27.4; DB 9; Length 108359;
Best Local Similarity 48.4%; Pred. No. 2e+03;
RESULT 1416
Query Match 10.0%; Score 27.4; DB 6; Length 110000;
Best Local Similarity 50.4%; Pred. No. 2.1e+03;
RESULT 1417
Query Match 10.0%; Score 27.4; DB 6; Length 110000;
Best Local Similarity 53.2%; Pred. No. 2.1e+03;
RESULT 1418
ID ADB12064 standard; DNA; 1754382 BP.
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.
FN WO2003048304-A2.
PD 12-JUN-2003.
PA (AWHP) WYETH HOLDINGS CORP.
Query Match 10.0%; Score 27.4; DB 9; Length 110000;

Best Local Similarity 53.2%; Pred. No. 2.1e+03;
RESULT 1419
Query Match 10.0%; Score 27.4; DB 12; Length 110000;
Best Local Similarity 50.4%; Pred. No. 2.1e+03;
RESULT 1420
Query Match 10.0%; Score 27.4; DB 12; Length 110000;
Best Local Similarity 50.4%; Pred. No. 2.1e+03;
RESULT 1421
Query Match 10.0%; Score 27.4; DB 12; Length 110000;
Best Local Similarity 50.4%; Pred. No. 2.1e+03;
RESULT 1422
ID AAF25833 standard; DNA; 130480 BP.
DE R. marinus bacteriophage RM387 genomic DNA.
PN WO200075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS BHF.
Query Match 10.0%; Score 27.4; DB 4; Length 130480;
Best Local Similarity 49.6%; Pred. No. 2.2e+03;
RESULT 1423
ID ABK83566 standard; cDNA; 147724 BP.
DE Human cDNA differentially expressed in granulocytic cells #137.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 27.4; DB 6; Length 147724;
Best Local Similarity 59.7%; Pred. No. 2.3e+03;
RESULT 1424
ID ABQ88179 standard; cDNA; 160771 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 86.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 10.0%; Score 27.4; DB 6; Length 160771;
Best Local Similarity 61.9%; Pred. No. 2.3e+03;
RESULT 1425
ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 27.4; DB 6; Length 174424;
Best Local Similarity 53.2%; Pred. No. 2.4e+03;
RESULT 1426
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 27.4; DB 12; Length 181343;
Best Local Similarity 53.2%; Pred. No. 2.4e+03;
RESULT 1427
ID ADL13825 standard; DNA; 192427 BP.
DE Osteoarthritis-associated polymorphic nucleotide #357.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.4; DB 10; Length 192427;
Best Local Similarity 51.2%; Pred. No. 2.5e+03;
RESULT 1428
ID ADO56277 standard; DNA; 200620 BP.
DE Human presynaptic cytomatrix protein, REPS2, genomic sequence.
PN WO2004044164-A2.
PD 27-MAY-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 10.0%; Score 27.4; DB 12; Length 200620;
Best Local Similarity 57.6%; Pred. No. 2.5e+03;
RESULT 1429
ID ASX42543 standard; cDNA; 317 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7708.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT-) BYATT J. C.

PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 10.0%; Score 27.2; DB 8; Length 317;
Best Local Similarity 50.8%; Pred. No. 2.9e+02;
RESULT 1430
ID AAQ61275 standard; DNA; 359 BP.
DE Human brain Expressed Sequence Tag EST01293.
PN WO9316178-A2.
PD 19-AUG-1993.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 10.0%; Score 27.2; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
RESULT 1431
ID ADF58449 standard; cDNA; 393 BP.
DE Human polynucleotide sequence SEQ ID NO:816.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 27.2; DB 10; Length 393;
Best Local Similarity 51.7%; Pred. No. 3.2e+02;
RESULT 1432
ID ACA23930 standard; DNA; 414 BP.
DE Prokaryotic essential gene #5587.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.0%; Score 27.2; DB 8; Length 414;
Best Local Similarity 53.8%; Pred. No. 3.2e+02;
RESULT 1433
ID AAI98875 standard; cDNA; 449 BP.
DE Human excretory related polynucleotide SEQ ID NO 319.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 4; Length 449;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
RESULT 1434
ID AAI64062 standard; cDNA; 449 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 50.
PN WO200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 4; Length 449;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
RESULT 1435
ID ADF71615 standard; cDNA; 449 BP.
DE Human bladder associated antigen cDNA #40.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 12; Length 449;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
RESULT 1436
ID ABL62616 standard; DNA; 451 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:953.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 10.0%; Score 27.2; DB 6; Length 451;
Best Local Similarity 48.7%; Pred. No. 3.3e+02;
RESULT 1437
ID ABN94889 standard; DNA; 451 BP.
DE Gene #1387 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 10.0%; Score 27.2; DB 6; Length 451;
Best Local Similarity 48.7%; Pred. No. 3.3e+02;
RESULT 1438
ID ABN67263 standard; DNA; 489 BP.
DE Streptococcus polynucleotide SEQ ID NO 2439.
PN WO200234771-A2.

PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
Query Match 10.0%; Score 27.2; DB 6; Length 489;
Best Local Similarity 53.8%; Pred. No. 3.4e+02;
RESULT 1439
ID ADN12790 standard; cDNA; 517 BP.
DE Human prostate/colon/lung/breast cancer-related cDNA 305, SEQ:305.
PN WC2004039943-A2.
PD 13-MAY-2004.
PA (CHIR-) CHIRON CORP.
Query Match 10.0%; Score 27.2; DB 12; Length 517;
Best Local Similarity 50.4%; Pred. No. 3.5e+02;
RESULT 1440
ID AAR26713 standard; DNA; 520 BP.
DE Candida albicans polynucleotide sequence #51.
PN EP982401-A2.
PD 01-MAR-2000.
PA (JANC) JANSSEN PHARM NV.
Query Match 10.0%; Score 27.2; DB 3; Length 520;
Best Local Similarity 54.1%; Pred. No. 3.5e+02;
RESULT 1441
ID ABV87968 standard; cDNA; 530 BP.
DE Human colon cancer related cDNA SEQ ID NO 1279.
PN WC200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.0%; Score 27.2; DB 6; Length 530;
Best Local Similarity 64.1%; Pred. No. 3.5e+02;
RESULT 1442
ID ADN12733 standard; cDNA; 582 BP.
DE Human prostate/colon/lung/breast cancer-related cDNA 248, SEQ:248.
PN WC2004039943-A2.
PD 13-MAY-2004.
PA (CHIR-) CHIRON CORP.
Query Match 10.0%; Score 27.2; DB 12; Length 582;
Best Local Similarity 50.4%; Pred. No. 3.7e+02;
RESULT 1443
ID ADN13758 standard; cDNA; 582 BP.
DE Human prostate/colon/lung/breast cancer-related cDNA 1273, SEQ:1273.
PN WC2004039943-A2.
PD 13-MAY-2004.
PA (CHIR-) CHIRON CORP.
Query Match 10.0%; Score 27.2; DB 12; Length 582;
Best Local Similarity 50.4%; Pred. No. 3.7e+02;
RESULT 1444
ID ABV21872 standard; cDNA; 683 BP.
DE Human prostate expression marker cDNA 21863.
PN WC200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.0%; Score 27.2; DB 5; Length 683;
Best Local Similarity 53.8%; Pred. No. 3.9e+02;
RESULT 1445
ID ABV27702 standard; cDNA; 683 BP.
DE Human prostate expression marker cDNA 27693.
PN WC200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 10.0%; Score 27.2; DB 5; Length 683;
Best Local Similarity 53.8%; Pred. No. 3.9e+02;
RESULT 1446
ID ABN91349 standard; DNA; 699 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:812.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 27.2; DB 6; Length 699;
Best Local Similarity 52.7%; Pred. No. 3.9e+02;
RESULT 1447
ID ABQ31082 standard; DNA; 784 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 17673.
PN WC200218632-A2.

PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 784;
Best Local Similarity 58.8%; Pred. No. 4.1e+02;
RESULT 1448
ID ABQ31083 standard; DNA; 784 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 17674.
PN WC200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 784;
Best Local Similarity 58.8%; Pred. No. 4.1e+02;
RESULT 1449
ID AAH03690 standard; cDNA; 788 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:525.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.2; DB 4; Length 788;
Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1450
ID AAI99487 standard; DNA; 957 BP.
DE Human excretory related polynucleotide SEQ ID NO 1251.
PN WC200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 4; Length 957;
Best Local Similarity 53.8%; Pred. No. 4.4e+02;
RESULT 1451
ID AAI64132 standard; cDNA; 957 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 165.
PN WC200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 4; Length 957;
Best Local Similarity 53.8%; Pred. No. 4.4e+02;
RESULT 1452
ID ADF71730 standard; DNA; 957 BP.
DE Human bladder associated antigen #40 genomic DNA #1.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 12; Length 957;
Best Local Similarity 53.8%; Pred. No. 4.4e+02;
RESULT 1453
ID AAV43035 standard; DNA; 965 BP.
DE Streptococcus pneumoniae polypeptide coding region.
PN WO9823631-A1.
PD 04-JUN-1998.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.0%; Score 27.2; DB 2; Length 965;
Best Local Similarity 50.8%; Pred. No. 4.4e+02;
RESULT 1454
ID ADB23199 standard; DNA; 1000 BP.
DE Environmental stress-responsive promoter, SEQ ID 37.
PN WC200304190-A1.
PD 30-MAY-2003.
PA (RIKE) RIKEN KK.
Query Match 10.0%; Score 27.2; DB 9; Length 1000;
Best Local Similarity 58.8%; Pred. No. 4.4e+02;
RESULT 1455
ID AAC33025 standard; DNA; 1033 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 1510.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (RIKE) RIKEN KK.
Query Match 10.0%; Score 27.2; DB 3; Length 1033;
Best Local Similarity 55.2%; Pred. No. 4.5e+02;
RESULT 1456
ID AAX97610 standard; DNA; 1153 BP.
DE Extended human secreted protein coding sequence, SEQ ID NO. 74.
PN WC200218632-A2.

PA (GEST) GENSET.
Query Match 10.0%; Score 27.2; DB 2; Length 1153;
Best Local Similarity 47.6%; Pred. No. 4.7e+02;
RESULT 1457
ID ADP18877 standard; cDNA; 1153 BP.
DE Human secreted polynucleotide #133.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 10.0%; Score 27.2; DB 12; Length 1153;
Best Local Similarity 47.6%; Pred. No. 4.7e+02;
RESULT 1458
ID ACA29019 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #10676.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.0%; Score 27.2; DB 8; Length 1275;
Best Local Similarity 47.6%; Pred. No. 4.9e+02;
RESULT 1459
ID ACA32458 standard; DNA; 1359 BP.
DE Prokaryotic essential gene #14115.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.0%; Score 27.2; DB 8; Length 1359;
Best Local Similarity 58.8%; Pred. No. 5e+02;
RESULT 1460
ID ADF02388 standard; DNA; 1428 BP.
DE Bacterial polynucleotide #2673.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.0%; Score 27.2; DB 10; Length 1428;
Best Local Similarity 48.7%; Pred. No. 5.1e+02;
RESULT 1461
ID ABZ14297 standard; DNA; 1467 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2102.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 1467;
Best Local Similarity 55.2%; Pred. No. 5.1e+02;
RESULT 1462
ID ADAG8572 standard; DNA; 1467 BP.
DE Arabidopsis thaliana gene, SEQ ID 484.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 10.0%; Score 27.2; DB 8; Length 1467;
Best Local Similarity 55.2%; Pred. No. 5.1e+02;
RESULT 1463
ID AAK99650 standard; cDNA; 1633 BP.
DE cDNA encoding human alpha 2, 3-sialyltransferase (ST3 GalVI) 9-13.
PN CN1329158-A.
PD 02-JAN-2002.
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
Query Match 10.0%; Score 27.2; DB 6; Length 1633;
Best Local Similarity 53.8%; Pred. No. 5.3e+02;
RESULT 1464
ID AAC51519 standard; DNA; 1723 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68821.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.0%; Score 27.2; DB 3; Length 1723;
Best Local Similarity 55.2%; Pred. No. 5.4e+02;
RESULT 1465
ID AAQ62810 standard; DNA; 1747 BP.
DE Riboflavin 1 gene (rib-1).
PN DE4238904-A1.
PD 26-MAY-1994.
PA (BADI) BASF AG.
Query Match 10.0%; Score 27.2; DB 10; Length 2520;
Best Local Similarity 56.8%; Pred. No. 5.4e+02;
RESULT 1466
ID ABL17101 standard; DNA; 1785 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2776.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 10.0%; Score 27.2; DB 4; Length 1785;
Best Local Similarity 61.1%; Pred. No. 5.5e+02;
RESULT 1467
ID ADA21174 standard; cDNA; 1854 BP.
DE Human secreted protein SECP-28 encoding cDNA SEQ ID NO:79.
PN WO2003068943-A2.
PD 21-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.2; DB 9; Length 1854;
Best Local Similarity 58.8%; Pred. No. 5.6e+02;
RESULT 1468
ID AAT09085 standard; cDNA; 1994 BP.
DE Achatina fulica cDNA.
PN JP07233195-A.
PD 05-SEP-1995.
PA (SUNR) SUNTORY LTD.
Query Match 10.0%; Score 27.2; DB 2; Length 1994;
Best Local Similarity 51.7%; Pred. No. 5.7e+02;
RESULT 1469
ID ACC61635 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 2052.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 10.0%; Score 27.2; DB 10; Length 2000;
Best Local Similarity 53.8%; Pred. No. 5.7e+02;
RESULT 1470
ID ADK64299 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #1226.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 10.0%; Score 27.2; DB 10; Length 2000;
Best Local Similarity 53.8%; Pred. No. 5.7e+02;
RESULT 1471
ID ABQ80054 standard; cDNA; 2399 BP.
DE Corn granule-bound starch synthase coding sequence.
PN CA2384605-A1.
PD 03-NOV-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 10.0%; Score 27.2; DB 8; Length 2399;
Best Local Similarity 56.8%; Pred. No. 6.1e+02;
RESULT 1472
ID AAA78420 standard; cDNA; 2520 BP.
DE Human secreted protein gene 40 SEQ ID NO:50.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 3; Length 2520;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
RESULT 1473
ID ADA40040 standard; cDNA; 2520 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 8; Length 2520;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
RESULT 1474
ID ADD37651 standard; cDNA; 2520 BP.
DE Human secreted protein encoding sequence #133.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 10; Length 2520;

Best Local Similarity 50.0%; Pred. No. 6.2e+02;
RESULT 1475
ID ADA56221 standard; DNA; 2520 BP.
DE Gene encoding human secreted protein #400.
PN WC2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 10; Length 2520;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
RESULT 1476
ID AAC85867 standard; cDNA; 2761 BP.
DE cDNA encoding CDIFF-27, Incyte ID No. 2573955CB1.
PN WC200119860-A2.
PD 22-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.2; DB 5; Length 2761;
Best Local Similarity 58.8%; Pred. No. 6.4e+02;
RESULT 1477
ID AAH54698 standard; DNA; 2982 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4062.
PN WC200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.2; DB 4; Length 2982;
Best Local Similarity 51.7%; Pred. No. 6.6e+02;
RESULT 1478
ID AAH54829 standard; DNA; 3041 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4193.
PN WC200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.2; DB 4; Length 3041;
Best Local Similarity 51.7%; Pred. No. 6.6e+02;
RESULT 1479
ID AAH18354 standard; cDNA; 3048 BP.
DE Human cDNA sequence SEQ ID NO:18387.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.0%; Score 27.2; DB 4; Length 3048;
Best Local Similarity 55.2%; Pred. No. 6.6e+02;
RESULT 1480
ID ABAG2165 standard; DNA; 3057 BP.
DE Arabidopsis ATP sulfurylase gene (APS1) promoter.
PN WC200216621-A2.
PD 28-FEB-2002.
PA (RHOB-) RHOBIO.
Query Match 10.0%; Score 27.2; DB 6; Length 3057;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
RESULT 1481
ID ABN68454 standard; DNA; 3096 BP.
DE Streptococcus polynucleotide SEQ ID NO 4821.
PN WC200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 10.0%; Score 27.2; DB 6; Length 3096;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
RESULT 1482
ID AAH54143 standard; DNA; 3349 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3507.
PN WC200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.2; DB 4; Length 3349;
Best Local Similarity 51.7%; Pred. No. 6.9e+02;
RESULT 1483
ID AAH54424 standard; DNA; 3673 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3788.
PN WC200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.0%; Score 27.2; DB 4; Length 3673;

Best Local Similarity 52.7%; Pred. No. 7.1e+02;
RESULT 1484
ID ADQ24396 standard; DNA; 3729 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7216.
PN WC2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 27.2; DB 12; Length 3729;
Best Local Similarity 44.4%; Pred. No. 7.2e+02;
RESULT 1485
ID AAX13036 standard; DNA; 3905 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:99.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 27.2; DB 2; Length 3905;
Best Local Similarity 59.5%; Pred. No. 7.3e+02;
RESULT 1486
ID ABS98831 standard; DNA; 3905 BP.
DE Enterococcus faecalis contig sequence #99.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 10.0%; Score 27.2; DB 6; Length 3905;
Best Local Similarity 59.5%; Pred. No. 7.3e+02;
RESULT 1487
ID ABL02188 standard; cDNA; 4235 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1046.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.2; DB 4; Length 4235;
Best Local Similarity 52.7%; Pred. No. 7.5e+02;
RESULT 1488
ID ABT23200 standard; DNA; 4384 BP.
DE Human protein modification + maintenance molecule DNA SEQ ID No 29.
PN WO2003000844-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 27.2; DB 8; Length 4384;
Best Local Similarity 52.7%; Pred. No. 7.6e+02;
RESULT 1489
ID ABL08292 standard; cDNA; 4742 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19358.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.2; DB 4; Length 4742;
Best Local Similarity 53.8%; Pred. No. 7.8e+02;
RESULT 1490
ID ABL34284 standard; DNA; 4920 BP.
DE Human immune system associated gene SEQ ID NO: 2357.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 4920;
Best Local Similarity 52.7%; Pred. No. 7.9e+02;
RESULT 1491
ID AAS44657 standard; DNA; 4936 BP.
DE Mouse full-length polynucleotide sequence #82.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 27.2; DB 4; Length 4936;
Best Local Similarity 55.2%; Pred. No. 7.9e+02;
RESULT 1492
ID AAL39475 standard; DNA; 5090 BP.
DE Genomic DNA of the CCBP2 gene.
PN WO200232926-A2.
PD 25-APR-2002.
PA (GENA-) GENAISANCE PHARM INC.

Query Match 10.0%; Score 27.2; DB 6; Length 5090;
Best Local Similarity 67.9%; Pred. No. 8e+02;
RESULT 1493
ID ADE63834 standard; DNA; 5382 BP.
DE Human gene U93574, SEQ ID NO 9778.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 27.2; DB 10; Length 5382;
Best Local Similarity 56.8%; Pred. No. 8.2e+02;
RESULT 1494
ID ADE63061 standard; DNA; 5468 BP.
DE Human gene M80340, SEQ ID NO 8996.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.0%; Score 27.2; DB 10; Length 5468;
Best Local Similarity 56.8%; Pred. No. 8.2e+02;
RESULT 1495
ID AAS46462 standard; DNA; 5686 BP.
DE Tumour suppressor gene derived chemically modified sequence #184.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 4; Length 5686;
Best Local Similarity 64.1%; Pred. No. 8.3e+02;
RESULT 1496
ID ABL19820 standard; DNA; 5690 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10933.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.2; DB 4; Length 5690;
Best Local Similarity 64.1%; Pred. No. 8.3e+02;
RESULT 1497
ID ABL07648 standard; cDNA; 5970 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17426.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 27.2; DB 4; Length 5970;
Best Local Similarity 53.8%; Pred. No. 8.5e+02;
RESULT 1498
ID ABL32878 standard; DNA; 5994 BP.
DE Human immune system associated gene SEQ ID NO: 851.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 5994;
Best Local Similarity 67.9%; Pred. No. 8.5e+02;
RESULT 1499
ID ABK31432 standard; DNA; 6099 BP.
DE Signal transduction associated gene modified DNA #138.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 6099;
Best Local Similarity 53.8%; Pred. No. 8.5e+02;
RESULT 1500
ID ABL70397 standard; DNA; 6099 BP.
DE Chemically treated cell signalling DNA sequence#144.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 10.0%; Score 27.2; DB 6; Length 6099;
Best Local Similarity 53.8%; Pred. No. 8.5e+02;

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OM nucleic - nucleic search, using sw model

Run on: December 1, 2004, 21:05:55 ; Search time 38.4858 Seconds
(without alignments)
5041.999 Million cell updates/sec

Perfect score: 273

Sequence: 1 atgacattttttgtctact.....gtgtaagaaaaaacacttag 273

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	273	100.0	713	4	US-10-140-002-473
2	77.6	28.4	2298	3	US-08-772-440-1
3	75.2	27.5	528	3	US-08-772-440-7
4	74	27.1	85	4	US-09-513-999C-28212
5	34.2	12.5	696	4	US-09-107-532A-1647
6	33.8	12.4	5144	4	US-09-824-735-1
7	32.4	11.9	7218	1	US-08-232-463-14
8	31.8	11.6	8478	3	US-08-676-818-1
9	31.8	11.6	8478	3	US-09-407-549-1
10	31.6	11.6	299	4	US-08-956-171E-1171
11	31.6	11.6	299	4	US-08-781-986A-1171
12	31.4	11.5	6156	4	US-10-204-708-59
13	31.2	11.4	1760	4	US-09-455-050A-139
14	31.2	11.4	3142	1	US-08-110-158-3
15	31.2	11.4	3142	4	US-09-407-549-1
16	31.2	11.4	3142	5	PCT-US91-05059-1
17	31	11.4	5433	3	US-08-929-329-1
18	30.8	11.3	517	4	US-09-621-976-17793
19	30.6	11.2	318	4	US-09-248-796A-3701
20	30.4	11.1	1038	4	US-09-248-796A-11086
21	30.2	11.1	1308	4	US-09-107-532A-3483
22	30	11.0	264	4	US-09-248-796A-9696
23	30	11.0	624	4	US-09-543-681A-2711
24	30	11.0	1590	4	US-09-543-681A-2561
25	30	11.0	14066	4	US-09-601-198-56
26	30	11.0	38059	4	US-09-328-925-4
27	29.8	10.9	690	4	US-09-540-236-1512
28	29.8	10.9	62909	4	US-09-596-002-32

Sequence 4105, Ap
Sequence 615, App
Sequence 545, App
Sequence 335, App
Sequence 4391, Ap
Sequence 3936, Ap
Sequence 48, Appl
Sequence 48, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 2913, Ap
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
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Sequence 2813, Ap
Sequence 1110, Ap
Sequence 38, Appl
Sequence 3, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 13, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 2798, Ap
Sequence 1947, Ap
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 81, Appl
Sequence 4683, Ap
Sequence 2038, Ap
Sequence 372, App
Sequence 4207, Ap
Sequence 3912, Ap
Sequence 1, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 2802, Ap
Sequence 103, App
Sequence 3, Appli
Sequence 372, App
Sequence 63, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 70, Appl
Sequence 6594, Ap
Sequence 20662, A
Sequence 13588, A
Sequence 8207, Ap
Sequence 220, App
Sequence 1, Appli
Sequence 1791, Ap
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Sequence 3265, Ap
Sequence 50, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 32753, A
Sequence 10261, A

102	28	10.3	783	4	US-09-489-039A-1532	Sequence 1532, Ap	175	27	9.9	9814	4	US-09-809-665A-31	Sequence 31, Appl
103	28	10.3	819	4	US-09-328-352-870	Sequence 870, App	c 176	27	9.9	10619	4	US-10-204-708-4	Sequence 4, Appl
c 104	28	10.3	1062	4	US-09-543-681A-3018	Sequence 3018, Ap	c 177	27	9.9	41100	4	US-09-755-665-46	Sequence 46, Appl
105	28	10.3	16397	4	US-08-956-171E-205	Sequence 205, App	c 178	27	9.9	56516	2	US-08-996-306-1	Sequence 1, Appl
c 106	28	10.3	16397	4	US-08-781-986A-205	Sequence 205, App	c 179	27	9.9	56516	3	US-09-338-907-1	Sequence 1, Appl
c 107	28	10.3	16950	3	US-09-453-702B-166	Sequence 166, App	c 180	27	9.9	56516	3	US-09-218-207-1	Sequence 1, Appl
c 108	28	10.3	51259	3	US-08-781-891-209	Sequence 209, App	c 181	27	9.9	56520	3	US-09-338-907-179	Sequence 179, App
c 109	28	10.3	51259	3	US-09-618-166-209	Sequence 209, App	c 182	27	9.9	56520	3	US-09-218-207-179	Sequence 179, App
c 110	28	10.3	786431	4	US-09-751-389-3	Sequence 3, Appl	c 183	27	9.9	128779	4	US-09-497-855A-38	Sequence 38, Appl
c 111	27.8	10.2	368	4	US-09-621-976-14001	Sequence 3, Appl	c 184	27	9.9	148567	4	US-09-801-876B-3	Sequence 3, Appl
c 112	27.8	10.2	524	4	US-09-621-976-16820	Sequence 14001, A	c 185	27	9.9	148567	4	US-10-254-869-3	Sequence 3, Appl
c 113	27.8	10.2	2872	4	US-10-204-708-92	Sequence 92, Appl	186	26.8	9.8	447	4	US-09-710-279-823	Sequence 823, App
c 114	27.8	10.2	68804	4	US-09-740-041-3	Sequence 3, Appl	187	26.8	9.8	489	4	US-09-489-039A-1563	Sequence 1563, App
c 115	27.6	10.1	888	4	US-09-710-279-2397	Sequence 2397, Ap	188	26.8	9.8	513	4	US-09-710-279-1953	Sequence 1953, Ap
c 116	27.6	10.1	1338	4	US-09-328-352-505	Sequence 505, App	189	26.8	9.8	555	4	US-09-248-796A-6488	Sequence 6488, Ap
c 117	27.6	10.1	3043	4	US-09-710-279-3576	Sequence 3576, App	c 189	26.8	9.8	539	3	US-09-134-001C-2502	Sequence 2502, Ap
c 118	27.6	10.1	3043	4	US-09-710-279-4088	Sequence 4088, Ap	190	26.8	9.8	539	3	US-09-134-001C-2502	Sequence 2502, Ap
c 119	27.6	10.1	3214	4	US-09-710-279-4318	Sequence 4318, Ap	191	26.8	9.8	729	4	US-09-248-796A-3070	Sequence 3070, Ap
c 120	27.6	10.1	3417	4	US-09-710-279-4318	Sequence 4318, Ap	192	26.8	9.8	834	4	US-09-710-279-1987	Sequence 1987, Ap
c 121	27.6	10.1	6543	4	US-09-963-137-131	Sequence 131, Appl	c 193	26.8	9.8	902	3	US-09-662-250A-16	Sequence 16, Appl
c 122	27.6	10.1	9465	4	US-09-206-551-1	Sequence 1, Appl	194	26.8	9.8	934	4	US-09-710-279-1531	Sequence 1531, Ap
c 123	27.4	10.0	201	4	US-09-134-000C-2372	Sequence 2372, Ap	195	26.8	9.8	1044	4	US-09-270-767-385	Sequence 385, App
c 124	27.4	10.0	468	3	US-08-943-731-121	Sequence 121, App	196	26.8	9.8	1044	4	US-09-270-767-15667	Sequence 15667, A
c 125	27.4	10.0	663	4	US-09-248-796A-2711	Sequence 2711, App	197	26.8	9.8	1089	3	US-09-134-001C-1220	Sequence 1220, Ap
c 126	27.4	10.0	1080	4	US-09-540-236-552	Sequence 552, App	198	26.8	9.8	1170	1	US-08-335-583C-1	Sequence 1, Appl
c 127	27.4	10.0	1254	4	US-09-248-796A-732	Sequence 732, App	199	26.8	9.8	1776	4	US-09-543-681A-999	Sequence 999, App
c 128	27.4	10.0	1378	1	US-08-137-175A-4	Sequence 4, Appl	200	26.8	9.8	2225	1	US-08-335-583C-7	Sequence 7, Appl
c 129	27.4	10.0	1978	3	US-08-479-017-4	Sequence 4, Appl	c 201	26.8	9.8	2231	4	US-09-270-767-9854	Sequence 9854, Ap
c 130	27.4	10.0	2030	4	US-09-620-312D-1090	Sequence 1090, Ap	c 202	26.8	9.8	2524	4	US-08-961-527-242	Sequence 242, App
c 131	27.4	10.0	2790	4	US-09-370-838-79	Sequence 79, Appl	c 203	26.8	9.8	2995	4	US-09-710-279-4272	Sequence 4272, Ap
c 132	27.4	10.0	2790	4	US-09-854-133-79	Sequence 79, Appl	204	26.8	9.8	3001	4	US-09-539-333D-207	Sequence 207, App
c 133	27.4	10.0	4041	4	US-09-710-279-3573	Sequence 3573, Ap	205	26.8	9.8	3086	4	US-09-710-279-4183	Sequence 4183, Ap
c 134	27.4	10.0	4342	4	US-09-710-279-3989	Sequence 3989, Ap	206	26.8	9.8	3383	4	US-09-710-279-3363	Sequence 3363, Ap
c 135	27.4	10.0	15109	4	US-08-956-171E-44	Sequence 44, Appl	c 207	26.8	9.8	3422	4	US-09-710-279-4400	Sequence 4400, Ap
c 136	27.4	10.0	24183	3	US-08-781-986A-44	Sequence 44, Appl	c 208	26.8	9.8	3518	4	US-09-710-279-4114	Sequence 4114, Ap
c 137	27.4	10.0	45613	4	US-08-943-731-3	Sequence 3, Appl	209	26.8	9.8	5925	3	US-08-470-260-4	Sequence 4, Appl
c 138	27.4	10.0	45613	4	US-09-596-002-22	Sequence 22, Appl	210	26.8	9.8	5925	3	US-08-471-491-4	Sequence 4, Appl
c 139	27.2	10.0	129908	4	US-09-585-858-1	Sequence 1, Appl	211	26.8	9.8	5925	3	US-08-466-662-4	Sequence 4, Appl
c 140	27.2	10.0	483	4	US-09-621-976-18418	Sequence 18418, A	212	26.8	9.8	10299	2	US-08-477-451-1	Sequence 1, Appl
c 141	27.2	10.0	699	3	US-09-134-001C-812	Sequence 812, App	213	26.8	9.8	10299	2	US-08-477-451-5	Sequence 5, Appl
c 142	27.2	10.0	720	4	US-09-248-796A-13178	Sequence 13178, A	214	26.8	9.8	19332	2	US-08-477-451-25	Sequence 25, Appl
c 143	27.2	10.0	916	4	US-09-248-796A-8625	Sequence 8625, Ap	c 215	26.8	9.8	48974	3	US-08-920-422-17	Sequence 17, Appl
c 144	27.2	10.0	9302	4	US-09-270-767-13902	Sequence 13902, A	c 216	26.8	9.8	64467	4	US-09-803-671B-3	Sequence 3, Appl
c 145	27.2	10.0	1014	4	US-09-248-796A-9456	Sequence 9456, Ap	c 217	26.8	9.8	161652	4	US-09-497-855A-40	Sequence 40, Appl
c 146	27.2	10.0	1020	4	US-09-270-767-1194	Sequence 1194, Ap	218	26.8	9.8	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 147	27.2	10.0	1020	4	US-09-270-767-16476	Sequence 16476, A	219	26.8	9.8	1830121	4	US-09-643-990A-1	Sequence 1, Appl
c 148	27.2	10.0	1428	4	US-09-543-681A-2673	Sequence 2673, Ap	220	26.8	9.8	1830121	4	US-10-329-960-1	Sequence 1, Appl
c 149	27.2	10.0	2982	4	US-09-710-279-4062	Sequence 4062, Ap	221	26.6	9.7	361	3	US-08-905-223-142	Sequence 142, App
c 150	27.2	10.0	3041	4	US-09-710-279-4193	Sequence 4193, Ap	c 222	26.6	9.7	442	4	US-09-270-767-4887	Sequence 4887, Ap
c 151	27.2	10.0	3349	4	US-09-710-279-3507	Sequence 3507, Ap	c 223	26.6	9.7	442	4	US-09-270-767-20269	Sequence 20269, Ap
c 152	27.2	10.0	3673	4	US-09-710-279-3788	Sequence 3788, Ap	c 224	26.6	9.7	448	4	US-09-270-767-1465	Sequence 1465, Ap
c 153	27.2	10.0	42571	4	US-09-810-347-3	Sequence 3, Appl	c 225	26.6	9.7	448	4	US-09-270-767-16747	Sequence 16747, A
c 154	27.2	10.0	269223	4	US-09-596-002-41	Sequence 41, Appl	c 226	26.6	9.7	489	4	US-09-621-976-14192	Sequence 14192, A
c 155	27	9.9	1101	4	US-09-638-715-1	Sequence 1, Appl	c 227	26.6	9.7	672	4	US-09-270-767-31194	Sequence 31194, A
c 156	27	9.9	1101	4	US-09-638-715-3	Sequence 3, Appl	c 228	26.6	9.7	808	4	US-09-270-767-7520	Sequence 7520, Ap
c 157	27	9.9	1101	4	US-10-060-509-1	Sequence 1, Appl	c 229	26.6	9.7	808	4	US-09-270-767-22802	Sequence 22802, A
c 158	27	9.9	1101	4	US-10-060-509-3	Sequence 3, Appl	c 230	26.6	9.7	1024	4	US-09-328-475C-1	Sequence 1, Appl
c 159	27	9.9	1101	4	US-10-060-506-1	Sequence 1, Appl	c 231	26.6	9.7	1083	4	US-09-543-681A-2146	Sequence 2146, Ap
c 160	27	9.9	1241	3	US-09-378-088A-42	Sequence 42, Appl	c 232	26.6	9.7	1141	4	US-09-806-708B-22	Sequence 22, Appl
c 161	27	9.9	1241	3	US-09-548-334A-42	Sequence 42, Appl	c 233	26.6	9.7	1422	4	US-09-248-796A-5892	Sequence 5892, Ap
c 162	27	9.9	1241	3	US-09-643-596B-42	Sequence 42, Appl	c 234	26.6	9.7	1560	4	US-09-248-796A-431	Sequence 431, App
c 163	27	9.9	1241	3	US/08/622	INFORMATION FOR	c 235	26.6	9.7	1796	4	US-09-270-767-30632	Sequence 30632, A
c 164	27	9.9	1347	3	US-09-165-922A-11	Sequence 11, Appl	c 236	26.6	9.7	2351	4	US-09-270-767-14459	Sequence 14459, A
c 165	27	9.9	3001	4	US-09-539-333D-134	Sequence 134, App	c 237	26.6	9.7	2409	4	US-09-484-970B-101	Sequence 101, App
c 166	27	9.9	3001	4	US-09-539-333D-155	Sequence 155, App	c 238	26.6	9.7	2595	4	US-09-270-767-14926	Sequence 14926, A
c 167	27	9.9	3001	4	US-09-539-333D-155	Sequence 155, App	c 239	26.6	9.7	2611	4	US-09-620-312D-995	Sequence 925, App
c 168	27	9.9	3300	1	US-08-620-312D-456	Sequence 456, App	c 240	26.6	9.7	2784	4	US-09-107-532A-681	Sequence 681, App
c 169	27	9.9	3637	1	US-08-445-640-3	Sequence 3, Appl	c 241	26.6	9.7	3581	2	US-08-738-349-1	Sequence 1, Appl
c 170	27	9.9	3637	3	US-08-170-558-3	Sequence 3, Appl	c 242	26.6	9.7	4209	4	US-09-248-796A-400	Sequence 400, App
c 171	27	9.9	3637	3	US-08-447-314-3	Sequence 3, Appl	c 243	26.6	9.7	4673	3	US-08-482-918-39	Sequence 39, Appl
c 172	27	9.9	3637	3	US-08-445-461-3	Sequence 3, Appl	c 244	26.6	9.7	4673	3	US-09-224-681-39	Sequence 39, Appl
c 173	27	9.9	4279	4	US-09-270-767-12174	Sequence 12174, A	c 245	26.6	9.7	4673	3	US-08-336-728A-39	Sequence 39, Appl
c 174	27	9.9	8878	1	US-08-206-176-3	Sequence 3, Appl	c 246	26.6	9.7	10754	2	US-09-635-251-39	Sequence 39, Appl
							247	26.6	9.7			US-08-966-958-1	Sequence 1, Appl

248	26.6	9.7	10754	2	US-09-215-817-1	Sequence 1, Appli	C 321	26.2	9.6	3803	4	US-09-710-279-3561	Sequence 3561, Ap
249	26.6	9.7	10754	3	US-09-342-353-1	Sequence 1, Appli	C 322	26.2	9.6	3889	4	US-09-710-279-4224	Sequence 4224, Ap
250	26.6	9.7	50000	3	US-09-146-053-3	Sequence 3, Appli	C 323	26.2	9.6	4736	4	US-09-526-193A-15	Sequence 15, Appl
251	26.6	9.7	90050	3	US-09-245-041-5	Sequence 5, Appli	C 324	26.2	9.6	6583	4	US-10-204-708-26	Sequence 26, Appl
252	26.6	9.7	90050	4	US-09-358-055B-5	Sequence 5, Appli	C 325	26.2	9.6	8537	4	US-10-204-708-41	Sequence 41, Appl
253	26.6	9.7	90050	4	US-09-893-238-5	Sequence 5, Appli	C 326	26.2	9.6	14231	4	US-08-961-527-81	Sequence 81, Appl
254	26.6	9.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 327	26.2	9.6	19446	4	US-08-961-527-51	Sequence 51, Appl
255	26.4	9.7	155	4	US-09-270-767-28279	Sequence 28279, A	C 328	26	9.5	331	4	US-09-513-999C-31630	Sequence 31630, A
256	26.4	9.7	184	4	US-09-513-999C-25441	Sequence 25441, A	C 329	26	9.5	466	4	US-09-621-976-10105	Sequence 10105, A
257	26.4	9.7	624	3	US-09-270-767-12500	Sequence 12500, A	C 330	26	9.5	472	4	US-09-976-594-1114	Sequence 1114, Ap
258	26.4	9.7	674	3	US-08-881-094-13	Sequence 13, Appl	C 331	26	9.5	575	3	US-09-328-111-325	Sequence 325, App
259	26.4	9.7	792	3	US-09-134-001C-2171	Sequence 2171, Ap	C 332	26	9.5	628	3	US-09-227-357-104	Sequence 104, App
260	26.4	9.7	1077	4	US-09-328-352-4025	Sequence 4025, Ap	C 333	26	9.5	726	3	US-08-896-164-72	Sequence 72, Appl
261	26.4	9.7	1322	4	US-09-461-325-67	Sequence 67, Appl	C 334	26	9.5	765	4	US-08-956-171B-1213	Sequence 1213, Ap
262	26.4	9.7	1322	4	US-10-115-123-67	Sequence 67, Appl	C 335	26	9.5	765	4	US-08-781-886A-1213	Sequence 1213, Ap
263	26.4	9.7	1322	4	US-09-270-767-2670	Sequence 2670, Ap	C 336	26	9.5	854	4	US-09-270-767-4954	Sequence 4954, Ap
264	26.4	9.7	1330	4	US-09-270-767-17952	Sequence 17952, A	C 337	26	9.5	854	4	US-09-270-767-20236	Sequence 20236, A
265	26.4	9.7	1330	4	US-09-583-110-591	Sequence 591, App	C 338	26	9.5	943	4	US-09-270-767-11459	Sequence 11459, A
266	26.4	9.7	1464	4	US-08-107-632A-1991	Sequence 1991, Ap	C 339	26	9.5	946	4	US-09-599-360B-42	Sequence 42, Appl
267	26.4	9.7	2109	4	US-08-785-071A-1	Sequence 1, Appli	C 340	26	9.5	1242	3	US-09-134-001C-865	Sequence 865, App
268	26.4	9.7	2631	3	US-09-012-872-1	Sequence 1, Appli	C 341	26	9.5	1329	4	US-09-248-796A-11266	Sequence 11266, A
269	26.4	9.7	2631	3	US-09-270-767-838	Sequence 1, Appli	C 342	26	9.5	1345	2	US-08-702-153-3	Sequence 3, Appli
270	26.4	9.7	2631	4	US-09-270-767-16120	Sequence 838, App	C 343	26	9.5	1443	4	US-09-248-796A-4907	Sequence 4907, Ap
271	26.4	9.7	2631	4	US-09-270-767-16120	Sequence 16120, A	C 344	26	9.5	1855	3	US-08-530-862B-3	Sequence 3, Appli
272	26.4	9.7	3003	4	US-09-248-796A-6805	Sequence 6805, Ap	C 345	26	9.5	1855	3	US-08-597-313B-3	Sequence 3, Appli
273	26.4	9.7	3119	3	US-09-112-450-1	Sequence 1, Appli	C 346	26	9.5	2679	3	US-08-904-284-4	Sequence 4, Appli
274	26.4	9.7	3119	4	US-09-419-291A-1	Sequence 1, Appli	C 347	26	9.5	3001	4	US-09-539-333D-227	Sequence 227, App
275	26.4	9.7	3374	4	US-09-710-279-3910	Sequence 3910, Ap	C 348	26	9.5	3670	2	US-08-898-038-1	Sequence 1, Appli
276	26.4	9.7	3537	4	US-09-311-021-7	Sequence 7, Appli	C 349	26	9.5	3670	2	US-09-352-125-1	Sequence 1, Appli
277	26.4	9.7	3825	4	US-09-710-279-3799	Sequence 3799, Ap	C 350	26	9.5	3704	2	US-08-702-153-1	Sequence 1, Appli
278	26.4	9.7	3853	3	US-09-245-248B-53	Sequence 53, Appl	C 351	26	9.5	4450	3	US-08-617-860B-2	Sequence 2, Appli
279	26.4	9.7	3964	4	US-08-961-527-136	Sequence 136, App	C 352	26	9.5	6409	4	US-09-967-908A-1	Sequence 1, Appli
280	26.4	9.7	4351	4	US-09-921-099A-1	Sequence 1, Appli	C 353	26	9.5	6409	4	US-10-159-151-1	Sequence 1, Appli
281	26.4	9.7	4351	4	US-09-921-099A-3	Sequence 3, Appli	C 354	26	9.5	6476	3	US-09-127-670-5	Sequence 5, Appli
282	26.4	9.7	4507	2	US-08-568-459A-3	Sequence 3, Appli	C 355	26	9.5	7424	4	US-09-596-002-8	Sequence 8, Appli
283	26.4	9.7	4507	2	US-08-487-826B-3	Sequence 3, Appli	C 356	26	9.5	11384	4	US-08-961-527-45	Sequence 45, Appl
284	26.4	9.7	4507	3	US-09-210-288-3	Sequence 3, Appli	C 357	26	9.5	14066	4	US-09-601-198-56	Sequence 56, Appl
285	26.4	9.7	6326	4	US-10-204-708-58	Sequence 58, Appl	C 358	26	9.5	28171	4	US-08-961-527-22	Sequence 22, Appl
286	26.4	9.7	8561	4	US-09-112-450-3	Sequence 3, Appli	C 359	26	9.5	80246	3	US-09-078-294-4	Sequence 4, Appli
287	26.4	9.7	8561	4	US-09-419-291A-3	Sequence 3, Appli	C 360	26	9.5	80595	3	US-09-078-294-3	Sequence 3, Appli
288	26.4	9.7	11443	4	US-08-961-527-49	Sequence 49, Appl	C 361	26	9.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli
289	26.4	9.7	31940	4	US-09-596-002-13	Sequence 13, Appl	C 362	25.8	9.5	121	4	US-08-956-171E-3292	Sequence 3292, Ap
290	26.4	9.7	640681	4	US-09-790-988-1	Sequence 1, Appli	C 363	25.8	9.5	121	4	US-08-781-886A-3292	Sequence 3292, Ap
291	26.2	9.6	213	3	US-09-134-001C-337	Sequence 337, App	C 364	25.8	9.5	186	4	US-09-248-796A-7940	Sequence 7940, Ap
292	26.2	9.6	286	4	US-09-621-976-10866	Sequence 10866, A	C 365	25.8	9.5	249	4	US-09-583-110-668	Sequence 668, App
293	26.2	9.6	285	2	US-08-607-384A-11	Sequence 11, Appl	C 366	25.8	9.5	239	4	US-09-513-999C-35561	Sequence 35561, A
294	26.2	9.6	327	4	US-09-710-279-1723	Sequence 1723, Ap	C 367	25.8	9.5	330	4	US-09-621-976-8443	Sequence 8443, Ap
295	26.2	9.6	337	4	US-09-270-767-30482	Sequence 30482, A	C 368	25.8	9.5	337	4	US-09-513-999C-13915	Sequence 13915, A
296	26.2	9.6	505	4	US-09-621-976-15639	Sequence 15639, A	C 369	25.8	9.5	438	4	US-09-328-352-3663	Sequence 3663, Ap
297	26.2	9.6	621	4	US-09-248-796A-3663	Sequence 3663, Ap	C 370	25.8	9.5	446	4	US-09-513-999C-28302	Sequence 28302, A
298	26.2	9.6	689	4	US-09-712-016-18	Sequence 18, Appl	C 371	25.8	9.5	447	4	US-09-517-431B-12	Sequence 12, Appl
299	26.2	9.6	696	4	US-09-248-796A-5270	Sequence 5270, Ap	C 372	25.8	9.5	474	4	US-09-621-976-18033	Sequence 18033, A
300	26.2	9.6	739	4	US-09-270-767-11458	Sequence 11458, A	C 373	25.8	9.5	670	4	US-09-221-017B-46	Sequence 46, Appl
301	26.2	9.6	759	4	US-09-710-279-1159	Sequence 1159, Ap	C 374	25.8	9.5	832	4	US-09-621-976-2813	Sequence 2813, Ap
302	26.2	9.6	1023	3	US-08-256-261-16	Sequence 16, Appl	C 375	25.8	9.5	1308	4	US-09-577-424-4	Sequence 4, Appli
303	26.2	9.6	1023	3	US-08-852-299-16	Sequence 16, Appl	C 376	25.8	9.5	1323	4	US-09-023-655-17	Sequence 17, Appl
304	26.2	9.6	1368	4	US-09-248-796A-3318	Sequence 3318, Ap	C 377	25.8	9.5	1347	3	US-09-134-001C-1309	Sequence 1309, Ap
305	26.2	9.6	1442	4	US-09-634-238-82	Sequence 82, Appl	C 378	25.8	9.5	1381	4	US-09-270-767-8613	Sequence 8613, Ap
306	26.2	9.6	1481	4	US-09-270-767-14334	Sequence 14334, A	C 379	25.8	9.5	1381	4	US-09-270-767-23895	Sequence 23895, A
307	26.2	9.6	1497	4	US-09-320-132-94	Sequence 94, Appl	C 380	25.8	9.5	1502	3	US-09-206-903A-2	Sequence 2, Appli
308	26.2	9.6	1505	1	US-07-915-246-1	Sequence 1, Appli	C 381	25.8	9.5	1502	3	US-09-206-936-3	Sequence 3, Appli
309	26.2	9.6	1972	3	US-08-961-083-203	Sequence 203, App	C 382	25.8	9.5	1502	3	US-09-202-122-2	Sequence 2, Appli
310	26.2	9.6	1972	4	US-09-536-784-203	Sequence 203, App	C 383	25.8	9.5	1502	3	US-09-202-122-11	Sequence 11, Appl
311	26.2	9.6	2614	4	US-09-004-056-1	Sequence 1, Appli	C 384	25.8	9.5	1502	3	US-09-206-935-2	Sequence 2, Appli
312	26.2	9.6	2950	4	US-09-489-847-92	Sequence 92, Appl	C 385	25.8	9.5	1502	3	US-09-206-936-2	Sequence 2, Appli
313	26.2	9.6	2964	4	US-09-578-063-25	Sequence 25, Appl	C 386	25.8	9.5	1502	3	US-09-206-936-2	Sequence 2, Appli
314	26.2	9.6	2978	4	US-09-710-279-4099	Sequence 4099, Ap	C 387	25.8	9.5	1502	3	US-09-206-936-3	Sequence 3, Appli
315	26.2	9.6	2993	4	US-09-710-279-3821	Sequence 3821, Ap	C 388	25.8	9.5	1502	4	US-09-919-622A-2	Sequence 2, Appli
316	26.2	9.6	3001	4	US-09-539-333D-168	Sequence 168, App	C 389	25.8	9.5	1502	4	US-09-919-622A-11	Sequence 11, Appl
317	26.2	9.6	3042	4	US-09-762-724-1	Sequence 1, Appli	C 390	25.8	9.5	1698	3	US-09-232-478-15	Sequence 15, Appl
318	26.2	9.6	3126	3	US-08-929-329-2	Sequence 2, Appli	C 391	25.8	9.5	1698	3	US-09-785-055-15	Sequence 15, Appl
319	26.2	9.6	3376	4	US-09-710-279-4055	Sequence 4055, Ap	C 392	25.8	9.5	1762	1	US-08-105-483-284	Sequence 284, App
320	26.2	9.6	3451	4	US-09-710-279-3716	Sequence 3716, Ap	C 393	25.8	9.5	1762	1	US-08-709-209-284	Sequence 284, App

C 394	25.8	9.5	1762	1	US-08-458-101-284	Sequence 284, App	C 467	25.6	9.4	978	3	US-09-443-184-38	Sequence 38, Appl
C 395	25.8	9.5	2017	3	US-09-436-983-1	Sequence 1, Appl	C 468	25.6	9.4	1008	4	US-08-328-352-1324	Sequence 1324, Ap
C 396	25.8	9.5	2427	4	US-09-543-681A-823	Sequence 823, App	C 469	25.6	9.4	1134	4	US-09-248-796A-1394	Sequence 1394, Ap
C 397	25.8	9.5	2697	4	US-09-583-110-666	Sequence 666, App	C 470	25.6	9.4	1134	4	US-09-248-796A-669	Sequence 669, App
C 398	25.8	9.5	2763	4	US-09-799-451-734	Sequence 734, App	C 471	25.6	9.4	1135	4	US-09-270-767-11635	Sequence 11635, A
C 399	25.8	9.5	3080	3	US-09-099-041A-25	Sequence 25, Appl	C 472	25.6	9.4	1251	4	US-09-710-279-2401	Sequence 2401, Ap
C 400	25.8	9.5	3080	3	US-09-245-281-25	Sequence 25, Appl	C 473	25.6	9.4	1254	3	US-09-134-001C-1969	Sequence 2169, Ap
C 401	25.8	9.5	3080	4	US-09-207-359B-25	Sequence 25, Appl	C 474	25.6	9.4	1533	4	US-09-543-681A-1905	Sequence 1905, Ap
C 402	25.8	9.5	3080	4	US-09-340-620A-25	Sequence 25, Appl	C 475	25.6	9.4	1899	4	US-09-328-352-659	Sequence 659, App
C 403	25.8	9.5	3080	4	US-09-865-364-25	Sequence 25, Appl	C 476	25.6	9.4	1993	4	US-09-071-035-243	Sequence 243, App
C 404	25.8	9.5	3840	3	US-09-245-248B-55	Sequence 55, Appl	C 477	25.6	9.4	2205	3	US-08-687-590-59	Sequence 59, Appl
C 405	25.8	9.5	4302	3	US-09-245-281-38	Sequence 38, Appl	C 478	25.6	9.4	2556	1	US-08-725-012-1	Sequence 1, Appl
C 406	25.8	9.5	4302	4	US-09-207-359B-38	Sequence 38, Appl	C 479	25.6	9.4	2625	4	US-10-116-370-1	Sequence 1, Appl
C 407	25.8	9.5	4302	4	US-09-340-620A-38	Sequence 38, Appl	C 480	25.6	9.4	2784	3	US-08-857-076-39	Sequence 39, Appl
C 408	25.8	9.5	4302	4	US-09-865-364-38	Sequence 38, Appl	C 481	25.6	9.4	3017	3	US-08-857-076-52	Sequence 52, Appl
C 409	25.8	9.5	4666	4	US-09-809-665A-23	Sequence 23, Appl	C 482	25.6	9.4	3119	3	US-08-857-076-53	Sequence 53, Appl
C 410	25.8	9.5	4699	1	US-08-487-890A-1	Sequence 1, Appl	C 483	25.6	9.4	3210	4	US-09-710-279-3922	Sequence 3922, Ap
C 411	25.8	9.5	4699	2	US-08-478-435-1	Sequence 1, Appl	C 484	25.6	9.4	3368	4	US-09-710-279-4169	Sequence 4169, Ap
C 412	25.8	9.5	4699	2	US-08-337-483-1	Sequence 1, Appl	C 485	25.6	9.4	3394	4	US-09-851-989-1	Sequence 1, Appl
C 413	25.8	9.5	4699	2	US-08-478-373-1	Sequence 1, Appl	C 486	25.6	9.4	3475	1	US-07-960-385-1	Sequence 1, Appl
C 414	25.8	9.5	4699	3	US-08-478-373-1	Sequence 1, Appl	C 487	25.6	9.4	3628	3	US-08-842-306B-47	Sequence 47, Appl
C 415	25.8	9.5	4699	3	US-08-483-577A-1	Sequence 1, Appl	C 488	25.6	9.4	3628	3	US-08-838-973B-47	Sequence 47, Appl
C 416	25.8	9.5	4699	3	US-08-897-438-1	Sequence 1, Appl	C 489	25.6	9.4	3755	4	US-09-710-279-3642	Sequence 3642, Ap
C 417	25.8	9.5	4699	3	US-08-637-654-1	Sequence 1, Appl	C 490	25.6	9.4	3802	4	US-09-071-035-235	Sequence 235, App
C 418	25.8	9.5	4699	3	US-08-649-518-1	Sequence 1, Appl	C 491	25.6	9.4	3924	4	US-09-071-035-237	Sequence 237, App
C 419	25.8	9.5	5152	4	US-10-204-708-74	Sequence 74, Appl	C 492	25.6	9.4	3924	4	US-09-071-035-241	Sequence 241, App
C 420	25.8	9.5	5609	3	US-09-313-677-14	Sequence 14, Appl	C 493	25.6	9.4	4059	4	US-09-385-219A-47	Sequence 47, Appl
C 421	25.8	9.5	5609	3	US-09-313-677-15	Sequence 15, Appl	C 494	25.6	9.4	4059	4	US-09-814-915A-66	Sequence 66, Appl
C 422	25.8	9.5	5707	2	US-08-472-809B-8	Sequence 8, Appl	C 495	25.6	9.4	5421	4	US-09-814-915A-66	Sequence 66, Appl
C 423	25.8	9.5	5874	4	US-09-561-709B-2	Sequence 2, Appl	C 496	25.6	9.4	5677	4	US-09-984-863-7	Sequence 7, Appl
C 424	25.8	9.5	6113	2	US-08-472-809B-7	Sequence 7, Appl	C 497	25.6	9.4	6113	2	US-09-851-985-3	Sequence 3, Appl
C 425	25.8	9.5	6345	2	US-08-472-809B-7	Sequence 7, Appl	C 498	25.6	9.4	6113	2	US-09-453-702B-206	Sequence 206, App
C 426	25.8	9.5	7026	3	US-09-313-677-20	Sequence 20, Appl	C 499	25.6	9.4	45325	3	US-09-453-702B-261	Sequence 261, App
C 427	25.8	9.5	7344	3	US-09-313-677-16	Sequence 16, Appl	C 500	25.6	9.4	116592	4	US-09-818-512-3	Sequence 3, Appl
C 428	25.8	9.5	11272	4	US-09-341-461-1	Sequence 1, Appl	C 501	25.6	9.4	168575	4	US-09-426-290-1	Sequence 1, Appl
C 429	25.8	9.5	12614	4	US-09-577-424-1	Sequence 1, Appl	C 502	25.4	9.3	179	4	US-09-313-294A-1084	Sequence 1084, Ap
C 430	25.8	9.5	14194	4	US-09-577-424-3	Sequence 3, Appl	C 503	25.4	9.3	195	4	US-09-248-796A-10278	Sequence 10278, A
C 431	25.8	9.5	15462	3	US-09-073-492-1	Sequence 1, Appl	C 504	25.4	9.3	215	4	US-09-513-999C-31998	Sequence 31998, A
C 432	25.8	9.5	15881	3	US-08-646-538-35	Sequence 35, Appl	C 505	25.4	9.3	216	4	US-09-107-532A-2805	Sequence 2805, Ap
C 433	25.8	9.5	15881	3	US-09-503-222-35	Sequence 35, Appl	C 506	25.4	9.3	258	4	US-09-248-796A-11356	Sequence 11356, A
C 434	25.8	9.5	33769	4	US-09-543-771-8	Sequence 8, Appl	C 507	25.4	9.3	266	2	US-08-378-235B-7	Sequence 7, Appl
C 435	25.8	9.5	3769	4	US-09-543-771-8	Sequence 8, Appl	C 508	25.4	9.3	288	4	US-09-513-999C-33934	Sequence 33934, A
C 436	25.6	9.4	211	4	US-09-621-976-17824	Sequence 17824, A	C 509	25.4	9.3	304	4	US-09-385-982-162	Sequence 162, App
C 437	25.6	9.4	226	4	US-09-513-999C-28903	Sequence 28903, A	C 510	25.4	9.3	349	4	US-09-513-999C-34991	Sequence 34991, A
C 438	25.6	9.4	367	4	US-09-513-999C-33451	Sequence 33451, A	C 511	25.4	9.3	349	4	US-09-270-767-3043	Sequence 3043, Ap
C 439	25.6	9.4	378	4	US-09-248-796A-2030	Sequence 2030, App	C 512	25.4	9.3	454	4	US-09-270-767-18325	Sequence 18325, A
C 440	25.6	9.4	428	4	US-09-270-767-425	Sequence 425, App	C 513	25.4	9.3	540	4	US-09-445-724B-13	Sequence 13, Appl
C 441	25.6	9.4	442	3	US-09-280-116-164	Sequence 164, App	C 514	25.4	9.3	582	4	US-09-445-724B-1	Sequence 1, Appl
C 442	25.6	9.4	454	4	US-09-621-976-14244	Sequence 14244, A	C 515	25.4	9.3	707	2	US-08-850-910A-40	Sequence 40, Appl
C 443	25.6	9.4	470	4	US-09-621-976-14244	Sequence 14244, A	C 516	25.4	9.3	775	4	US-09-586-106D-42	Sequence 42, Appl
C 444	25.6	9.4	579	4	US-09-248-796A-6575	Sequence 6575, App	C 517	25.4	9.3	867	4	US-09-248-796A-5780	Sequence 5780, Ap
C 445	25.6	9.4	588	3	US-09-488-295-4	Sequence 4, Appl	C 518	25.4	9.3	1042	1	US-08-596-864-2	Sequence 2, Appl
C 446	25.6	9.4	610	4	US-09-270-767-27909	Sequence 27909, A	C 519	25.4	9.3	1042	1	US-08-989-667-2	Sequence 2, Appl
C 447	25.6	9.4	638	4	US-09-270-767-12180	Sequence 12180, A	C 520	25.4	9.3	1349	4	US-09-634-238-37	Sequence 37, Appl
C 448	25.6	9.4	661	4	US-09-976-594-444	Sequence 444, App	C 521	25.4	9.3	1427	4	US-09-445-724B-5	Sequence 5, Appl
C 449	25.6	9.4	755	3	US-09-020-956-21	Sequence 21, Appl	C 522	25.4	9.3	1454	4	US-09-614-912-63	Sequence 63, Appl
C 450	25.6	9.4	755	3	US-09-030-607-21	Sequence 21, Appl	C 523	25.4	9.3	1507	2	US-08-850-910A-17	Sequence 17, Appl
C 451	25.6	9.4	755	3	US-09-439-313-21	Sequence 21, Appl	C 524	25.4	9.3	1507	2	US-08-850-910A-17	Sequence 38, Appl
C 452	25.6	9.4	755	3	US-09-352-616A-21	Sequence 21, Appl	C 525	25.4	9.3	2274	3	US-08-492-459-13	Sequence 13, Appl
C 453	25.6	9.4	755	3	US-09-232-149A-21	Sequence 21, Appl	C 526	25.4	9.3	2274	3	US-08-423-752-13	Sequence 13, Appl
C 454	25.6	9.4	755	4	US-09-159-812-21	Sequence 21, Appl	C 527	25.4	9.3	2274	3	US-08-716-873-27	Sequence 27, Appl
C 455	25.6	9.4	755	4	US-09-636-215-21	Sequence 21, Appl	C 528	25.4	9.3	2274	3	US-09-368-431-27	Sequence 27, Appl
C 456	25.6	9.4	755	4	US-09-685-166A-21	Sequence 21, Appl	C 529	25.4	9.3	2274	3	US-09-414-006-13	Sequence 13, Appl
C 457	25.6	9.4	755	4	US-09-115-453-21	Sequence 21, Appl	C 530	25.4	9.3	2274	4	US-09-447-223-13	Sequence 13, Appl
C 458	25.6	9.4	755	4	US-09-688-489-21	Sequence 21, Appl	C 531	25.4	9.3	2274	4	US-09-951-217-27	Sequence 27, Appl
C 459	25.6	9.4	755	4	US-09-679-426-21	Sequence 21, Appl	C 532	25.4	9.3	2521	4	US-09-620-312D-1015	Sequence 1015, Ap
C 460	25.6	9.4	773	4	US-09-359-301A-20	Sequence 20, Appl	C 533	25.4	9.3	2550	4	US-09-248-796A-3954	Sequence 3954, Ap
C 461	25.6	9.4	773	4	US-09-771-035A-52	Sequence 52, Appl	C 534	25.4	9.3	3771	4	US-08-480-784-21	Sequence 21, Appl
C 462	25.6	9.4	789	4	US-09-710-279-3157	Sequence 3157, Ap	C 535	25.4	9.3	4249	1	US-08-483-553-21	Sequence 21, Appl
C 463	25.6	9.4	792	3	US-09-134-001C-1675	Sequence 1675, Ap	C 536	25.4	9.3	4249	1	US-08-487-002-21	Sequence 21, Appl
C 464	25.6	9.4	798	4	US-09-328-352-1947	Sequence 1947, Ap	C 537	25.4	9.3	4249	1	US-08-483-554B-21	Sequence 21, Appl
C 465	25.6	9.4	888	4	US-09-134-000C-1658	Sequence 1658, Ap	C 538	25.4	9.3	4249	1	US-08-488-011B-21	Sequence 21, Appl
C 466	25.6	9.4					C 539	25.4	9.3	4249	1		

540	25.4	9.3	4249	3	US-08-850-727-21	Sequence 21, Appl	C 613	25.4	9.3	15598	4	US-08-956-171E-82	Sequence 82, Appl
541	25.4	9.3	4249	5	PCT-US95-10202-21	Sequence 21, Appl	C 614	25.4	9.3	15598	4	US-08-781-986A-82	Sequence 82, Appl
542	25.4	9.3	4249	5	PCT-US95-10203-21	Sequence 21, Appl	C 615	25.2	9.2	255	4	US-09-513-999C-2456	Sequence 2456, Ap
543	25.4	9.3	4249	5	PCT-US95-10220-21	Sequence 21, Appl	C 616	25.2	9.2	264	4	US-09-248-796A-9696	Sequence 9696, Ap
544	25.4	9.3	4758	4	US-09-620-312D-840	Sequence 840, Appl	C 617	25.2	9.2	273	4	US-09-248-796A-7359	Sequence 7359, Ap
C 545	25.4	9.3	5562	4	US-10-204-708-64	Sequence 1, Appl	C 618	25.2	9.2	277	4	US-09-513-999C-27659	Sequence 27659, A
546	25.4	9.3	5656	1	US-08-825-061-1	Sequence 1, Appl	C 619	25.2	9.2	364	4	US-09-270-767-28765	Sequence 28765, A
547	25.4	9.3	5656	1	US-08-825-886-1	Sequence 1, Appl	C 620	25.2	9.2	388	4	US-09-513-999C-17462	Sequence 17462, A
548	25.4	9.3	5656	4	US-08-989-890-1	Sequence 1, Appl	C 621	25.2	9.2	392	4	US-09-513-999C-14215	Sequence 14215, A
549	25.4	9.3	5689	1	US-08-825-061-3	Sequence 3, Appl	C 622	25.2	9.2	442	4	US-09-621-976-14788	Sequence 14788, A
550	25.4	9.3	5689	1	US-08-825-886-3	Sequence 3, Appl	C 623	25.2	9.2	487	4	US-09-257-179-22	Sequence 22, Appl
551	25.4	9.3	5689	4	US-08-989-890-3	Sequence 3, Appl	C 624	25.2	9.2	633	4	US-09-248-796A-7507	Sequence 7507, Ap
552	25.4	9.3	5707	1	US-08-825-061-11	Sequence 11, Appl	C 625	25.2	9.2	635	3	US-09-328-111-630	Sequence 630, App
553	25.4	9.3	5707	1	US-08-825-886-11	Sequence 11, Appl	C 626	25.2	9.2	652	3	US-09-328-111-717	Sequence 717, App
554	25.4	9.3	5707	4	US-08-989-890-11	Sequence 11, Appl	C 627	25.2	9.2	746	4	US-09-902-331B-15	Sequence 15, Appl
555	25.4	9.3	5709	1	US-08-825-061-2	Sequence 2, Appl	C 628	25.2	9.2	747	4	US-09-714-767A-8	Sequence 8, Appl
556	25.4	9.3	5709	1	US-08-825-061-7	Sequence 7, Appl	C 629	25.2	9.2	951	4	US-09-248-796A-4213	Sequence 4213, Ap
557	25.4	9.3	5709	1	US-08-825-061-8	Sequence 8, Appl	C 630	25.2	9.2	984	4	US-09-248-796A-3639	Sequence 3639, Ap
558	25.4	9.3	5709	1	US-08-825-061-9	Sequence 9, Appl	C 631	25.2	9.2	1001	4	US-09-641-638-373	Sequence 373, App
559	25.4	9.3	5709	1	US-08-825-886-2	Sequence 2, Appl	C 632	25.2	9.2	1001	4	US-09-641-638-374	Sequence 374, App
560	25.4	9.3	5709	1	US-08-825-886-7	Sequence 7, Appl	C 633	25.2	9.2	1001	4	US-09-641-638-375	Sequence 375, App
561	25.4	9.3	5709	1	US-08-825-886-8	Sequence 8, Appl	C 634	25.2	9.2	1001	4	US-10-170-097-373	Sequence 373, App
562	25.4	9.3	5709	1	US-08-825-886-9	Sequence 9, Appl	C 635	25.2	9.2	1001	4	US-10-170-097-374	Sequence 374, App
563	25.4	9.3	5709	4	US-08-989-890-2	Sequence 2, Appl	C 636	25.2	9.2	1001	4	US-10-170-097-375	Sequence 375, App
564	25.4	9.3	5709	4	US-08-989-890-7	Sequence 7, Appl	C 637	25.2	9.2	1155	4	US-09-248-796A-5987	Sequence 5987, Ap
565	25.4	9.3	5709	4	US-08-989-890-8	Sequence 8, Appl	C 638	25.2	9.2	1218	4	US-09-248-796A-3862	Sequence 3862, Ap
566	25.4	9.3	5709	4	US-08-989-890-9	Sequence 9, Appl	C 639	25.2	9.2	1262	3	US-09-227-351A-284	Sequence 27, Appl
567	25.4	9.3	5710	1	US-08-825-061-6	Sequence 6, Appl	C 640	25.2	9.2	1368	4	US-09-614-221A-284	Sequence 284, App
568	25.4	9.3	5710	1	US-08-825-886-6	Sequence 6, Appl	C 641	25.2	9.2	1523	4	US-09-270-767-12905	Sequence 12905, A
569	25.4	9.3	5710	4	US-08-989-890-6	Sequence 6, Appl	C 642	25.2	9.2	1557	4	US-09-248-796A-5742	Sequence 5742, Ap
570	25.4	9.3	5711	1	US-08-825-061-4	Sequence 4, Appl	C 643	25.2	9.2	1561	2	US-08-532-547-2	Sequence 2, Appl
571	25.4	9.3	5711	1	US-08-825-061-10	Sequence 10, Appl	C 644	25.2	9.2	1561	2	US-08-379-658B-2	Sequence 2, Appl
572	25.4	9.3	5711	1	US-08-598-591-1	Sequence 1, Appl	C 645	25.2	9.2	1561	3	US-08-455-838-2	Sequence 2, Appl
573	25.4	9.3	5711	1	US-08-798-691-1	Sequence 1, Appl	C 646	25.2	9.2	1561	3	US-09-019-809-2	Sequence 2, Appl
574	25.4	9.3	5711	1	US-08-798-691-3	Sequence 3, Appl	C 647	25.2	9.2	1561	3	US-09-471-177-2	Sequence 2, Appl
575	25.4	9.3	5711	1	US-08-798-691-5	Sequence 5, Appl	C 648	25.2	9.2	1561	4	US-09-220-806-2	Sequence 2, Appl
576	25.4	9.3	5711	1	US-08-825-886-4	Sequence 4, Appl	C 649	25.2	9.2	1677	4	US-09-436-699C-27	Sequence 27, Appl
577	25.4	9.3	5711	2	US-08-825-886-10	Sequence 10, Appl	C 650	25.2	9.2	1677	4	US-09-328-352-1376	Sequence 1376, Ap
578	25.4	9.3	5711	2	US-08-558-322-1	Sequence 1, Appl	C 651	25.2	9.2	1917	4	US-09-614-912-173	Sequence 173, App
579	25.4	9.3	5711	3	US-08-825-487A-1	Sequence 1, Appl	C 652	25.2	9.2	2667	4	US-09-614-221A-335	Sequence 335, App
580	25.4	9.3	5711	3	US-08-825-487A-3	Sequence 3, Appl	C 653	25.2	9.2	2727	4	US-09-328-352-3042	Sequence 3042, Ap
581	25.4	9.3	5711	3	US-08-825-487A-5	Sequence 5, Appl	C 654	25.2	9.2	2914	1	US-08-454-097-11	Sequence 11, Appl
582	25.4	9.3	5711	3	US-09-074-476-1	Sequence 1, Appl	C 655	25.2	9.2	2914	3	US-08-185-359-11	Sequence 11, Appl
583	25.4	9.3	5711	3	US-09-074-476-3	Sequence 3, Appl	C 656	25.2	9.2	2922	4	US-08-683-262B-74	Sequence 74, Appl
584	25.4	9.3	5711	3	US-09-074-476-5	Sequence 5, Appl	C 657	25.2	9.2	2922	3	US-09-361-704-74	Sequence 74, Appl
585	25.4	9.3	5711	4	US-08-989-890-4	Sequence 4, Appl	C 658	25.2	9.2	2950	5	PCT-US93-08386-7	Sequence 7, Appl
586	25.4	9.3	5711	4	US-08-989-890-10	Sequence 10, Appl	C 659	25.2	9.2	2968	5	PCT-US93-08386-1	Sequence 1, Appl
587	25.4	9.3	5711	4	US-10-022-819-1	Sequence 1, Appl	C 660	25.2	9.2	3261	4	US-09-543-681A-3524	Sequence 3524, Ap
588	25.4	9.3	5711	4	US-09-462-401A-1	Sequence 1, Appl	C 661	25.2	9.2	3321	4	US-09-023-655-1361	Sequence 1361, Ap
589	25.4	9.3	5712	1	US-08-825-061-12	Sequence 12, Appl	C 662	25.2	9.2	4344	2	US-08-532-547-4	Sequence 4, Appl
590	25.4	9.3	5712	1	US-08-825-886-12	Sequence 12, Appl	C 663	25.2	9.2	4344	2	US-08-379-658B-4	Sequence 4, Appl
591	25.4	9.3	5712	2	US-08-603-753D-1	Sequence 1, Appl	C 664	25.2	9.2	4344	3	US-08-455-838-4	Sequence 4, Appl
592	25.4	9.3	5712	3	US-09-099-753-1	Sequence 1, Appl	C 665	25.2	9.2	4344	3	US-09-019-809-4	Sequence 4, Appl
593	25.4	9.3	5712	3	US-08-986-106-1	Sequence 1, Appl	C 666	25.2	9.2	4344	4	US-09-471-177-4	Sequence 4, Appl
594	25.4	9.3	5712	3	US-09-007-678B-47	Sequence 47, Appl	C 667	25.2	9.2	4344	4	US-09-220-806-4	Sequence 4, Appl
595	25.4	9.3	5712	4	US-08-989-890-12	Sequence 12, Appl	C 668	25.2	9.2	4866	1	US-08-110-158-5	Sequence 5, Appl
596	25.4	9.3	5712	2	US-08-637-759B-38	Sequence 38, Appl	C 669	25.2	9.2	4867	3	US-09-177-325-12	Sequence 12, Appl
597	25.4	9.3	5746	3	US-08-871-355A-38	Sequence 38, Appl	C 670	25.2	9.2	4967	3	US-09-411-812A-12	Sequence 12, Appl
598	25.4	9.3	5746	3	US-09-201-945-38	Sequence 38, Appl	C 671	25.2	9.2	4967	3	US-09-590-113-12	Sequence 12, Appl
599	25.4	9.3	5770	1	US-08-825-061-5	Sequence 5, Appl	C 672	25.2	9.2	5501	4	US-10-204-708-37	Sequence 37, Appl
600	25.4	9.3	5770	1	US-08-825-886-5	Sequence 5, Appl	C 673	25.2	9.2	5590	4	US-09-773-416-13	Sequence 13, Appl
601	25.4	9.3	5770	4	US-08-989-890-5	Sequence 5, Appl	C 674	25.2	9.2	5590	4	US-09-620-312D-823	Sequence 823, App
602	25.4	9.3	5914	1	US-08-480-784-1	Sequence 1, Appl	C 675	25.2	9.2	5683	4	US-10-204-708-25	Sequence 25, Appl
603	25.4	9.3	5914	1	US-08-483-553-1	Sequence 1, Appl	C 676	25.2	9.2	42571	4	US-09-810-347-3	Sequence 3, Appl
604	25.4	9.3	5914	1	US-08-487-002-1	Sequence 1, Appl	C 677	25.2	9.2	43795	3	US-08-742-185-101	Sequence 101, App
605	25.4	9.3	5914	1	US-08-483-554B-1	Sequence 1, Appl	C 678	25.2	9.2	70000	4	US-09-851-896-3	Sequence 3, Appl
606	25.4	9.3	5914	3	US-08-488-011B-1	Sequence 1, Appl	C 679	25.2	9.2	89047	4	US-09-596-002-34	Sequence 34, Appl
607	25.4	9.3	5914	3	US-08-850-727-1	Sequence 1, Appl	C 680	25	9.2	399	4	US-09-621-976-8976	Sequence 8976, Ap
608	25.4	9.3	5914	5	PCT-US95-10202-1	Sequence 1, Appl	C 681	25	9.2	449	4	US-09-621-976-13952	Sequence 13952, A
609	25.4	9.3	5914	5	PCT-US95-10203-1	Sequence 1, Appl	C 682	25	9.2	462	3	US-09-227-357-124	Sequence 124, App
610	25.4	9.3	5914	5	PCT-US95-10220-1	Sequence 1, Appl	C 683	25	9.2	474	4	US-09-513-999C-32431	Sequence 32431, A
C 611	25.4	9.3	5982	4	US-09-576-594-68	Sequence 68, Appl	C 684	25	9.2	477	3	US-09-026-343-12	Sequence 12, Appl
612	25.4	9.3	9636	4	US-09-150-867-2	Sequence 2, Appl	C 685	25	9.2	477	3	US-09-362-871-12	Sequence 12, Appl

686	25	9.2	510	4	US-09-621-976-2430	Sequence 2430, Ap	759	24.8	9.1	344	4	US-09-513-999C-10414	Sequence 10414, A
687	25	9.2	564	4	US-09-248-796A-2164	Sequence 2164, Ap	c 760	24.8	9.1	375	4	US-09-621-976-17190	Sequence 17190, A
688	25	9.2	567	4	US-08-270-767-11215	Sequence 11215, A	c 761	24.8	9.1	382	4	US-09-513-999C-32861	Sequence 32861, A
689	25	9.2	700	3	US-09-236-097-11	Sequence 11, Appl	762	24.8	9.1	396	4	US-09-640-173-16	Sequence 16, Appl
690	25	9.2	724	3	US-08-936-165A-226	Sequence 226, App	763	24.8	9.1	396	4	US-09-713-550-16	Sequence 16, Appl
691	25	9.2	744	4	US-09-710-279-2069	Sequence 2069, Ap	764	24.8	9.1	396	4	US-08-825-294-16	Sequence 16, Appl
692	25	9.2	822	4	US-09-248-796A-13402	Sequence 13402, A	765	24.8	9.1	396	4	US-09-970-966-16	Sequence 16, Appl
693	25	9.2	852	3	US-09-461-697-1	Sequence 1, Appli	c 766	24.8	9.1	398	4	US-09-621-976-8399	Sequence 8399, Ap
694	25	9.2	888	4	US-08-270-767-10771	Sequence 10771, A	c 767	24.8	9.1	472	4	US-09-621-976-13817	Sequence 13817, A
695	25	9.2	924	4	US-09-248-796A-6148	Sequence 6148, Ap	c 768	24.8	9.1	561	4	US-09-107-532A-1311	Sequence 1311, Ap
696	25	9.2	978	4	US-09-328-352-604	Sequence 604, App	769	24.8	9.1	561	4	US-09-710-279-2529	Sequence 2529, Ap
697	25	9.2	1086	4	US-09-016-434-1335	Sequence 1335, Ap	770	24.8	9.1	685	3	US-08-881-094-14	Sequence 14, Appl
698	25	9.2	1086	4	US-09-944-807-7	Sequence 7, Appli	771	24.8	9.1	688	4	US-09-270-767-12682	Sequence 12682, A
699	25	9.2	1152	4	US-09-710-279-2167	Sequence 2167, Ap	772	24.8	9.1	762	4	US-09-248-796A-2764	Sequence 2764, Ap
700	25	9.2	1257	4	US-09-248-796A-4211	Sequence 4211, Ap	773	24.8	9.1	785	1	US-08-463-090B-2	Sequence 2, Appli
701	25	9.2	1359	3	US-09-134-001C-1098	Sequence 1098, Ap	c 774	24.8	9.1	885	4	US-09-248-796A-2033	Sequence 2033, Ap
702	25	9.2	1422	3	US-09-227-357-18	Sequence 18, Appl	775	24.8	9.1	951	3	US-09-134-001C-1418	Sequence 1418, Ap
703	25	9.2	1422	4	US-09-107-532A-1717	Sequence 1717, Ap	776	24.8	9.1	951	1	US-07-855-412B-2	Sequence 2, Appli
704	25	9.2	1519	1	US-07-971-759-19	Sequence 19, Appl	777	24.8	9.1	951	2	US-08-308-887A-2	Sequence 2, Appli
705	25	9.2	1604	3	US-09-438-938-9	Sequence 9, Appli	778	24.8	9.1	951	3	US-08-881-094-2	Sequence 2, Appli
706	25	9.2	1604	4	US-09-668-885A-9	Sequence 9, Appli	779	24.8	9.1	993	3	US-08-969-644-21	Sequence 21, Appl
707	25	9.2	1776	3	US-08-676-882-1	Sequence 1, Appli	780	24.8	9.1	993	3	US-08-444-189-21	Sequence 21, Appl
708	25	9.2	1779	4	US-09-248-796A-291	Sequence 291, App	781	24.8	9.1	993	3	US-08-468-544-21	Sequence 21, Appl
709	25	9.2	2121	2	US-08-897-340-6	Sequence 6, Appli	c 782	24.8	9.1	1053	4	US-09-107-532A-3626	Sequence 3626, Ap
710	25	9.2	2121	3	US-09-252-329-6	Sequence 6, Appli	c 783	24.8	9.1	1141	4	US-09-806-708B-22	Sequence 22, Appl
711	25	9.2	2232	4	US-09-248-796A-3250	Sequence 3250, Ap	784	24.8	9.1	1430	4	US-09-369-247-31	Sequence 31, Appl
712	25	9.2	2598	4	US-09-248-796A-3589	Sequence 3589, Ap	785	24.8	9.1	1433	4	US-09-369-247-57	Sequence 57, Appl
713	25	9.2	2869	4	US-08-809-955-18	Sequence 18, Appl	786	24.8	9.1	1530	4	US-03-248-796A-6635	Sequence 6635, Ap
714	25	9.2	3117	4	US-09-710-279-3427	Sequence 3427, Ap	787	24.8	9.1	1554	4	US-09-976-594-1115	Sequence 1115, Ap
715	25	9.2	3117	4	US-09-710-279-4005	Sequence 4005, Ap	788	24.8	9.1	1581	3	US-09-313-300-1	Sequence 1, Appli
716	25	9.2	3280	2	US-09-710-279-3500	Sequence 3500, Ap	c 789	24.8	9.1	1695	4	US-09-506-286B-9	Sequence 9, Appli
717	25	9.2	3290	2	US-08-729-955A-1	Sequence 1, Appli	c 790	24.8	9.1	1695	4	US-09-506-286B-12	Sequence 12, Appl
718	25	9.2	3663	4	US-09-540-236-1091	Sequence 1091, Ap	c 791	24.8	9.1	1695	4	US-09-762-861B-9	Sequence 9, Appli
719	25	9.2	3927	4	US-09-134-000C-3183	Sequence 3183, Ap	c 792	24.8	9.1	1695	4	US-09-762-861B-12	Sequence 12, Appl
720	25	9.2	4702	1	US-08-038-682-8	Sequence 8, Appli	c 793	24.8	9.1	1695	4	US-10-065-133A-9	Sequence 9, Appli
721	25	9.2	4702	1	US-08-302-832-8	Sequence 8, Appli	c 794	24.8	9.1	1695	4	US-10-065-133A-12	Sequence 12, Appl
722	25	9.2	4702	2	US-08-530-198-8	Sequence 8, Appli	c 795	24.8	9.1	1698	4	US-09-622-951-1	Sequence 1, Appli
723	25	9.2	4702	2	US-08-469-880-8	Sequence 8, Appli	796	24.8	9.1	1737	4	US-09-248-796A-699	Sequence 699, App
724	25	9.2	4702	2	US-08-728-470-8	Sequence 8, Appli	797	24.8	9.1	1751	4	US-09-270-767-11403	Sequence 11403, A
725	25	9.2	4702	3	US-08-719-641-8	Sequence 8, Appli	c 798	24.8	9.1	1762	1	US-08-105-483-300	Sequence 300, App
726	25	9.2	4803	1	US-08-617-697-8	Sequence 8, Appli	c 799	24.8	9.1	1762	1	US-08-709-209-300	Sequence 300, App
727	25	9.2	4866	1	US-08-110-158-5	Sequence 5, Appli	c 800	24.8	9.1	1762	1	US-08-458-101-300	Sequence 300, App
728	25	9.2	5197	1	US-08-131-365B-53	Sequence 53, Appl	c 801	24.8	9.1	1762	4	US-09-506-286B-7	Sequence 7, Appli
729	25	9.2	5197	2	US-08-668-123-53	Sequence 53, Appl	c 802	24.8	9.1	1762	4	US-09-506-286B-10	Sequence 10, Appl
730	25	9.2	6314	4	US-09-620-312D-98	Sequence 98, Appl	c 803	24.8	9.1	1762	4	US-09-762-861B-7	Sequence 7, Appli
731	25	9.2	7672	4	US-09-220-132-24	Sequence 24, Appl	c 804	24.8	9.1	1762	4	US-09-762-861B-10	Sequence 10, Appl
732	25	9.2	9700	4	US-09-698-295-9	Sequence 9, Appli	c 805	24.8	9.1	1762	4	US-10-065-133A-7	Sequence 7, Appli
733	25	9.2	9865	4	US-09-698-295-2	Sequence 2, Appli	c 806	24.8	9.1	1762	4	US-10-065-133A-10	Sequence 10, Appl
734	25	9.2	11049	4	US-10-204-708-24	Sequence 24, Appl	c 807	24.8	9.1	2004	4	US-09-710-279-197	Sequence 197, App
735	25	9.2	11485	3	US-09-410-464-9	Sequence 9, Appli	c 808	24.8	9.1	2046	4	US-09-248-796A-4279	Sequence 4279, Ap
736	25	9.2	15222	2	US-08-801-898A-23	Sequence 23, Appl	c 809	24.8	9.1	2108	4	US-09-221-017B-305	Sequence 305, App
737	25	9.2	15222	3	US-08-962-690-12	Sequence 12, Appl	810	24.8	9.1	2192	4	US-08-855-323-6	Sequence 6, Appli
738	25	9.2	15223	2	US-08-892-403A-1	Sequence 1, Appli	811	24.8	9.1	2467	2	US-08-701-240-1	Sequence 1, Appli
739	25	9.2	15223	3	US-08-720-132-1	Sequence 1, Appli	812	24.8	9.1	2467	3	US-09-138-236-1	Sequence 1, Appli
740	25	9.2	15223	4	US-09-291-894-1	Sequence 1, Appli	c 813	24.8	9.1	2595	4	US-09-134-000C-2620	Sequence 2620, Ap
741	25	9.2	15223	4	US-09-847-173-1	Sequence 1, Appli	c 814	24.8	9.1	2835	4	US-09-614-221A-162	Sequence 162, App
742	25	9.2	18596	3	US-09-318-448-11	Sequence 11, Appl	c 815	24.8	9.1	2886	4	US-09-976-594-960	Sequence 960, App
743	25	9.2	18597	4	US-09-962-665-8	Sequence 8, Appli	c 816	24.8	9.1	3036	4	US-09-710-279-3822	Sequence 3822, Ap
744	25	9.2	18597	4	US-09-963-333-8	Sequence 8, Appli	817	24.8	9.1	3323	4	US-09-341-505-5	Sequence 5, Appli
745	25	9.2	18597	4	US-09-962-677-8	Sequence 8, Appli	c 818	24.8	9.1	3323	4	US-09-341-505-6	Sequence 6, Appli
746	25	9.2	193300	4	US-09-966-451-10	Sequence 10, Appl	c 819	24.8	9.1	3350	3	US-08-617-860B-3	Sequence 3, Appli
747	25	9.2	193303	4	US-09-596-002-20	Sequence 20, Appl	820	24.8	9.1	3390	1	US-08-453-742-26	Sequence 26, Appl
748	25	9.2	98844	4	US-09-791-211-10	Sequence 10, Appl	821	24.8	9.1	3390	1	US-08-454-464-26	Sequence 26, Appl
749	25	9.2	99916	4	US-09-816-095-3	Sequence 3, Appli	822	24.8	9.1	3390	1	US-08-453-222-26	Sequence 26, Appl
750	25	9.2	128779	4	US-09-497-855A-38	Sequence 38, Appl	823	24.8	9.1	3390	1	US-08-452-802-26	Sequence 26, Appl
751	25	9.2	148567	4	US-09-801-876B-3	Sequence 3, Appli	824	24.8	9.1	3416	1	US-08-453-742-24	Sequence 24, Appl
752	25	9.2	148567	4	US-10-254-869-3	Sequence 3, Appli	825	24.8	9.1	3416	1	US-08-454-464-24	Sequence 24, Appl
753	25	9.2	193303	4	US-09-497-855A-37	Sequence 37, Appl	826	24.8	9.1	3416	1	US-08-453-222-24	Sequence 24, Appl
754	25	9.2	193303	4	US-09-497-855A-44	Sequence 44, Appl	827	24.8	9.1	3416	1	US-08-452-802-24	Sequence 24, Appl
755	25	9.2	202001	4	US-09-734-674-3	Sequence 3, Appli	c 828	24.8	9.1	3504	4	US-09-710-279-3859	Sequence 3859, Ap
756	24.8	9.1	267	4	US-09-513-999C-13172	Sequence 13172, A	c 829	24.8	9.1	3556	4	US-09-270-767-10439	Sequence 10439, A
757	24.8	9.1	285	4	US-09-270-767-26978	Sequence 26978, A	830	24.8	9.1	3588	1	US-07-792-885A-2	Sequence 2, Appli
758	24.8	9.1	291	4	US-09-621-976-17250	Sequence 17250, A	831	24.8	9.1	3588	4	US-09-016-434-1839	Sequence 1189, Ap

832	24.8	9.1	3674	4	US-09-482-273-73	Sequence 73, Appl	C 905	24.6	9.0	866	4	US-09-736-457-1824	Sequence 1824, Ap
833	24.8	9.1	5285	3	US-09-402-328-1	Sequence 1, Appli	C 906	24.6	9.0	866	4	US-09-671-325-1824	Sequence 1824, Ap
C 834	24.8	9.1	5333	4	US-08-956-171E-170	Sequence 170, App	C 907	24.6	9.0	879	4	US-09-270-767-11336	Sequence 11336, A
C 835	24.8	9.1	5333	4	US-08-956-171E-170	Sequence 170, App	C 908	24.6	9.0	902	4	US-09-149-476-169	Sequence 169, App
836	24.8	9.1	5948	2	US-08-662-227-1	Sequence 1, Appli	C 909	24.6	9.0	927	4	US-09-484-970B-12	Sequence 12, Appl
837	24.8	9.1	5948	4	US-09-017-947-1	Sequence 1, Appli	C 910	24.6	9.0	956	4	US-09-221-017B-484	Sequence 484, App
838	24.8	9.1	5948	4	US-09-925-442-1	Sequence 1, Appli	C 911	24.6	9.0	1089	3	US-09-004-731-15	Sequence 15, Appl
839	24.8	9.1	6005	4	US-09-023-655-341	Sequence 341, App	C 912	24.6	9.0	1089	3	US-09-004-731-17	Sequence 17, Appl
C 840	24.8	9.1	6249	4	US-09-634-238-404	Sequence 404, App	C 913	24.6	9.0	1089	3	US-08-749-699-15	Sequence 15, Appl
C 841	24.8	9.1	7502	3	US-08-969-644-6	Sequence 6, Appli	C 914	24.6	9.0	1089	3	US-08-749-699-17	Sequence 17, Appl
C 842	24.8	9.1	7502	3	US-08-444-189-6	Sequence 6, Appli	C 915	24.6	9.0	1089	3	US-09-134-001C-1833	Sequence 1833, Ap
C 843	24.8	9.1	7502	3	US-08-468-544-6	Sequence 6, Appli	C 916	24.6	9.0	1089	3	US-09-004-729-15	Sequence 15, Appl
C 844	24.8	9.1	13715	4	US-08-956-171E-195	Sequence 195, App	C 917	24.6	9.0	1089	4	US-09-004-729-17	Sequence 17, Appl
C 845	24.8	9.1	13715	4	US-08-781-986A-195	Sequence 195, App	C 918	24.6	9.0	1113	4	US-09-340-236-1169	Sequence 1169, Ap
C 846	24.8	9.1	13830	4	US-09-614-981-8	Sequence 8, Appli	C 919	24.6	9.0	1233	4	US-09-248-796A-1779	Sequence 1779, Ap
C 847	24.8	9.1	40000	4	US-09-780-049-18	Sequence 18, Appl	C 920	24.6	9.0	1278	4	US-09-248-796A-1321	Sequence 1321, Ap
C 848	24.8	9.1	70559	4	US-09-409-800B-1	Sequence 1, Appli	C 921	24.6	9.0	1421	4	US-09-592-054-3	Sequence 5, Appli
849	24.8	9.1	162450	3	US-09-345-882-1	Sequence 1, Appli	C 922	24.6	9.0	1455	4	US-09-592-054-5	Sequence 5, Appli
850	24.8	9.1	392000	4	US-10-037-983-11	Sequence 11, Appl	C 923	24.6	9.0	1522	3	US-09-248-796A-6254	Sequence 6254, Ap
C 851	24.8	9.0	189	4	US-09-248-796A-14100	Sequence 14100, A	C 924	24.6	9.0	1533	4	US-09-056-783-1	Sequence 1, Appli
C 852	24.6	9.0	195	4	US-09-248-796A-8271	Sequence 8271, Ap	C 925	24.6	9.0	1542	4	US-09-134-000C-3330	Sequence 3330, Ap
C 853	24.6	9.0	231	4	US-09-248-796A-9774	Sequence 9774, Ap	C 926	24.6	9.0	1569	4	US-09-543-681A-1015	Sequence 1015, Ap
C 854	24.6	9.0	258	4	US-09-248-796A-10108	Sequence 10108, A	C 927	24.6	9.0	1695	4	US-09-592-054-3	Sequence 3, Appli
C 855	24.6	9.0	318	4	US-09-248-796A-12743	Sequence 12743, A	C 928	24.6	9.0	1827	4	US-09-792-024-6	Sequence 6, Appli
C 856	24.6	9.0	340	4	US-09-702-705-34	Sequence 34, Appl	C 929	24.6	9.0	1920	4	US-09-543-681A-3546	Sequence 3546, Ap
C 857	24.6	9.0	340	4	US-09-736-457-34	Sequence 34, Appl	C 930	24.6	9.0	1929	4	US-09-614-221A-285	Sequence 285, App
C 858	24.6	9.0	340	4	US-09-614-124B-34	Sequence 34, Appl	C 931	24.6	9.0	2003	4	US-09-665-479A-1	Sequence 1, Appli
C 859	24.6	9.0	340	4	US-09-671-325-34	Sequence 34, Appl	C 932	24.6	9.0	2007	2	US-08-743-637B-169	Sequence 169, App
860	24.6	9.0	340	4	US-09-589-184-34	Sequence 34, Appl	C 933	24.6	9.0	2028	3	US-08-526-840B-169	Sequence 169, App
861	24.6	9.0	340	4	US-09-658-824-34	Sequence 34, Appl	C 934	24.6	9.0	2036	3	US-09-134-001C-1710	Sequence 1710, Ap
862	24.6	9.0	351	4	US-09-248-796A-11005	Sequence 11005, A	C 935	24.6	9.0	2044	1	US-08-071-601-3	Sequence 3, Appli
863	24.6	9.0	354	4	US-09-248-796A-1703	Sequence 1703, Ap	C 936	24.6	9.0	2044	2	US-08-621-100-3	Sequence 3, Appli
864	24.6	9.0	355	4	US-09-513-999C-11365	Sequence 11365, A	C 937	24.6	9.0	2044	2	US-09-543-681A-1015	Sequence 1015, Ap
865	24.6	9.0	359	4	US-09-270-767-3877	Sequence 3877, Ap	C 938	24.6	9.0	2183	3	US-09-592-054-3	Sequence 3, Appli
866	24.6	9.0	359	4	US-09-270-767-19159	Sequence 19159, A	C 939	24.6	9.0	2259	4	US-09-710-279-347	Sequence 347, App
867	24.6	9.0	417	4	US-09-643-597-189	Sequence 189, App	C 940	24.6	9.0	2336	3	US-09-228-986-10	Sequence 10, Appl
868	24.6	9.0	417	4	US-09-480-884A-189	Sequence 189, App	C 941	24.6	9.0	2336	4	US-10-101-464A-10	Sequence 10, Appl
869	24.6	9.0	417	4	US-09-542-615A-189	Sequence 189, App	C 942	24.6	9.0	2415	3	US-09-134-001C-2381	Sequence 2381, Ap
870	24.6	9.0	417	4	US-09-606-421B-189	Sequence 189, App	C 943	24.6	9.0	2482	1	US-09-626-959D-1	Sequence 1, Appli
871	24.6	9.0	417	4	US-09-466-396A-189	Sequence 189, App	C 944	24.6	9.0	2625	2	US-08-468-036-2	Sequence 2, Appli
872	24.6	9.0	417	4	US-09-476-496A-189	Sequence 189, App	C 945	24.6	9.0	2625	2	US-08-736-843-2	Sequence 2, Appli
873	24.6	9.0	417	4	US-09-630-940B-189	Sequence 189, App	C 946	24.6	9.0	2677	4	US-09-221-017B-959	Sequence 959, App
874	24.6	9.0	442	3	US-09-040-984-24	Sequence 24, Appl	C 947	24.6	9.0	2739	4	US-09-248-796A-2638	Sequence 2638, Ap
875	24.6	9.0	442	3	US-09-123-912-24	Sequence 24, Appl	C 948	24.6	9.0	2949	3	US-09-412-554A-3	Sequence 3, Appli
876	24.6	9.0	442	4	US-09-643-597-24	Sequence 24, Appl	C 949	24.6	9.0	3066	4	US-09-710-279-3818	Sequence 110, App
877	24.6	9.0	442	4	US-09-480-884A-24	Sequence 24, Appl	C 950	24.6	9.0	3141	4	US-09-569-098A-110	Sequence 110, App
878	24.6	9.0	442	4	US-09-542-615A-24	Sequence 24, Appl	C 951	24.6	9.0	3189	4	US-09-447-399-1	Sequence 1, Appli
879	24.6	9.0	442	4	US-09-606-421B-24	Sequence 24, Appl	C 952	24.6	9.0	3285	4	US-09-206-942-68	Sequence 68, Appl
880	24.6	9.0	442	4	US-09-221-107-24	Sequence 24, Appl	C 953	24.6	9.0	3300	3	US-08-913-842-4	Sequence 4, Appli
881	24.6	9.0	442	4	US-09-466-396A-24	Sequence 24, Appl	C 954	24.6	9.0	3328	4	US-09-710-279-3446	Sequence 3446, Ap
882	24.6	9.0	442	4	US-09-476-496A-24	Sequence 24, Appl	C 955	24.6	9.0	3420	4	US-09-447-399-3	Sequence 3, Appli
883	24.6	9.0	442	4	US-09-630-940B-24	Sequence 24, Appl	C 956	24.6	9.0	3518	4	US-10-014-882-3	Sequence 3, Appli
C 884	24.6	9.0	471	4	US-09-248-796A-8789	Sequence 8789, Ap	C 957	24.6	9.0	3657	4	US-09-710-279-3888	Sequence 3888, Ap
885	24.6	9.0	472	4	US-09-621-976-10170	Sequence 10170, A	C 958	24.6	9.0	3701	4	US-09-710-279-3392	Sequence 3392, Ap
886	24.6	9.0	472	4	US-09-513-999C-3922	Sequence 3922, Ap	C 959	24.6	9.0	3922	3	US-09-148-751-1	Sequence 1, Appli
C 887	24.6	9.0	527	4	US-09-270-767-26896	Sequence 26896, A	C 960	24.6	9.0	3922	3	US-09-252-509-3	Sequence 3, Appli
C 888	24.6	9.0	545	4	US-09-621-976-3524	Sequence 3524, Ap	C 961	24.6	9.0	3937	4	US-09-620-312D-280	Sequence 280, App
889	24.6	9.0	675	3	US-09-334-001C-811	Sequence 811, App	C 962	24.6	9.0	4348	4	US-09-595-684B-22	Sequence 22, Appl
890	24.6	9.0	688	3	US-09-328-111-292	Sequence 292, App	C 963	24.6	9.0	4532	4	US-09-930-377B-1	Sequence 1, Appli
891	24.6	9.0	711	3	US-09-004-731-21	Sequence 21, Appl	C 964	24.6	9.0	5107	4	US-09-358-383C-15	Sequence 15, Appl
892	24.6	9.0	711	3	US-08-749-699-21	Sequence 21, Appl	C 965	24.6	9.0	5116	1	US-08-038-882-1	Sequence 1, Appli
C 893	24.6	9.0	711	4	US-09-004-729-21	Sequence 21, Appl	C 966	24.6	9.0	5116	1	US-08-302-832-1	Sequence 1, Appli
C 894	24.6	9.0	715	4	US-09-270-767-788	Sequence 788, App	C 967	24.6	9.0	5116	2	US-08-530-198-1	Sequence 1, Appli
C 895	24.6	9.0	715	4	US-09-270-767-16070	Sequence 16070, A	C 968	24.6	9.0	5116	2	US-08-469-880-1	Sequence 1, Appli
C 896	24.6	9.0	774	3	US-09-004-731-18	Sequence 18, Appl	C 969	24.6	9.0	5116	2	US-08-728-470-1	Sequence 1, Appli
C 897	24.6	9.0	774	3	US-09-004-731-20	Sequence 20, Appl	C 970	24.6	9.0	5116	2	US-08-617-697-1	Sequence 1, Appli
C 898	24.6	9.0	774	3	US-08-749-699-18	Sequence 18, Appl	C 971	24.6	9.0	5116	3	US-08-719-641-1	Sequence 1, Appli
C 899	24.6	9.0	774	3	US-08-749-699-20	Sequence 20, Appl	C 972	24.6	9.0	5316	4	US-09-206-942-66	Sequence 66, Appl
C 900	24.6	9.0	774	4	US-09-004-729-18	Sequence 18, Appl	C 973	24.6	9.0	5340	4	US-09-627-123-21	Sequence 21, Appl
C 901	24.6	9.0	774	4	US-09-004-729-20	Sequence 20, Appl	C 974	24.6	9.0	5432	1	US-08-592-214A-20	Sequence 20, Appl
C 902	24.6	9.0	804	4	US-09-270-767-6966	Sequence 6966, Ap	C 975	24.6	9.0	5855	3	US-09-149-976-20	Sequence 20, Appl
C 903	24.6	9.0	804	4	US-09-270-767-22248	Sequence 22248, A	C 976	24.6	9.0	5855	3	US-09-358-383C-14	Sequence 14, Appl
C 904	24.6	9.0	866	4	US-09-702-705-1824	Sequence 1824, Ap	C 977	24.6	9.0	5955	4		

978	24.6	9.0	9171	1	US-08-038-682-5	Sequence 5, Appli	c1051	24.4	8.9	1107	1	US-08-621-081A-3	Sequence 3, Appli
979	24.6	9.0	9171	1	US-08-302-832-5	Sequence 5, Appli	c1052	24.4	8.9	1107	2	US-08-876-781-3	Sequence 3, Appli
980	24.6	9.0	9171	2	US-08-530-188-5	Sequence 5, Appli	c1053	24.4	8.9	1110	4	US-09-248-796A-2045	Sequence 2045, Ap
981	24.6	9.0	9171	2	US-08-469-880-5	Sequence 5, Appli	c1054	24.4	8.9	1140	4	US-09-540-236-1565	Sequence 1565, Ap
982	24.6	9.0	9171	2	US-08-728-470-5	Sequence 5, Appli	c1055	24.4	8.9	1275	4	US-09-248-796A-7220	Sequence 7220, Ap
983	24.6	9.0	9171	2	US-08-617-697-5	Sequence 5, Appli	c1056	24.4	8.9	1338	4	US-09-328-352-2543	Sequence 2543, Ap
984	24.6	9.0	9171	3	US-08-713-641-5	Sequence 5, Appli	c1057	24.4	8.9	1659	1	US-08-231-729B-1	Sequence 1, Appli
c 985	24.6	9.0	9370	1	US-08-320-559-27	Sequence 27, Appl	c1058	24.4	8.9	1659	1	US-08-231-729B-2	Sequence 2, Appli
c 986	24.6	9.0	9370	1	US-08-545-860D-27	Sequence 27, Appl	c1059	24.4	8.9	1806	4	US-10-140-002-121	Sequence 121, App
c 987	24.6	9.0	9370	5	PCT-US94-04496-27	Sequence 27, Appl	c1060	24.4	8.9	1823	4	US-08-956-171E-371	Sequence 371, App
c 988	24.6	9.0	9391	1	US-08-320-559-25	Sequence 25, Appl	c1061	24.4	8.9	1823	4	US-08-781-986A-371	Sequence 371, App
c 989	24.6	9.0	9391	3	US-08-545-860D-25	Sequence 25, Appl	c1062	24.4	8.9	1833	4	US-09-248-796A-3296	Sequence 3296, Ap
c 990	24.6	9.0	9391	5	PCT-US94-04496-25	Sequence 25, Appl	c1063	24.4	8.9	2069	4	US-09-678-300-3	Sequence 3, Appli
c 991	24.6	9.0	11056	3	US-09-004-838-23	Sequence 23, Appl	c1064	24.4	8.9	2106	4	US-09-248-796A-2525	Sequence 2525, Ap
c 992	24.6	9.0	11093	5	PCT-US87-723-306-5	Sequence 5, Appli	c1065	24.4	8.9	2124	4	US-09-678-300-6	Sequence 6, Appli
c 993	24.6	9.0	11093	5	PCT-US96-10041-5	Sequence 5, Appli	c1066	24.4	8.9	2165	4	US-09-678-300-9	Sequence 9, Appli
c 994	24.6	9.0	14335	4	US-09-596-002-11	Sequence 11, Appl	c1067	24.4	8.9	2220	4	US-09-917-254-28	Sequence 28, Appl
c 995	24.6	9.0	15062	3	US-09-004-838-89	Sequence 89, Appl	c1068	24.4	8.9	2229	4	US-09-774-528-283	Sequence 283, App
c 996	24.6	9.0	19233	4	US-10-204-708-45	Sequence 45, Appl	c1069	24.4	8.9	2232	4	US-09-678-300-12	Sequence 12, Appl
c 997	24.6	9.0	20199	4	US-08-961-527-6	Sequence 6, Appli	c1070	24.4	8.9	2333	1	US-08-427-993B-2	Sequence 2, Appli
c 998	24.6	9.0	36159	4	US-09-749-588-3	Sequence 3, Appli	c1071	24.4	8.9	2333	2	US-08-478-609A-2	Sequence 2, Appli
c 999	24.6	9.0	36159	4	US-10-135-687-3	Sequence 3, Appli	c1072	24.4	8.9	2380	4	US-09-270-767-5110	Sequence 5110, Ap
c1000	24.6	9.0	58407	4	US-08-916-421B-2	Sequence 2, Appli	c1073	24.4	8.9	2380	4	US-09-270-767-20392	Sequence 20392, A
c1001	24.6	9.0	59407	4	US-09-692-570-2	Sequence 2, Appli	c1074	24.4	8.9	2466	4	US-09-248-796A-5058	Sequence 5058, Ap
c1002	24.6	9.0	63588	4	US-09-873-404-3	Sequence 3, Appli	c1075	24.4	8.9	2476	4	US-09-270-767-14107	Sequence 14107, A
c1003	24.6	9.0	63588	4	US-10-243-735-3	Sequence 3, Appli	c1076	24.4	8.9	2808	4	US-09-678-300-2	Sequence 2, Appli
c1004	24.6	9.0	113211	4	US-09-596-002-40	Sequence 40, Appl	c1077	24.4	8.9	2863	4	US-09-678-300-5	Sequence 5, Appli
c1005	24.6	9.0	392000	4	US-10-027-983-11	Sequence 11, Appl	c1078	24.4	8.9	2880	4	US-09-016-434-1125	Sequence 1125, Ap
c1006	24.4	8.9	178	4	US-09-513-999C-33265	Sequence 33265, A	c1079	24.4	8.9	2904	4	US-09-678-300-8	Sequence 8, Appli
c1007	24.4	8.9	240	4	US-09-513-999C-31139	Sequence 31139, A	c1080	24.4	8.9	2971	4	US-09-678-300-11	Sequence 11, Appl
c1008	24.4	8.9	333	4	US-09-513-999C-35549	Sequence 35549, A	c1081	24.4	8.9	3025	4	US-09-976-594-552	Sequence 552, App
c1009	24.4	8.9	381	4	US-09-248-796A-429	Sequence 429, App	c1082	24.4	8.9	3033	4	US-09-525-160B-9	Sequence 9, Appli
c1010	24.4	8.9	382	4	US-09-232-785-275	Sequence 275, App	c1083	24.4	8.9	3038	4	US-09-710-279-3383	Sequence 3383, Ap
c1011	24.4	8.9	429	4	US-09-248-796A-13031	Sequence 13031, A	c1084	24.4	8.9	3138	1	US-07-867-106-4	Sequence 4, Appli
c1012	24.4	8.9	482	4	US-09-513-999C-9104	Sequence 9104, Ap	c1085	24.4	8.9	3213	4	US-09-525-160B-4	Sequence 4, Appli
c1013	24.4	8.9	490	4	US-09-621-976-2432	Sequence 2432, Ap	c1086	24.4	8.9	3270	3	US-08-637-732A-1	Sequence 1, Appli
c1014	24.4	8.9	490	4	US-09-854-133-685	Sequence 685, App	c1087	24.4	8.9	3714	4	US-09-678-300-1	Sequence 1, Appli
c1015	24.4	8.9	518	4	US-10-101-464A-409	Sequence 409, App	c1088	24.4	8.9	3756	4	US-09-710-279-3933	Sequence 3933, Ap
c1016	24.4	8.9	528	4	US-09-543-681A-4036	Sequence 4036, Ap	c1089	24.4	8.9	3834	4	US-09-614-221A-353	Sequence 353, App
c1017	24.4	8.9	530	4	US-09-702-705-721	Sequence 721, App	c1090	24.4	8.9	4053	4	US-09-620-312D-156	Sequence 156, App
c1018	24.4	8.9	530	4	US-09-736-457-721	Sequence 721, App	c1091	24.4	8.9	4201	3	US-08-945-056-4	Sequence 4, Appli
c1019	24.4	8.9	530	4	US-09-614-124B-721	Sequence 721, App	c1092	24.4	8.9	4244	4	US-09-526-193A-27	Sequence 27, Appl
c1020	24.4	8.9	530	4	US-09-671-325-721	Sequence 721, App	c1093	24.4	8.9	4295	4	US-09-620-312D-338	Sequence 338, App
c1021	24.4	8.9	530	4	US-09-589-184-721	Sequence 721, App	c1094	24.4	8.9	4295	3	US-08-781-891-205	Sequence 205, App
c1022	24.4	8.9	530	4	US-09-658-824-721	Sequence 721, App	c1095	24.4	8.9	4792	4	US-09-618-156-205	Sequence 205, App
c1023	24.4	8.9	533	4	US-09-536-059-15	Sequence 15, Appl	c1096	24.4	8.9	4792	4	US-09-345-236B-10	Sequence 10, Appl
c1024	24.4	8.9	543	3	US-08-530-862B-1	Sequence 1, Appli	c1097	24.4	8.9	4792	4	US-09-345-236B-19	Sequence 19, Appl
c1025	24.4	8.9	543	3	US-08-597-313D-1	Sequence 1, Appli	c1098	24.4	8.9	4792	4	US-09-345-236B-33	Sequence 33, Appl
c1026	24.4	8.9	551	4	US-08-956-171E-994	Sequence 994, App	c1099	24.4	8.9	4792	4	US-09-345-236B-36	Sequence 36, Appl
c1027	24.4	8.9	551	4	US-08-781-986A-994	Sequence 994, App	c1100	24.4	8.9	4792	4	US-10-204-708-6	Sequence 6, Appli
c1028	24.4	8.9	555	4	US-09-543-681A-3355	Sequence 3355, Ap	c1101	24.4	8.9	6669	4	US-08-956-171E-175	Sequence 175, App
c1029	24.4	8.9	570	4	US-09-248-796A-13813	Sequence 13813, A	c1102	24.4	8.9	8339	4	US-08-781-986A-175	Sequence 175, App
c1030	24.4	8.9	621	4	US-09-248-796A-109	Sequence 109, App	c1103	24.4	8.9	8339	4	US-10-204-708-23	Sequence 23, Appl
c1031	24.4	8.9	621	4	US-09-248-796A-4638	Sequence 4638, Ap	c1104	24.4	8.9	8339	4	US-08-956-171E-4	Sequence 4, Appli
c1032	24.4	8.9	696	4	US-09-270-767-14786	Sequence 14786, A	c1105	24.4	8.9	8339	4	US-08-781-986A-4	Sequence 4, Appli
c1033	24.4	8.9	723	4	US-09-107-532A-2567	Sequence 2567, Ap	c1106	24.4	8.9	8339	4	US-08-961-527-40	Sequence 40, Appl
c1034	24.4	8.9	807	4	US-09-134-000C-2956	Sequence 2956, Ap	c1107	24.4	8.9	8339	4	US-09-952-060-31	Sequence 31, Appl
c1035	24.4	8.9	822	4	US-09-248-796A-6474	Sequence 6474, Ap	c1108	24.4	8.9	8339	4	US-09-952-060-26	Sequence 26, Appl
c1036	24.4	8.9	857	1	US-08-308-883-1	Sequence 1, Appli	c1109	24.4	8.9	8339	4	US-09-952-060-28	Sequence 28, Appl
c1037	24.4	8.9	857	1	US-08-730-163-1	Sequence 1, Appli	c1110	24.4	8.9	8339	4	US-09-952-060-29	Sequence 29, Appl
c1038	24.4	8.9	857	3	US-08-256-799-1	Sequence 1, Appli	c1111	24.4	8.9	8339	4	US-09-952-060-28	Sequence 28, Appl
c1039	24.4	8.9	857	3	US-08-462-437-1	Sequence 1, Appli	c1112	24.4	8.9	8339	4	US-09-784-316-3	Sequence 3, Appli
c1040	24.4	8.9	867	2	US-09-036-582-36	Sequence 36, Appl	c1113	24.4	8.9	8339	4	US-10-229-124-3	Sequence 3, Appli
c1041	24.4	8.9	867	4	US-09-318-141-36	Sequence 36, Appl	c1114	24.4	8.9	8339	4	US-09-798-096-10	Sequence 10, Appl
c1042	24.4	8.9	885	4	US-09-540-236-1751	Sequence 1751, Ap	c1115	24.4	8.9	8339	4	US-09-596-002-39	Sequence 39, Appl
c1043	24.4	8.9	912	4	US-09-107-532A-1538	Sequence 1538, Ap	c1116	24.4	8.9	8339	4	US-09-822-871-3	Sequence 3, Appli
c1044	24.4	8.9	915	4	US-09-149-476-159	Sequence 159, App	c1117	24.4	8.9	8339	4	US-09-621-976-13589	Sequence 13589, A
c1045	24.4	8.9	915	4	US-09-149-476-294	Sequence 294, App	c1118	24.4	8.9	8339	4	US-09-513-999C-12741	Sequence 12741, A
c1046	24.4	8.9	1036	4	US-09-513-999C-755	Sequence 755, App	c1119	24.4	8.9	8339	4	US-09-621-976-8934	Sequence 8934, Ap
c1047	24.4	8.9	1041	4	US-09-710-279-2033	Sequence 2033, Ap	c1120	24.4	8.9	8339	4	US-09-621-976-9493	Sequence 9493, Ap
c1048	24.4	8.9	1068	3	US-09-134-000C-1915	Sequence 1915, Ap	c1121	24.4	8.9	8339	4	US-09-328-352-1404	Sequence 1404, Ap
c1049	24.4	8.9	1087	4	US-09-919-039-69	Sequence 69, Appli	c1122	24.4	8.9	8339	4	US-09-948-004-9	Sequence 9, Appli
c1050	24.4	8.9	1107	1	US-08-165-038-3	Sequence 3, Appli	c1123	24.4	8.9	8339	4	US-09-702-705-1718	Sequence 1718, Ap

1124	24.2	8.9	343	4	US-09-736-457-1718	Sequence 1718, Ap	1197	24.2	8.9	202001	4	US-09-734-674-3	Sequence 3, Appli
1125	24.2	8.9	343	4	US-09-671-325-1718	Sequence 1718, Ap	1198	24	8.8	192	4	US-09-621-976-19086	Sequence 19086, A
1126	24.2	8.9	343	4	US-09-658-824-1718	Sequence 1718, Ap	1199	24	8.8	194	4	US-09-513-993C-29033	Sequence 29033, A
1127	24.2	8.9	366	4	US-09-107-532A-1621	Sequence 1621, Ap	1200	24	8.8	198	4	US-09-107-532A-2536	Sequence 2536, Ap
1128	24.2	8.9	393	4	US-09-248-796A-7234	Sequence 7234, Ap	1201	24	8.8	282	4	US-09-513-999C-10366	Sequence 10366, A
1129	24.2	8.9	439	4	US-09-270-767-27929	Sequence 27929, A	1202	24	8.8	322	4	US-09-621-976-10214	Sequence 10214, A
1130	24.2	8.9	451	4	US-09-513-999C-21258	Sequence 21258, A	1203	24	8.8	359	4	US-09-513-999C-471	Sequence 471, App
1131	24.2	8.9	474	4	US-09-621-976-16748	Sequence 16748, A	1204	24	8.8	363	4	US-09-710-279-219	Sequence 219, App
1132	24.2	8.9	480	4	US-09-107-532A-385	Sequence 385, App	1205	24	8.8	366	3	US-09-134-001C-319	Sequence 319, App
1133	24.2	8.9	485	4	US-09-270-767-5062	Sequence 5062, Ap	1206	24	8.8	384	4	US-09-248-796A-12750	Sequence 12750, A
1134	24.2	8.9	485	4	US-09-270-767-20344	Sequence 20344, A	1207	24	8.8	396	4	US-09-248-796A-7480	Sequence 7480, Ap
1135	24.2	8.9	564	4	US-09-702-705-729	Sequence 729, App	1208	24	8.8	399	4	US-09-621-976-8976	Sequence 8976, Ap
1136	24.2	8.9	564	4	US-09-736-457-729	Sequence 729, App	1209	24	8.8	406	2	US-08-967-101-22	Sequence 22, Appl
1137	24.2	8.9	564	4	US-09-614-124B-729	Sequence 729, App	1210	24	8.8	406	2	US-08-592-541-22	Sequence 22, Appl
1138	24.2	8.9	564	4	US-09-671-325-729	Sequence 729, App	1211	24	8.8	406	3	US-09-124-698-22	Sequence 22, Appl
1139	24.2	8.9	564	4	US-09-589-184-729	Sequence 729, App	1212	24	8.8	406	3	US-09-127-480-22	Sequence 22, Appl
1140	24.2	8.9	564	4	US-09-658-824-729	Sequence 729, App	1213	24	8.8	406	3	US-08-496-841C-22	Sequence 22, Appl
1141	24.2	8.9	564	4	US-09-248-796A-2884	Sequence 2884, Ap	1214	24	8.8	406	3	US-09-124-523-22	Sequence 22, Appl
1142	24.2	8.9	624	4	US-09-248-796A-1073	Sequence 1073, Ap	1215	24	8.8	406	4	US-09-636-796A-22	Sequence 22, Appl
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1146	24.2	8.9	738	4	US-09-134-000C-3216	Sequence 3216, Ap	1219	24	8.8	441	4	US-09-621-976-9679	Sequence 9679, Ap
1147	24.2	8.9	753	4	US-09-248-796A-13439	Sequence 13439, A	1220	24	8.8	643	4	US-09-513-999C-1863	Sequence 1863, Ap
1148	24.2	8.9	967	4	US-09-453-323-5	Sequence 5, Appli	1221	24	8.8	459	4	US-09-513-999C-32194	Sequence 32194, A
1149	24.2	8.9	1101	3	US-08-945-056-7	Sequence 7, Appli	1222	24	8.8	461	4	US-09-270-767-4475	Sequence 4475, Ap
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1153	24.2	8.9	1835	4	US-09-564-808-5	Sequence 5, Appli	1226	24	8.8	643	4	US-08-781-986A-914	Sequence 914, App
1154	24.2	8.9	2178	4	US-09-248-796A-6746	Sequence 6746, Ap	1227	24	8.8	704	4	US-09-270-767-12416	Sequence 12416, A
1155	24.2	8.9	2237	4	US-09-148-545-104	Sequence 104, App	1228	24	8.8	788	4	US-09-270-767-30059	Sequence 30059, A
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1157	24.2	8.9	2264	3	US-09-126-109-9	Sequence 9, Appli	1230	24	8.8	819	4	US-09-270-767-12417	Sequence 12417, A
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1161	24.2	8.9	3159	4	US-09-134-000C-3215	Sequence 3215, Ap	1234	24	8.8	913	4	US-09-774-528-410	Sequence 410, App
1162	24.2	8.9	3164	4	US-09-710-279-3828	Sequence 3828, Ap	1235	24	8.8	921	3	US-09-247-153-133	Sequence 133, App
1163	24.2	8.9	3172	1	US-07-741-940-3	Sequence 3, Appli	1236	24	8.8	995	3	US-08-976-259-101	Sequence 101, App
1164	24.2	8.9	3172	1	US-08-289-548A-3	Sequence 3, Appli	1237	24	8.8	995	4	US-09-956-004-101	Sequence 101, App
1165	24.2	8.9	3172	1	US-08-452-654-3	Sequence 3, Appli	1238	24	8.8	999	4	US-09-702-705-1664	Sequence 1664, Ap
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1170	24.2	8.9	3234	4	US-09-710-279-3853	Sequence 3853, Ap	1243	24	8.8	1001	3	US-09-671-317-384	Sequence 384, App
1171	24.2	8.9	3243	4	US-09-543-681A-1875	Sequence 1875, Ap	1244	24	8.8	1011	3	US-09-134-001C-1508	Sequence 1508, Ap
1172	24.2	8.9	3268	4	US-09-566-921-91	Sequence 91, Appl	1245	24	8.8	1014	4	US-09-248-796A-9763	Sequence 9763, Ap
1173	24.2	8.9	3384	3	US-08-923-992A-5	Sequence 5, Appli	1246	24	8.8	1107	4	US-09-248-796A-12180	Sequence 12180, A
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1175	24.2	8.9	3609	4	US-09-710-279-3919	Sequence 3919, Ap	1248	24	8.8	1146	4	US-09-328-352-3712	Sequence 3712, Ap
1176	24.2	8.9	3962	1	US-08-336-343A-1	Sequence 1, Appli	1249	24	8.8	1185	4	US-09-248-796A-8117	Sequence 8117, Ap
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1179	24.2	8.9	4465	3	US-08-930-996A-3	Sequence 3, Appli	1252	24	8.8	1226	3	US-09-598-401C-3	Sequence 3, Appli
1180	24.2	8.9	4529	2	US-08-449-645A-16	Sequence 16, Appl	1253	24	8.8	1263	3	US-09-443-184-37	Sequence 37, Appli
1181	24.2	8.9	4529	4	US-08-702-367A-16	Sequence 16, Appl	1254	24	8.8	1266	3	US-09-134-078-3	Sequence 3, Appli
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1183	24.2	8.9	4597	4	US-08-961-527-175	Sequence 175, App	1256	24	8.8	1362	4	US-09-134-000C-2330	Sequence 2330, Ap
1184	24.2	8.9	6326	4	US-10-204-708-57	Sequence 57, Appl	1257	24	8.8	1379	4	US-09-690-454-18	Sequence 18, Appl
1185	24.2	8.9	7780	4	US-08-961-527-18	Sequence 18, Appl	1258	24	8.8	1410	4	US-09-107-532A-18	Sequence 18, Appl
1186	24.2	8.9	8076	4	US-09-532-806-2	Sequence 2, Appli	1259	24	8.8	1413	4	US-09-248-796A-1026	Sequence 1026, Ap
1187	24.2	8.9	9002	4	US-09-532-806-3	Sequence 3, Appli	1260	24	8.8	1424	2	US-08-915-972A-21	Sequence 21, Appl
1188	24.2	8.9	11225	6	5182210-9	Patent No. 5182210	1261	24	8.8	1424	3	US-09-177-909-21	Sequence 21, Appl
1189	24.2	8.9	17136	4	US-08-956-171B-112	Sequence 158, App	1262	24	8.8	1424	3	US-09-056-105-21	Sequence 21, Appl
1190	24.2	8.9	18613	4	US-08-781-986A-112	Sequence 112, App	1263	24	8.8	1494	4	US-09-134-000C-2050	Sequence 2050, Ap
1191	24.2	8.9	18613	4	US-09-820-924-3	Sequence 3, Appli	1264	24	8.8	1710	4	US-09-350-729A-4	Sequence 4, Appli
1192	24.2	8.9	39982	4	US-10-369-626-3	Sequence 3, Appli	1265	24	8.8	1788	4	US-09-583-110-1283	Sequence 1283, Ap
1193	24.2	8.9	39982	4	US-09-146-053-6	Sequence 6, Appli	1266	24	8.8	1906	4	US-09-149-476-137	Sequence 137, App
1194	24.2	8.9	45546	3	US-09-811-469-3	Sequence 3, Appli	1267	24	8.8	1946	2	US-08-755-584-1	Sequence 1, Appli
1195	24.2	8.9	83450	4	US-10-370-659-3	Sequence 3, Appli	1268	24	8.8	1946	3	US-09-192-611-1	Sequence 1, Appli
1196	24.2	8.9	83450	4	US-10-370-659-3	Sequence 3, Appli	1269	24	8.8	1946	4	US-08-755-592A-5	Sequence 5, Appli

c1270	24	8.8	1946	4	US-09-617-923-1	Sequence 1, Appli	1343	24	8.8	319608	4	US-09-539-333D-1	Sequence 1, Appli
1271	24	8.8	2064	3	US-09-276-599-2	Sequence 2, Appli	1344	24	8.8	319608	4	US-09-679-409-1	Sequence 1, Appli
1272	24	8.8	2064	4	US-09-598-401C-2	Sequence 2, Appli	c1345	24	8.8	580073	4	US-08-545-528D-1	Sequence 1, Appli
1273	24	8.8	2097	4	US-09-107-532A-2031	Sequence 2031, Ap	c1346	23.8	8.7	190	4	US-09-513-999C-23294	Sequence 23294, A
1274	24	8.8	2107	3	US-09-180-852-1	Sequence 1, Appli	c1347	23.8	8.7	210	4	US-09-248-796A-12532	Sequence 12532, A
1275	24	8.8	2152	4	US-09-023-655-58	Sequence 58, Appl	c1348	23.8	8.7	258	4	US-08-956-171E-4617	Sequence 4617, Ap
1276	24	8.8	2160	4	US-08-082-849B-30	Sequence 30, Appl	c1349	23.8	8.7	258	4	US-08-781-986A-4617	Sequence 4617, Ap
1277	24	8.8	2160	5	PT-US94-01624-30	Sequence 30, Appl	c1350	23.8	8.7	291	4	US-09-513-999C-22523	Sequence 22523, A
c1278	24	8.8	2169	4	US-09-134-000C-2322	Sequence 2322, Ap	c1351	23.8	8.7	316	4	US-09-513-999C-25024	Sequence 25024, A
1279	24	8.8	2211	2	US-08-799-138-5	Sequence 5, Appli	1352	23.8	8.7	347	3	US-09-134-001C-2127	Sequence 2127, Ap
1280	24	8.8	2211	3	US-09-392-362-5	Sequence 5, Appli	c1353	23.8	8.7	388	4	US-09-513-999C-32074	Sequence 32074, A
1281	24	8.8	2211	4	US-09-350-729A-2	Sequence 2, Appli	c1354	23.8	8.7	397	4	US-09-270-767-26285	Sequence 26285, A
1282	24	8.8	2292	4	US-09-350-729A-3	Sequence 3, Appli	c1355	23.8	8.7	402	4	US-09-248-796A-6258	Sequence 6258, Ap
1283	24	8.8	2295	4	US-09-350-729A-1	Sequence 1, Appli	1356	23.8	8.7	414	1	US-08-256-261-13	Sequence 13, Appl
c1284	24	8.8	2367	3	US-08-278-968A-17	Sequence 17, Appl	1357	23.8	8.7	414	3	US-08-852-239-13	Sequence 13, Appl
c1285	24	8.8	2436	4	US-09-149-476-282	Sequence 282, App	c1358	23.8	8.7	443	4	US-09-397-787-272	Sequence 272, App
1286	24	8.8	2461	1	US-08-832-883-3	Sequence 3, Appli	1359	23.8	8.7	444	4	US-09-543-681A-3762	Sequence 3762, Ap
1287	24	8.8	2461	2	US-08-832-877-113	Sequence 113, App	1360	23.8	8.7	447	3	US-09-134-001C-998	Sequence 998, App
c1288	24	8.8	2604	4	US-09-107-532A-739	Sequence 739, App	1361	23.8	8.7	449	4	US-09-270-767-8502	Sequence 8502, Ap
1289	24	8.8	2610	4	US-09-134-000C-1647	Sequence 1647, Ap	1362	23.8	8.7	449	4	US-09-270-767-23784	Sequence 23784, A
1290	24	8.8	2709	1	US-08-021-601-11	Sequence 11, Appl	1363	23.8	8.7	450	4	US-09-621-976-18513	Sequence 18513, A
1291	24	8.8	2709	1	US-08-082-849B-11	Sequence 11, Appl	1364	23.8	8.7	453	4	US-09-107-532A-3443	Sequence 3443, Ap
1292	24	8.8	2709	5	PT-US94-01624-11	Sequence 11, Appl	c1365	23.8	8.7	563	4	US-09-880-006-4	Sequence 4, Appli
1293	24	8.8	2750	3	US-08-617-860B-33	Sequence 33, Appl	c1366	23.8	8.7	631	4	US-09-270-767-2848	Sequence 2848, Ap
c1294	24	8.8	2757	4	US-09-016-434-1201	Sequence 1201, Ap	c1367	23.8	8.7	631	4	US-09-270-767-18130	Sequence 18130, A
c1295	24	8.8	2757	4	US-10-215-448-4	Sequence 4, Appli	c1368	23.8	8.7	670	3	US-08-961-083-161	Sequence 161, App
1296	24	8.8	2885	4	US-09-620-312D-900	Sequence 900, App	c1369	23.8	8.7	670	4	US-09-536-784-161	Sequence 161, App
1297	24	8.8	3083	3	US-09-276-599-1	Sequence 1, Appli	1370	23.8	8.7	693	4	US-09-270-767-29615	Sequence 29615, A
1298	24	8.8	3083	4	US-09-598-401C-1	Sequence 1, Appli	c1371	23.8	8.7	715	4	US-09-270-767-10815	Sequence 10815, A
c1299	24	8.8	3320	4	US-09-710-279-3337	Sequence 3337, Ap	1372	23.8	8.7	735	4	US-09-248-796A-6082	Sequence 6082, Ap
c1300	24	8.8	3454	4	US-09-710-279-3998	Sequence 3998, Ap	c1373	23.8	8.7	765	4	US-09-248-796A-6256	Sequence 6256, Ap
1301	24	8.8	3462	4	US-09-710-279-4440	Sequence 4440, Ap	1374	23.8	8.7	765	4	US-09-248-796A-8429	Sequence 8429, Ap
c1302	24	8.8	3504	2	US-08-760-797A-2	Sequence 2, Appli	1375	23.8	8.7	788	4	US-09-016-434-314	Sequence 314, App
c1303	24	8.8	3504	2	US-08-760-797A-4	Sequence 4, Appli	1376	23.8	8.7	795	4	US-09-919-172-17	Sequence 17, Appl
c1304	24	8.8	3504	3	US-08-932-929B-2	Sequence 2, Appli	c1377	23.8	8.7	852	4	US-09-248-796A-1077	Sequence 1077, Ap
c1305	24	8.8	3504	3	US-08-932-929B-4	Sequence 4, Appli	c1378	23.8	8.7	885	4	US-09-248-796A-3614	Sequence 3614, Ap
c1306	24	8.8	3577	3	US-08-932-929B-4	Sequence 4, Appli	1379	23.8	8.7	888	4	US-09-543-681A-2259	Sequence 2259, Ap
c1307	24	8.8	3824	1	US-09-326-529-3	Sequence 3, Appli	1380	23.8	8.7	897	4	US-09-540-236-144	Sequence 144, App
1308	24	8.8	4235	1	US-08-021-601-3	Sequence 3, Appli	1381	23.8	8.7	914	3	US-09-177-234-2	Sequence 2, Appli
1309	24	8.8	4235	1	US-08-082-849B-3	Sequence 3, Appli	1382	23.8	8.7	929	4	US-09-270-767-14462	Sequence 14462, A
1310	24	8.8	4235	5	PT-US94-01624-3	Sequence 3, Appli	1383	23.8	8.7	948	4	US-09-270-767-6477	Sequence 6477, Ap
1311	24	8.8	4267	4	US-09-023-655-1379	Sequence 1379, Ap	1384	23.8	8.7	948	4	US-09-270-767-21759	Sequence 21759, A
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c1313	24	8.8	5554	4	US-09-815-923-1	Sequence 1, Appli	1386	23.8	8.7	957	4	US-09-543-681A-913	Sequence 913, App
c1314	24	8.8	6376	4	US-09-799-451-48	Sequence 48, Appl	1387	23.8	8.7	984	4	US-09-248-796A-10304	Sequence 10304, A
1315	24	8.8	7100	3	US-09-308-375-1	Sequence 1, Appli	1388	23.8	8.7	1026	4	US-09-248-796A-5057	Sequence 5057, Ap
c1316	24	8.8	8920	2	US-08-446-855A-1	Sequence 1, Appli	c1389	23.8	8.7	1032	4	US-09-543-681A-1681	Sequence 1681, Ap
c1317	24	8.8	8920	3	US-09-150-741-1	Sequence 1, Appli	c1390	23.8	8.7	1034	4	US-09-880-006-3	Sequence 3, Appli
1318	24	8.8	10144	4	US-10-204-708-93	Sequence 93, Appl	1391	23.8	8.7	1043	4	US-09-976-594-159	Sequence 159, App
1319	24	8.8	10640	4	US-09-417-485D-5	Sequence 5, Appli	c1392	23.8	8.7	1055	4	US-09-806-708B-23	Sequence 23, Appl
1320	24	8.8	11049	4	US-10-204-708-22	Sequence 22, Appl	1393	23.8	8.7	1096	4	US-09-177-419C-10	Sequence 10, Appl
1321	24	8.8	13425	4	US-08-961-527-151	Sequence 151, App	1394	23.8	8.7	1106	4	US-09-177-419C-5	Sequence 5, Appli
c1322	24	8.8	16550	4	US-08-916-421B-3	Sequence 3, Appli	c1395	23.8	8.7	1107	4	US-09-583-110-2432	Sequence 110, App
c1323	24	8.8	16550	4	US-09-692-570-3	Sequence 3, Appli	1396	23.8	8.7	1122	3	US-08-936-165A-104	Sequence 104, App
c1324	24	8.8	16568	4	US-09-525-906-1	Sequence 1, Appli	c1397	23.8	8.7	1122	4	US-09-583-110-2428	Sequence 2428, Ap
c1325	24	8.8	16569	3	US-09-097-889-2	Sequence 2, Appli	1398	23.8	8.7	1182	4	US-09-134-000C-3346	Sequence 3346, Ap
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c1328	24	8.8	16569	4	US-09-098-079-2	Sequence 2, Appli	c1401	23.8	8.7	1266	4	US-09-543-681A-3619	Sequence 3619, Ap
c1329	24	8.8	16569	4	US-10-053-611-1	Sequence 1, Appli	c1402	23.8	8.7	1271	4	US-09-270-767-11058	Sequence 11058, A
c1330	24	8.8	16995	4	US-08-961-527-82	Sequence 82, Appl	1403	23.8	8.7	1336	4	US-09-270-767-13609	Sequence 13609, A
c1331	24	8.8	20986	4	US-08-961-527-54	Sequence 54, Appl	c1404	23.8	8.7	1348	4	US-09-614-474-5	Sequence 5, Appli
1332	24	8.8	23439	4	US-08-956-171E-38	Sequence 38, Appl	c1405	23.8	8.7	1393	4	US-09-710-279-2725	Sequence 2725, Ap
1333	24	8.8	23439	4	US-08-781-986A-38	Sequence 38, Appl	c1406	23.8	8.7	1407	4	US-09-543-681A-499	Sequence 499, App
c1334	24	8.8	44848	4	US-09-435-739-42	Sequence 42, Appl	1407	23.8	8.7	1425	4	US-09-248-796A-2625	Sequence 2625, Ap
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c1336	24	8.8	49136	3	US-09-422-869-1	Sequence 1, Appli	c1409	23.8	8.7	1461	4	US-09-121-211-18	Sequence 18, Appl
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Listing first 1500 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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214	273	100.0	713	15	US-10-175-590-473	Sequence 473, App
518	140	51.3	1018	15	US-10-270-470-5	Sequence 5, Appli
519	140	51.3	1281	9	US-09-764-870-223	Sequence 223, App
520	140	51.3	1281	14	US-10-125-540-223	Sequence 223, App
521	35.2	12.9	608	18	US-10-425-115-17501	Sequence 77501, A
522	35	12.8	630	13	US-10-027-632-185809	Sequence 185809,
523	35	12.8	630	15	US-10-027-632-185809	Sequence 185809,
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c 527	34.4	12.6	1446	11	US-09-764-875-329	Sequence 329, App

c 528	34.4	12.6	1969	15	US-10-104-047-1747	Sequence 1747, Ap
c 529	34.4	12.6	2086	9	US-09-764-877-3431	Sequence 3431, Ap
c 530	34.4	12.6	2086	16	US-10-242-515-3431	Sequence 3431, Ap
531	34.4	12.6	2772	15	US-10-369-493-25421	Sequence 25421, A
532	34.4	12.5	513509	10	US-09-754-853A-4	Sequence 4, Appli
c 533	34	12.5	140040	16	US-10-275-762-69	Sequence 69, Appl
c 534	33.8	12.4	5144	9	US-09-824-735-1	Sequence 1, Appli
c 535	33.6	12.3	321	11	US-09-864-408A-3941	Sequence 3941, Ap
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c 538	33.6	12.3	9646	15	US-10-311-455-1662	Sequence 1662, Ap
c 539	33.6	12.3	18218	15	US-10-311-455-1921	Sequence 1921, Ap
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542	33.2	12.2	418	18	US-10-425-115-130803	Sequence 130803,
543	33	12.1	462	9	US-09-796-692-8243	Sequence 8243, Ap
544	33	12.1	462	14	US-10-040-862-8243	Sequence 8243, Ap
545	33	12.1	462	16	US-10-057-475B-8243	Sequence 8243, Ap
546	33	12.1	462	16	US-10-154-884B-8243	Sequence 8243, Ap
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c 551	32.8	12.0	9832	15	US-10-311-455-630	Sequence 630, App
c 552	32.8	12.0	65253	15	US-10-085-117-331	Sequence 331, App
c 553	32.6	11.9	489	10	US-09-918-995-10135	Sequence 10135, A
c 554	32.6	11.9	598	13	US-10-027-632-201440	Sequence 201440,
c 555	32.6	11.9	598	15	US-10-027-632-201440	Sequence 201440,
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c 557	32.6	11.9	256190	17	US-10-367-094-163	Sequence 163, App
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c 559	32.4	11.9	427	16	US-10-242-535A-14888	Sequence 14888, A
c 560	32.4	11.9	572	13	US-10-085-783A-14888	Sequence 14888, A
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c 584	31.8	11.6	851	15	US-10-106-698-493	Sequence 493, App
c 585	31.8	11.6	1343	18	US-10-425-115-102080	Sequence 102080,
c 586	31.8	11.6	2680	15	US-10-096-534-37	Sequence 37, Appl
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599	31.4	11.5	6156	15	US-10-204-708-59	Sequence 59, Appl
600	31.4	11.5	6156	16	US-10-240-589C-97	Sequence 97, Appl

601	31.4	11.5	299598	17	US-10-322-696-16	Sequence 16, Appl	C 674	30.6	11.2	68571	15	US-10-401-194-1	Sequence 1, Appl
C 602	31.2	11.4	536	9	US-09-864-761-13184	Sequence 13184, A	C 675	30.6	11.2	81199	13	US-10-087-192-1150	Sequence 1150, Ap
C 603	31.2	11.4	1760	13	US-10-044-090-53	Sequence 53, Appl	C 676	30.6	11.2	85548	14	US-10-175-523-75	Sequence 75, Appl
C 604	31.2	11.4	1072	15	US-10-313-542-139	Sequence 139, App	C 677	30.6	11.2	90043	13	US-10-087-192-1141	Sequence 1141, Ap
C 605	31.2	11.4	1811	17	US-09-764-875-17	Sequence 17, Appl	C 678	30.6	11.2	322101	15	US-10-060-902-1	Sequence 1, Appl
C 606	31.2	11.4	3117	17	US-10-741-601-255	Sequence 255, App	C 679	30.6	11.2	322101	15	US-10-354-247-1	Sequence 1, Appl
C 607	31.2	11.4	3142	16	US-10-641-601-1090	Sequence 1090, Ap	C 680	30.4	11.1	324	9	US-09-983-965-3647	Sequence 3647, A
C 608	31.2	11.4	3142	17	US-10-717-597-161	Sequence 161, App	C 681	30.4	11.1	375	9	US-09-960-352-15014	Sequence 15014, A
C 609	31.2	11.4	3183	17	US-10-741-601-254	Sequence 254, App	C 682	30.4	11.1	423	16	US-10-40-425-265	Sequence 265, App
C 610	31.2	11.4	3199	17	US-10-741-601-257	Sequence 257, App	C 683	30.4	11.1	536	18	US-10-424-599-5497	Sequence 5497, Ap
C 611	31.2	11.4	3303	17	US-10-741-601-256	Sequence 256, App	C 684	30.4	11.1	574	18	US-10-425-115-53609	Sequence 53609, A
C 612	31.2	11.4	3660	15	US-10-341-200-22	Sequence 22, Appl	C 685	30.4	11.1	612	10	US-09-764-891-2532	Sequence 2532, Ap
C 613	31.2	11.4	3670	15	US-10-311-455-1038	Sequence 1038, Ap	C 686	30.4	11.1	760	16	US-10-424-599-44716	Sequence 44716, A
C 614	31.2	11.4	53323	17	US-10-741-601-5695	Sequence 5695, Ap	C 687	30.4	11.1	779	16	US-10-424-599-88179	Sequence 88179, A
C 615	31.2	11.4	84409	17	US-10-741-601-5696	Sequence 5696, Ap	C 688	30.4	11.1	1031	15	US-10-082-828-66	Sequence 66, Appl
C 616	31.2	11.4	172637	9	US-09-805-4584-3	Sequence 3, Appl	C 689	30.4	11.1	1183	13	US-10-027-632-100779	Sequence 100779, A
C 617	31	11.4	397	10	US-09-814-353-20772	Sequence 20772, A	C 690	30.4	11.1	1183	15	US-10-027-632-100779	Sequence 100779, A
C 618	31	11.4	400	10	US-09-814-353-3415	Sequence 3415, Ap	C 691	30.4	11.1	1721	10	US-09-814-353-21087	Sequence 21087, A
C 619	31	11.4	400	10	US-09-814-353-9733	Sequence 9733, Ap	C 692	30.4	11.1	2538	16	US-10-282-122A-35894	Sequence 35894, A
C 620	31	11.4	494	10	US-09-814-353-16117	Sequence 16117, A	C 693	30.4	11.1	2741	17	US-10-437-963-102249	Sequence 102249, A
C 621	31	11.4	603	13	US-10-027-632-185970	Sequence 185970, A	C 694	30.2	11.1	383	16	US-10-242-535A-18104	Sequence 18104, A
C 622	31	11.4	603	13	US-10-027-632-185971	Sequence 185971, A	C 695	30.2	11.1	383	16	US-10-085-783A-18104	Sequence 18104, A
C 623	31	11.4	603	15	US-10-027-632-185970	Sequence 185970, A	C 696	30.2	11.1	896	17	US-10-451-467A-21	Sequence 21, Appl
C 624	31	11.4	603	15	US-10-027-632-185971	Sequence 185971, A	C 697	30.2	11.1	980	13	US-10-027-632-9387	Sequence 9387, Ap
C 625	31	11.4	4233	16	US-10-221-613-419	Sequence 419, App	C 698	30.2	11.1	980	15	US-10-027-632-9387	Sequence 9387, Ap
C 626	31	11.4	4233	18	US-10-473-126-129	Sequence 129, App	C 699	30.2	11.1	980	15	US-10-027-632-9387	Sequence 9387, Ap
C 627	31	11.4	4233	31	US-10-473-126-233	Sequence 233, App	C 700	30.2	11.1	980	15	US-10-027-632-30826	Sequence 30826, A
C 628	31	11.4	4233	31	US-10-473-126-275	Sequence 275, App	C 701	30.2	11.1	1217	9	US-09-822-830A-479	Sequence 479, App
C 629	31	11.4	4233	18	US-10-473-126-379	Sequence 379, App	C 702	30.2	11.1	1246	13	US-10-027-632-122821	Sequence 122821, A
C 630	31	11.4	32248	9	US-09-764-864-1769	Sequence 1769, Ap	C 703	30.2	11.1	1246	15	US-10-027-632-122821	Sequence 122821, A
C 631	31	11.4	32248	9	US-09-764-877-3487	Sequence 3487, Ap	C 704	30.2	11.1	1246	15	US-10-027-632-122821	Sequence 122821, A
C 632	31	11.4	32248	16	US-10-242-515-3487	Sequence 3487, Ap	C 705	30.2	11.1	1246	15	US-10-027-632-122821	Sequence 122821, A
C 633	30.8	11.3	349	16	US-10-424-599-20868	Sequence 20868, A	C 706	30.2	11.1	3589	13	US-10-027-632-258595	Sequence 258595, A
C 634	30.8	11.3	451	13	US-10-027-632-67512	Sequence 67512, A	C 707	30.2	11.1	32192	10	US-09-764-891-7049	Sequence 7049, Ap
C 635	30.8	11.3	451	13	US-10-027-632-306656	Sequence 306656, A	C 708	30.2	11.1	32192	10	US-09-764-891-7049	Sequence 7049, Ap
C 636	30.8	11.3	451	13	US-10-027-632-306656	Sequence 306656, A	C 709	30.2	11.1	32192	10	US-09-764-891-7049	Sequence 7049, Ap
C 637	30.8	11.3	451	13	US-10-027-632-306656	Sequence 306656, A	C 710	30.2	11.1	32192	10	US-09-764-891-7049	Sequence 7049, Ap
C 638	30.8	11.3	451	15	US-10-027-632-67512	Sequence 67512, A	C 711	30.2	11.1	96598	16	US-10-394-948-25	Sequence 25, Appl
C 639	30.8	11.3	451	15	US-10-027-632-67512	Sequence 67512, A	C 712	30.2	11.1	96598	16	US-10-052-482-115	Sequence 115, Appl
C 640	30.8	11.3	451	15	US-10-027-632-306655	Sequence 306655, A	C 713	30	11.0	180	14	US-10-149-121-25	Sequence 25, Appl
C 641	30.8	11.3	451	15	US-10-027-632-306656	Sequence 306656, A	C 714	30	11.0	368	16	US-10-131-827-8547	Sequence 8547, Ap
C 642	30.8	11.3	483	13	US-10-027-632-37791	Sequence 37791, A	C 715	30	11.0	368	17	US-10-437-963-66636	Sequence 66636, A
C 643	30.8	11.3	483	15	US-10-027-632-37791	Sequence 37791, A	C 716	30	11.0	368	17	US-10-437-963-66636	Sequence 66636, A
C 644	30.8	11.3	649	13	US-10-027-632-106912	Sequence 106912, A	C 717	30	11.0	727	13	US-10-027-632-133213	Sequence 133213, A
C 645	30.8	11.3	649	13	US-10-027-632-106913	Sequence 106913, A	C 718	30	11.0	727	13	US-10-027-632-133213	Sequence 133213, A
C 646	30.8	11.3	649	13	US-10-027-632-128127	Sequence 128127, A	C 719	30	11.0	727	13	US-10-027-632-151704	Sequence 151704, A
C 647	30.8	11.3	649	15	US-10-027-632-106912	Sequence 106912, A	C 720	30	11.0	727	13	US-10-027-632-151705	Sequence 151705, A
C 648	30.8	11.3	649	15	US-10-027-632-106913	Sequence 106913, A	C 721	30	11.0	727	15	US-10-027-632-133213	Sequence 133213, A
C 649	30.8	11.3	649	15	US-10-027-632-106913	Sequence 106913, A	C 722	30	11.0	727	15	US-10-027-632-151703	Sequence 151703, A
C 650	30.8	11.3	653	13	US-10-027-632-25280	Sequence 25280, A	C 723	30	11.0	727	15	US-10-027-632-151704	Sequence 151704, A
C 651	30.8	11.3	653	13	US-10-027-632-25281	Sequence 25281, A	C 724	30	11.0	727	15	US-10-027-632-151705	Sequence 151705, A
C 652	30.8	11.3	653	15	US-10-027-632-25280	Sequence 25280, A	C 725	30	11.0	839	18	US-10-739-930-1363	Sequence 1363, Ap
C 653	30.8	11.3	653	15	US-10-027-632-25281	Sequence 25281, A	C 726	30	11.0	1258	18	US-10-425-115-168155	Sequence 168155, A
C 654	30.8	11.3	798	13	US-10-027-632-157032	Sequence 157032, A	C 727	30	11.0	1258	18	US-10-425-115-168155	Sequence 168155, A
C 655	30.8	11.3	798	15	US-10-027-632-157032	Sequence 157032, A	C 728	30	11.0	1575	16	US-10-282-122A-32474	Sequence 32474, A
C 656	30.8	11.3	1236	16	US-10-282-122A-10410	Sequence 10410, A	C 729	30	11.0	1917	9	US-09-974-300-2294	Sequence 2294, Ap
C 657	30.8	11.3	1794	16	US-10-282-122A-40523	Sequence 40523, A	C 730	30	11.0	3009	17	US-10-437-963-90698	Sequence 90698, A
C 658	30.8	11.3	2028	17	US-10-437-963-51016	Sequence 51016, A	C 731	30	11.0	3732	17	US-10-437-963-58220	Sequence 58220, A
C 659	30.8	11.3	2469	16	US-10-260-238-1188	Sequence 1188, Ap	C 732	30	11.0	3736	17	US-10-775-920-314	Sequence 314, App
C 660	30.8	11.3	2593	18	US-10-425-115-83395	Sequence 83395, A	C 733	30	11.0	7809	18	US-10-473-126-264	Sequence 264, App
C 661	30.8	11.3	2717	17	US-10-437-963-51019	Sequence 51019, A	C 734	30	11.0	14066	15	US-10-349-680-149	Sequence 149, App
C 662	30.8	11.3	76272	16	US-10-352-179-83	Sequence 83, Appl	C 735	30	11.0	14067	9	US-10-282-122A-40681	Sequence 40681, A
C 663	30.8	11.3	83836	13	US-10-087-192-1849	Sequence 1849, Ap	C 736	30	11.0	28588	16	US-09-764-887-399	Sequence 399, App
C 664	30.8	11.3	100944	17	US-10-322-696-4	Sequence 4, Appl	C 737	30	11.0	28588	14	US-10-073-961-399	Sequence 399, App
C 665	30.8	11.3	18276	13	US-10-087-192-142	Sequence 142, App	C 738	30	11.0	38059	9	US-09-880-107-2125	Sequence 2125, Ap
C 666	30.8	11.3	177249	15	US-10-085-117-223	Sequence 223, App	C 739	30	11.0	67191	11	US-09-997-722-169	Sequence 169, App
C 667	30.6	11.2	387	9	US-09-783-590-627	Sequence 827, App	C 740	30	11.0	67191	15	US-10-105-612-1	Sequence 1, Appl
C 668	30.6	11.2	744	17	US-10-767-795-2234	Sequence 2234, Ap	C 741	30	11.0	238484	13	US-10-087-192-544	Sequence 544, App
C 669	30.6	11.2	1000	16	US-10-264-237-741	Sequence 741, App	C 742	29.8	10.9	457	15	US-10-027-632-313504	Sequence 313504, A
C 670	30.6	11.2	1587	15	US-10-106-698-1956	Sequence 1956, Ap	C 743	29.8	10.9	457	15	US-10-027-632-313504	Sequence 313504, A
C 671	30.6	11.2	2377	15	US-10-104-047-1029	Sequence 1029, Ap	C 744	29.8	10.9	498	10	US-09-918-995-9365	Sequence 9365, Ap
C 672	30.6	11.2	2942	15	US-10-104-047-609	Sequence 609, App	C 745	29.8	10.9	617	13	US-10-282-122A-27173	Sequence 27173, A
C 673	30.6	11.2	6292	16	US-10-221-714A-462	Sequence 462, App	C 746	29.8	10.9	657	13	US-10-027-632-231973	Sequence 231973, A

747	29.8	10.9	657	13	US-10-027-632-231974	Sequence 231974, A	820	29.4	10.8	1342	15	US-10-292-798-775	Sequence 775, App
748	29.8	10.9	657	15	US-10-027-632-231973	Sequence 231973, A	821	29.4	10.8	3095	14	US-10-116-802-510	Sequence 510, App
749	29.8	10.9	657	15	US-10-027-632-231974	Sequence 231974, A	822	29.4	10.8	6167	14	US-10-239-676-41	Sequence 41, Appl
C 750	29.8	10.9	1066	18	US-10-425-115-162832	Sequence 162832, A	C 823	29.4	10.8	6167	15	US-10-311-455-615	Sequence 615, App
751	29.8	10.9	1296	13	US-10-027-632-203409	Sequence 203409, A	C 824	29.4	10.8	6167	15	US-10-240-453-45	Sequence 45, Appl
752	29.8	10.9	1296	15	US-10-027-632-203409	Sequence 203409, A	C 825	29.4	10.8	6167	16	US-10-221-613-109	Sequence 109, App
C 753	29.8	10.9	1952	16	US-10-424-599-30375	Sequence 30375, A	C 826	29.4	10.8	29793	9	US-09-973-451-38	Sequence 38, Appl
C 754	29.8	10.9	3685	15	US-10-104-047-301	Sequence 301, App	C 827	29.4	10.8	48436	9	US-09-927-602-38	Sequence 38, Appl
C 755	29.8	10.9	6352	16	US-10-221-613-195	Sequence 195, App	C 828	29.4	10.8	100685	17	US-10-388-838-93	Sequence 93, Appl
C 756	29.8	10.9	7589	15	US-10-240-453-263	Sequence 263, App	C 829	29.4	10.8	113000	15	US-10-376-566-16	Sequence 16, Appl
C 757	29.8	10.9	13605	9	US-09-764-877-3446	Sequence 3446, App	C 830	29.4	10.8	118502	13	US-10-087-192-397	Sequence 397, App
C 758	29.8	10.9	13605	16	US-10-242-515-3446	Sequence 3446, App	C 831	29.4	10.8	325791	11	US-09-768-185A-1	Sequence 1, Appl
C 759	29.8	10.9	16373	15	US-10-311-455-592	Sequence 592, App	C 832	29.4	10.8	397658	9	US-09-813-320-3	Sequence 3, Appl
C 760	29.8	10.9	62909	16	US-10-672-787-32	Sequence 32, Appl	C 833	29.4	10.8	1830121	14	US-10-323-960-1	Sequence 1, Appl
C 761	29.8	10.9	207433	16	US-10-277-216-5	Sequence 5, Appl	C 834	29.4	10.8	1830121	16	US-10-329-670-1	Sequence 1, Appl
C 762	29.8	10.9	207433	17	US-10-126-022-5	Sequence 20, Appl	C 835	29.4	10.8	1830121	18	US-10-158-865-1	Sequence 1, Appl
C 763	29.8	10.9	224112	17	US-10-367-094-80	Sequence 20, Appl	C 836	29.2	10.7	386	16	US-10-242-535A-29124	Sequence 29124, A
C 764	29.8	10.9	659158	9	US-09-771-208-20	Sequence 3939, App	C 837	29.2	10.7	537	17	US-10-085-783A-29124	Sequence 29124, A
C 765	29.6	10.8	316	18	US-10-674-124A-3939	Sequence 10921, A	C 838	29.2	10.7	537	17	US-10-021-323-1726	Sequence 1736, App
C 766	29.6	10.8	367	18	US-10-425-115-10921	Sequence 28764, A	C 839	29.2	10.7	599	18	US-10-739-930-3329	Sequence 3329, App
C 767	29.6	10.8	476	10	US-09-918-995-28764	Sequence 1497, App	C 840	29.2	10.7	596	13	US-10-027-632-222980	Sequence 222980, A
C 768	29.6	10.8	511	16	US-10-264-049-1497	Sequence 2257, App	C 841	29.2	10.7	596	15	US-10-027-632-222980	Sequence 222980, A
C 769	29.6	10.8	563	17	US-10-021-323-2257	Sequence 8506, App	C 842	29.2	10.7	621	13	US-10-027-632-3094	Sequence 3094, App
C 770	29.6	10.8	588	17	US-10-021-323-8506	Sequence 131714, A	C 843	29.2	10.7	621	15	US-10-027-632-3094	Sequence 3094, App
C 771	29.6	10.8	607	13	US-10-027-632-131714	Sequence 131714, A	C 844	29.2	10.7	686	13	US-10-027-632-145079	Sequence 145079, A
C 772	29.6	10.8	607	15	US-10-027-632-131714	Sequence 13776, A	C 845	29.2	10.7	686	15	US-10-027-632-145079	Sequence 145079, A
C 773	29.6	10.8	686	13	US-10-027-632-13776	Sequence 13776, A	C 846	29.2	10.7	719	16	US-10-424-599-43471	Sequence 43471, A
C 774	29.6	10.8	686	13	US-10-027-632-13776	Sequence 13776, A	C 847	29.2	10.7	1027	16	US-10-424-599-130026	Sequence 130026, A
C 775	29.6	10.8	686	13	US-10-027-632-13776	Sequence 13776, A	C 848	29.2	10.7	1137	16	US-10-282-122A-21834	Sequence 21834, A
C 776	29.6	10.8	686	15	US-10-027-632-13776	Sequence 13776, A	C 849	29.2	10.7	1137	9	US-09-880-107-3286	Sequence 3286, App
C 777	29.6	10.8	686	15	US-10-027-632-13776	Sequence 13776, A	C 850	29.2	10.7	4220	16	US-10-416-110-1	Sequence 1, Appl
C 778	29.6	10.8	686	15	US-10-027-632-13776	Sequence 13776, A	C 851	29.2	10.7	4220	16	US-10-416-110-1	Sequence 1, Appl
C 779	29.6	10.8	686	15	US-10-027-632-13776	Sequence 13776, A	C 852	29.2	10.7	4887	17	US-10-437-963-68104	Sequence 68104, A
C 780	29.6	10.8	686	15	US-10-027-632-13776	Sequence 13776, A	C 853	29.2	10.7	5071	17	US-10-437-963-23612	Sequence 23612, A
C 781	29.6	10.8	825	13	US-10-027-632-166166	Sequence 166166, A	C 854	29.2	10.7	5501	15	US-10-204-708-38	Sequence 38, Appl
C 782	29.6	10.8	825	13	US-10-027-632-166166	Sequence 166166, A	C 855	29.2	10.7	5501	16	US-10-221-613-204	Sequence 204, App
C 783	29.6	10.8	825	13	US-10-027-632-166166	Sequence 166166, A	C 856	29.2	10.7	5501	16	US-10-240-589C-64	Sequence 64, Appl
C 784	29.6	10.8	825	13	US-10-027-632-166166	Sequence 166166, A	C 857	29.2	10.7	5937	15	US-10-240-489-95	Sequence 95, Appl
C 785	29.6	10.8	1118	13	US-10-027-632-258629	Sequence 258629, A	C 858	29.2	10.7	9110	15	US-10-311-455-2401	Sequence 2401, App
C 786	29.6	10.8	1118	15	US-10-027-632-258629	Sequence 258629, A	C 859	29.2	10.7	73334	15	US-10-311-455-2097	Sequence 2097, App
C 787	29.6	10.8	1118	15	US-10-027-632-258629	Sequence 5482, App	C 860	29.2	10.7	73334	16	US-10-240-589C-127	Sequence 127, App
C 788	29.6	10.8	1158	17	US-10-437-963-5482	Sequence 1316, App	C 861	29.2	10.7	75899	9	US-09-854-883-243	Sequence 243, App
C 789	29.6	10.8	1158	18	US-10-739-930-1316	Sequence 123215, A	C 862	29.2	10.7	75899	15	US-10-360-510-243	Sequence 243, App
C 790	29.6	10.8	1295	13	US-10-027-632-123215	Sequence 123215, A	C 863	29.2	10.7	102374	13	US-10-087-192-667	Sequence 667, App
C 791	29.6	10.8	1295	13	US-10-027-632-123215	Sequence 123216, A	C 864	29.2	10.7	102374	13	US-10-087-192-895	Sequence 895, App
C 792	29.6	10.8	1295	13	US-10-027-632-123215	Sequence 123217, A	C 865	29.2	10.7	111252	13	US-10-087-192-895	Sequence 895, App
C 793	29.6	10.8	1295	15	US-10-027-632-123215	Sequence 123216, A	C 866	29.2	10.7	403035	17	US-10-741-601-5729	Sequence 5729, App
C 794	29.6	10.8	1295	15	US-10-027-632-123216	Sequence 123216, A	C 867	29.2	10.7	278	18	US-10-425-115-175361	Sequence 175361, A
C 795	29.6	10.8	1330	10	US-10-027-632-123217	Sequence 123217, A	C 868	29.2	10.6	327	18	US-10-674-124A-23694	Sequence 23694, A
C 796	29.6	10.8	1876	16	US-09-814-353-21895	Sequence 21895, A	C 869	29.2	10.6	451	16	US-10-424-599-8687	Sequence 8687, App
C 797	29.6	10.8	2864	17	US-10-424-599-26755	Sequence 26755, A	C 870	29.2	10.6	637	13	US-10-027-632-190237	Sequence 190237, A
C 798	29.6	10.8	3032	18	US-10-433-793-201	Sequence 201, App	C 871	29.2	10.6	637	15	US-10-027-632-190237	Sequence 190237, A
C 799	29.6	10.8	4407	17	US-10-425-115-138292	Sequence 138292, A	C 872	29.2	10.6	650	13	US-10-027-632-207520	Sequence 207520, A
C 800	29.6	10.8	5982	16	US-10-398-221-2058	Sequence 51006, A	C 873	29.2	10.6	650	13	US-10-027-632-207520	Sequence 207520, A
C 801	29.6	10.8	6074	15	US-10-398-221-2058	Sequence 2185, App	C 874	29.2	10.6	650	13	US-10-027-632-207522	Sequence 207522, A
C 802	29.6	10.8	6074	15	US-10-172-086-43	Sequence 43, Appl	C 875	29.2	10.6	650	15	US-10-027-632-207520	Sequence 207520, A
C 803	29.6	10.8	6074	18	US-10-311-507-75	Sequence 75, Appl	C 876	29.2	10.6	650	15	US-10-027-632-207521	Sequence 207521, A
C 804	29.6	10.8	6074	18	US-10-480-846-43	Sequence 43, Appl	C 877	29.2	10.6	650	15	US-10-027-632-207522	Sequence 207522, A
C 805	29.6	10.8	15951	15	US-10-433-793-80	Sequence 80, Appl	C 878	29.2	10.6	854	16	US-10-424-599-90510	Sequence 90510, A
C 806	29.6	10.8	15951	15	US-10-311-455-1653	Sequence 1653, App	C 879	29.2	10.6	918	13	US-10-027-632-9957	Sequence 9957, App
C 807	29.6	10.8	19634	18	US-10-240-489-133	Sequence 133, Appl	C 880	29.2	10.6	918	13	US-10-027-632-9958	Sequence 9958, App
C 808	29.6	10.8	19634	18	US-10-473-126-31	Sequence 31, Appl	C 881	29.2	10.6	918	15	US-10-027-632-9957	Sequence 9957, App
C 809	29.6	10.8	149612	13	US-10-087-192-1960	Sequence 1960, App	C 882	29.2	10.6	950	13	US-10-027-632-9958	Sequence 9958, App
C 810	29.6	10.8	196008	15	US-10-147-603-1	GENERAL INFORMAT	C 883	29.2	10.6	950	15	US-10-027-632-121677	Sequence 121677, A
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C 813	29.4	10.8	166	9	US-09-770-696-376	Sequence 376, App	C 886	29.2	10.6	1205	18	US-10-027-632-78784	Sequence 78784, A
C 814	29.4	10.8	738	17	US-10-767-795-2668	Sequence 2668, App	C 887	29.2	10.6	1358	13	US-10-027-632-78784	Sequence 78784, A
C 815	29.4	10.8	865	13	US-10-027-632-173980	Sequence 173980, A	C 888	29.2	10.6	1358	15	US-10-027-632-78784	Sequence 78784, A
C 816	29.4	10.8	865	15	US-10-027-632-173980	Sequence 173980, A	C 889	29.2	10.6	1401	17	US-10-767-701-15454	Sequence 15454, A
C 817	29.4	10.8	1029	9	US-09-815-242-6861	Sequence 6861, App	C 890	29.2	10.6	1573	11	US-09-938-842A-4776	Sequence 4776, App
C 818	29.4	10.8	1029	16	US-10-282-122A-21877	Sequence 21877, A	C 891	29.2	10.6	1573	11	US-09-938-842A-4776	Sequence 4776, App
C 819	29.4	10.8	1191	17	US-10-473-518-137	Sequence 137, App	C 892	29.2	10.6	3125	15	US-10-104-047-1355	Sequence 1355, App
C 820	29.4	10.8	1342	15	US-10-017-161-901	Sequence 901, App	C 893	29.2	10.6	5046	9	US-09-725-735A-13	Sequence 13, Appl

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C 894	29	10.6	5878	16	US-10-424-599-3160	Sequence 3160, Ap	C 967	28.6	648	11	US-09-969-034-484	Sequence 484, App
C 895	29	10.6	6718	16	US-10-424-599-3162	Sequence 3162, Ap	C 968	28.6	651	9	US-09-867-550-1393	Sequence 1393, Ap
C 896	29	10.6	15674	15	US-10-311-455-336	Sequence 336, Appl	C 969	28.6	720	18	US-10-425-115-145508	Sequence 145508,
C 897	29	10.6	15674	15	US-10-424-599-3162	Sequence 336, Appl	C 970	28.6	736	15	US-10-425-115-145508	Sequence 145508,
C 898	29	10.6	21500	13	US-10-087-192-169	Sequence 169, Appl	C 971	28.6	751	16	US-10-424-599-115836	Sequence 115836, A
C 899	29	10.6	41498	13	US-10-087-192-169	Sequence 169, Appl	C 972	28.6	838	17	US-10-767-701-15322	Sequence 15322, A
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C 906	28.8	10.5	778	14	US-10-198-846-9621	Sequence 9621, Ap	C 979	28.6	1094	15	US-10-027-632-119162	Sequence 119162,
C 907	28.8	10.5	856	16	US-10-425-114-36497	Sequence 36497, A	C 980	28.6	1094	15	US-10-027-632-119162	Sequence 119162,
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C 910	28.8	10.5	1347	13	US-10-027-632-209894	Sequence 209894, A	C 983	28.6	1509	10	US-09-925-299-159	Sequence 159, App
C 911	28.8	10.5	1347	15	US-10-027-632-209894	Sequence 209894, A	C 984	28.6	1650	16	US-10-282-122A-9683	Sequence 9683, Ap
C 912	28.8	10.5	2218	16	US-10-425-114-33630	Sequence 33630, A	C 985	28.6	1764	18	US-10-425-115-135127	Sequence 135127,
C 913	28.8	10.5	2255	16	US-10-425-114-36149	Sequence 36149, A	C 986	28.6	1880	16	US-10-425-114-13588	Sequence 13588, A
C 914	28.8	10.5	2255	18	US-10-425-115-122407	Sequence 122407, A	C 987	28.6	2000	16	US-10-260-238-1941	Sequence 1941, Ap
C 915	28.8	10.5	3079	18	US-10-425-115-136976	Sequence 136976, A	C 988	28.6	2153	18	US-10-425-115-104664	Sequence 104664,
C 916	28.8	10.5	5476	14	US-10-239-676-207	Sequence 207, App	C 989	28.6	3013	9	US-09-925-302-353	Sequence 353, App
C 917	28.8	10.5	5476	15	US-10-204-708-81	Sequence 81, Appl	C 990	28.6	3013	10	US-09-925-302-353	Sequence 353, App
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C 919	28.8	10.5	5521	18	US-10-425-115-122402	Sequence 122402, A	C 992	28.6	3323	16	US-10-169-395-22	Sequence 22, Appl
C 920	28.8	10.5	11805	15	US-10-311-455-1722	Sequence 700, App	C 993	28.6	3661	15	US-10-000-897-35	Sequence 35, Appl
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C 922	28.8	10.5	16602	17	US-10-433-793-114	Sequence 725, App	C 995	28.6	4263	15	US-10-032-585-6606	Sequence 323, Ap
C 923	28.8	10.5	22684	15	US-10-017-161-725	Sequence 8034, Ap	C 996	28.6	5236	15	US-10-311-455-323	Sequence 28, Appl
C 924	28.8	10.5	27062	10	US-09-764-891-8034	Sequence 8034, Ap	C 997	28.6	6246	15	US-10-172-086-28	Sequence 990, App
C 925	28.8	10.5	23221	15	US-10-282-798-635	Sequence 635, App	C 998	28.6	6246	17	US-10-311-455-990	Sequence 50, Appl
C 926	28.8	10.5	59365	17	US-10-367-094-74	Sequence 74, Appl	C 999	28.6	6246	18	US-10-480-846-28	Sequence 28, Appl
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C 928	28.8	10.5	116858	13	US-10-087-192-547	Sequence 547, App	C1001	28.6	7746	15	US-10-257-166-130	Sequence 1, Appl
C 929	28.8	10.5	212321	13	US-10-087-192-1126	Sequence 1126, Ap	C1002	28.6	7746	15	US-10-257-166-130	Sequence 1, Appl
C 930	28.8	10.5	439892	13	US-10-087-192-454	Sequence 454, App	C1003	28.6	8201	15	US-10-363-798-1	Sequence 52, Appl
C 931	28.6	10.5	265	9	US-09-923-876-4819	Sequence 4819, Ap	C1004	28.6	8201	15	US-10-790-988-1	Sequence 1, Appl
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C 933	28.6	10.5	426	9	US-09-917-800A-888	Sequence 888, App	C1006	28.6	10766	10	US-10-027-632-174961	Sequence 174961,
C 934	28.6	10.5	454	15	US-10-000-897-34	Sequence 34, Appl	C1007	28.6	200418	13	US-10-087-192-568	Sequence 568, App
C 935	28.6	10.5	454	17	US-10-818-168-34	Sequence 34, Appl	C1008	28.6	325348	15	US-10-085-117-358	Sequence 358, App
C 936	28.6	10.5	455	18	US-10-674-124A-19189	Sequence 19189, A	C1009	28.6	337022	17	US-10-322-696-52	Sequence 52, Appl
C 937	28.6	10.5	459	17	US-10-767-795-4501	Sequence 4501, Ap	C1010	28.6	640681	9	US-09-790-988-1	Sequence 1, Appl
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C 940	28.6	10.5	497	13	US-10-027-632-85316	Sequence 85316, A	C1013	28.6	3673778	15	US-10-312-841-1	Sequence 1, Appl
C 941	28.6	10.5	497	13	US-10-027-632-85316	Sequence 85316, A	C1014	28.4	336	17	US-10-437-963-63215	Sequence 63215, A
C 942	28.6	10.5	497	13	US-10-027-632-85316	Sequence 85316, A	C1015	28.4	358	14	US-10-198-846-12854	Sequence 12854, A
C 943	28.6	10.5	497	13	US-10-027-632-85316	Sequence 85316, A	C1016	28.4	358	18	US-10-425-115-108948	Sequence 108948,
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C 946	28.6	10.5	497	13	US-10-027-632-85316	Sequence 85316, A	C1019	28.4	457	15	US-10-170-481A-432	Sequence 432, App
C 947	28.6	10.5	497	15	US-10-027-632-85316	Sequence 85316, A	C1020	28.4	457	15	US-10-210-028-432	Sequence 432, App
C 948	28.6	10.5	497	15	US-10-027-632-85316	Sequence 85316, A	C1021	28.4	457	15	US-10-162-521A-432	Sequence 432, App
C 949	28.6	10.5	497	15	US-10-027-632-85316	Sequence 85316, A	C1022	28.4	514	13	US-10-027-632-70648	Sequence 70648, A
C 950	28.6	10.5	497	15	US-10-027-632-85316	Sequence 85316, A	C1023	28.4	514	13	US-10-027-632-70648	Sequence 70648, A
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C 955	28.6	10.5	571	13	US-10-027-632-215230	Sequence 215230, A	C1028	28.4	549	15	US-10-027-632-94924	Sequence 94924, A
C 956	28.6	10.5	571	13	US-10-027-632-215230	Sequence 215230, A	C1029	28.4	549	15	US-10-027-632-181461	Sequence 181461,
C 957	28.6	10.5	571	15	US-10-027-632-215230	Sequence 215230, A	C1030	28.4	556	14	US-10-027-632-181461	Sequence 181461,
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C 959	28.6	10.5	640	15	US-10-027-632-237655	Sequence 237655, A	C1032	28.4	556	14	US-10-027-632-181461	Sequence 181461,
C 960	28.6	10.5	641	13	US-10-027-632-77502	Sequence 77502, A	C1033	28.4	556	14	US-10-027-632-181461	Sequence 181461,
C 961	28.6	10.5	641	13	US-10-027-632-77502	Sequence 77502, A	C1034	28.4	556	14	US-10-027-632-181461	Sequence 181461,
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C 964	28.6	10.5	641	13	US-10-027-632-77502	Sequence 77502, A	C1037	28.4	556	14	US-10-027-632-181461	Sequence 181461,
C 965	28.6	10.5	641	15	US-10-027-632-77502	Sequence 77502, A	C1038	28.4	556	14	US-10-027-632-181461	Sequence 181461,

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c1137	28.4	10.4	1069	14	US-10-206-576-7	Sequence 7, App	c1210	28.2	10.3	568	15	US-10-027-632-285031	Sequence 285031, A
c1138	28.4	10.4	1161	9	US-09-071-035-5	Sequence 5, App	c1211	28.2	10.3	631	15	US-10-027-632-237754	Sequence 237754, A
c1139	28.4	10.4	1161	14	US-10-206-576-5	Sequence 5, App	c1212	28.2	10.3	631	15	US-10-027-632-237754	Sequence 237754, A
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c1141	28.4	10.4	1324	15	US-10-017-161-23	Sequence 23, App	c1214	28.2	10.3	650	14	US-10-198-846-13701	Sequence 13701, A
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c1144	28.4	10.4	1540	18	US-10-425-115-90285	Sequence 90285, A	c1217	28.2	10.3	709	9	US-09-770-149-214	Sequence 214, App
c1145	28.4	10.4	1584	15	US-10-369-493-25428	Sequence 25428, A	c1218	28.2	10.3	856	9	US-09-770-149-214	Sequence 214, App
c1146	28.4	10.4	2074	16	US-10-403-571-67	Sequence 67, App	c1219	28.2	10.3	856	9	US-09-770-149-214	Sequence 214, App
c1147	28.4	10.4	2281	15	US-10-369-493-45144	Sequence 45144, A	c1220	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1148	28.4	10.4	2281	16	US-10-220-120-159	Sequence 159, App	c1221	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1149	28.4	10.4	2562	15	US-10-131-827-8851	Sequence 8851, App	c1222	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1150	28.4	10.4	2562	15	US-10-311-455-1259	Sequence 1259, App	c1223	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1151	28.4	10.4	6440	15	US-10-311-455-1630	Sequence 1630, App	c1224	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1152	28.4	10.4	7219	17	US-10-437-963-13743	Sequence 13743, A	c1225	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1153	28.4	10.4	7393	15	US-10-037-270-372	Sequence 372, App	c1226	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1154	28.4	10.4	7393	15	US-10-117-722-372	Sequence 372, App	c1227	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1155	28.4	10.4	7574	9	US-09-070-9278A-152	Sequence 152, App	c1228	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1156	28.4	10.4	7809	18	US-10-473-126-118	Sequence 118, App	c1229	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1157	28.4	10.4	10696	15	US-10-311-455-292	Sequence 292, App	c1230	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1158	28.4	10.4	10696	15	US-10-240-452-40	Sequence 40, App	c1231	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1159	28.4	10.4	13919	16	US-10-240-589C-113	Sequence 113, App	c1232	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1160	28.4	10.4	17703	16	US-10-257-166-33	Sequence 33, App	c1233	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1161	28.4	10.4	31314	9	US-09-764-877-3875	Sequence 3875, App	c1234	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1162	28.4	10.4	31314	16	US-10-242-515-3875	Sequence 3875, App	c1235	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1163	28.4	10.4	31949	13	US-09-764-891-8098	Sequence 8098, App	c1236	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1164	28.4	10.4	32186	10	US-09-764-891-8099	Sequence 8099, App	c1237	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1165	28.4	10.4	38736	17	US-10-433-287-78	Sequence 78, App	c1238	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1166	28.4	10.4	41907	9	US-09-967-013-5	Sequence 5, App	c1239	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1167	28.4	10.4	74788	13	US-10-087-192-1906	Sequence 1906, App	c1240	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1168	28.4	10.4	96599	11	US-09-997-722-13	Sequence 13, App	c1241	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1169	28.4	10.4	163321	13	US-10-087-192-63	Sequence 63, App	c1242	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1170	28.4	10.4	168174	17	US-10-071-411-63	Sequence 63, App	c1243	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1171	28.4	10.4	168273	17	US-10-071-411-63	Sequence 63, App	c1244	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1172	28.4	10.4	326014	9	US-09-731-231A-3	Sequence 3, App	c1245	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1173	28.4	10.4	326014	9	US-10-751-985-3	Sequence 3, App	c1246	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1174	28.4	10.4	326014	17	US-10-751-985-3	Sequence 3, App	c1247	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1175	28.4	10.4	465237	9	US-09-933-267A-1	Sequence 1, App	c1248	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1176	28.4	10.4	495269	16	US-10-398-221-8	Sequence 8, App	c1249	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1177	28.4	10.4	684707	16	US-10-398-221-9	Sequence 9, App	c1250	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1178	28.4	10.4	1223197	13	US-10-027-632-179264	Sequence 179264, App	c1251	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1179	28.4	10.4	1223197	15	US-10-027-632-179264	Sequence 179264, App	c1252	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1180	28.4	10.4	3011208	16	US-10-398-221-2058	Sequence 2058, App	c1253	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1181	28.2	10.3	291	14	US-10-083-357-326	Sequence 326, App	c1254	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1182	28.2	10.3	332	9	US-09-880-107-1366	Sequence 1366, App	c1255	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1183	28.2	10.3	339	18	US-10-425-115-30161	Sequence 30161, A	c1256	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1184	28.2	10.3	454	17	US-10-437-963-94544	Sequence 94544, A	c1257	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1185	28.2	10.3	482	18	US-10-674-124A-3765	Sequence 3765, App	c1258	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1186	28.2	10.3	483	13	US-10-027-632-74581	Sequence 74581, A	c1259	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1187	28.2	10.3	483	15	US-10-027-632-74581	Sequence 74581, A	c1260	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1188	28.2	10.3	516	15	US-10-170-385-198	Sequence 198, App	c1261	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1189	28.2	10.3	528	13	US-10-027-632-39878	Sequence 39878, A	c1262	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1190	28.2	10.3	528	15	US-10-027-632-39878	Sequence 39878, A	c1263	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1191	28.2	10.3	538	16	US-10-424-599-88702	Sequence 88702, A	c1264	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1192	28.2	10.3	568	13	US-10-027-632-77475	Sequence 77475, A	c1265	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1193	28.2	10.3	568	13	US-10-027-632-77476	Sequence 77476, A	c1266	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1194	28.2	10.3	568	13	US-10-027-632-77477	Sequence 77477, A	c1267	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App
c1195	28.2	10.3	568	13	US-10-027-632-80426	Sequence 80426, A	c1268	28.2	10.3	994	17	US-10-767-701-9274	Sequence 9274, App

c1269	28	10.3	268	9	US-09-867-701-9358	Sequence 9358, Ap	1342	28	10.3	32174	9	US-09-860-670-232	Sequence 232, App
1270	28	10.3	309	17	US-10-437-963-68450	Sequence 68450, A	1343	28	10.3	32174	9	US-09-764-904-90	Sequence 90, Appl
1271	28	10.3	327	13	US-10-021-162-5	Sequence 5, Appl	1344	28	10.3	32174	10	US-09-764-891-6480	Sequence 6480, Ap
1272	28	10.3	363	14	US-10-198-846-13161	Sequence 13161, A	c1345	28	10.3	32174	10	US-09-764-891-10135	Sequence 10135, A
1273	28	10.3	369	9	US-09-560-863-784	Sequence 784, App	1346	28	10.3	32174	10	US-09-764-891-10179	Sequence 10179, A
c1274	28	10.3	387	16	US-10-264-049-1913	Sequence 1913, Ap	1347	28	10.3	32174	14	US-10-091-548-90	Sequence 90, Appl
1275	28	10.3	389	9	US-09-815-242-4485	Sequence 4485, Ap	1348	28	10.3	32174	14	US-10-074-095-1134	Sequence 1134, Ap
1276	28	10.3	438	9	US-09-815-242-8127	Sequence 8127, Ap	1349	28	10.3	32174	15	US-10-212-872-1134	Sequence 1134, Ap
1277	28	10.3	441	9	US-09-815-242-8127	Sequence 8127, Ap	1350	28	10.3	32174	15	US-10-091-414-256	Sequence 256, App
1278	28	10.3	441	9	US-09-815-242-8127	Sequence 8127, Ap	c1351	28	10.3	32174	15	US-10-074-024-609	Sequence 609, App
1279	28	10.3	441	9	US-09-815-242-8951	Sequence 8951, Ap	c1352	28	10.3	32174	15	US-10-227-646-232	Sequence 232, App
1280	28	10.3	441	16	US-10-282-122A-7892	Sequence 7892, Ap	1353	28	10.3	32174	16	US-10-242-515-2645	Sequence 2645, Ap
c1281	28	10.3	535	15	US-10-027-632-182395	Sequence 182395, A	c1354	28	10.3	32174	16	US-10-741-601-5670	Sequence 5670, Ap
c1282	28	10.3	535	15	US-10-027-632-182395	Sequence 182395, A	c1355	28	10.3	32174	16	US-10-374-077-209	Sequence 209, App
c1283	28	10.3	546	13	US-10-027-632-214805	Sequence 214805, A	c1356	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1284	28	10.3	546	13	US-10-027-632-214805	Sequence 214805, A	c1357	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1285	28	10.3	573	18	US-10-363-345A-20415	Sequence 20415, A	c1358	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1286	28	10.3	573	18	US-10-363-345A-20415	Sequence 20415, A	c1359	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1287	28	10.3	573	18	US-10-363-345A-22106	Sequence 22106, A	c1360	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1288	28	10.3	580	13	US-10-027-632-230788	Sequence 230788, A	c1361	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
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1291	28	10.3	580	13	US-10-027-632-230788	Sequence 230788, A	c1364	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1292	28	10.3	580	13	US-10-027-632-230788	Sequence 230788, A	c1365	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1293	28	10.3	603	9	US-09-917-800A-1217	Sequence 1217, Ap	c1366	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1294	28	10.3	603	9	US-09-917-800A-1217	Sequence 1217, Ap	c1367	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1295	28	10.3	624	13	US-10-027-632-241899	Sequence 241899, A	c1368	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1296	28	10.3	624	13	US-10-027-632-241899	Sequence 241899, A	c1369	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1297	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1370	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1298	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1371	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1299	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1372	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1300	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1373	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1301	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1374	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1302	28	10.3	663	13	US-10-027-632-245888	Sequence 245888, A	c1375	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1303	28	10.3	673	13	US-10-027-632-205850	Sequence 205850, A	c1376	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1304	28	10.3	736	16	US-10-424-599-60906	Sequence 60906, A	c1377	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1305	28	10.3	736	16	US-10-424-599-60906	Sequence 60906, A	c1378	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1306	28	10.3	1002	16	US-10-282-122A-101676	Sequence 101676, A	c1379	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1307	28	10.3	1047	16	US-10-425-115-80196	Sequence 80196, A	c1380	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1308	28	10.3	1133	13	US-10-027-632-256471	Sequence 256471, A	c1381	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1309	28	10.3	1133	13	US-10-027-632-256471	Sequence 256471, A	c1382	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1310	28	10.3	1294	16	US-10-424-599-54504	Sequence 54504, A	c1383	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1311	28	10.3	1335	15	US-10-424-599-60917	Sequence 60917, A	c1384	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1312	28	10.3	1413	15	US-10-369-493-47357	Sequence 47357, A	c1385	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1313	28	10.3	1496	18	US-10-425-115-89024	Sequence 89024, A	c1386	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1314	28	10.3	1804	16	US-10-425-115-89024	Sequence 89024, A	c1387	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1315	28	10.3	1885	16	US-10-424-599-104369	Sequence 104369, A	c1388	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1316	28	10.3	1938	16	US-10-424-599-35625	Sequence 35625, A	c1389	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1317	28	10.3	2070	16	US-10-425-115-95183	Sequence 95183, A	c1390	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1318	28	10.3	2304	16	US-10-282-122A-40693	Sequence 40693, A	c1391	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1319	28	10.3	2483	17	US-10-437-963-16745	Sequence 16745, A	c1392	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1320	28	10.3	2841	16	US-10-282-122A-18265	Sequence 18265, A	c1393	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1321	28	10.3	2871	15	US-10-007-926A-241	Sequence 241, App	c1394	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1322	28	10.3	2871	16	US-10-159-563-392	Sequence 392, App	c1395	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1323	28	10.3	4911	17	US-09-814-353-19968	Sequence 19968, A	c1396	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1324	28	10.3	5323	17	US-10-437-963-67553	Sequence 67553, A	c1397	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1325	28	10.3	5496	17	US-10-437-963-68976	Sequence 68976, A	c1398	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1326	28	10.3	6176	9	US-09-823-109-6	Sequence 6, Appl	c1399	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1327	28	10.3	7461	9	US-09-764-860-1135	Sequence 1135, Ap	c1400	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1328	28	10.3	7461	9	US-09-764-860-1135	Sequence 1135, Ap	c1401	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1329	28	10.3	7461	14	US-10-091-548-91	Sequence 91, Appl	c1402	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1330	28	10.3	7461	14	US-10-074-095-1135	Sequence 1135, Ap	c1403	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1331	28	10.3	7461	15	US-10-212-872-1135	Sequence 1135, Ap	c1404	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1332	28	10.3	9415	15	US-10-311-455-267	Sequence 267, App	c1405	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1333	28	10.3	10528	15	US-10-311-455-308	Sequence 308, App	c1406	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1334	28	10.3	13469	16	US-10-221-714A-316	Sequence 316, App	c1407	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1335	28	10.3	16397	8	US-08-781-986A-205	Sequence 205, App	c1408	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1336	28	10.3	16397	16	US-10-329-624-205	Sequence 205, App	c1409	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
c1337	28	10.3	16950	14	US-10-114-170-166	Sequence 166, App	c1410	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1338	28	10.3	23683	15	US-10-240-485-175	Sequence 175, App	c1411	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1339	28	10.3	32174	9	US-09-908-711-158	Sequence 158, App	c1412	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1340	28	10.3	32174	9	US-09-764-860-1134	Sequence 1134, Ap	c1413	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap
1341	28	10.3	32174	9	US-09-764-877-2645	Sequence 2645, Ap	c1414	28	10.3	32174	16	US-10-087-192-1948	Sequence 1948, Ap

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1416	27.8	10.2	1803	11	US-10-104-047-1436	Sequence 1436, Ap	c1489	27.6	10.1	599	15	US-10-027-632-36273	Sequence 36273, A
1417	27.8	10.2	2370	15	US-09-754-947-2	Sequence 2, Appli	c1490	27.6	10.1	599	15	US-10-027-632-36274	Sequence 36274, A
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Job time : 307.595 secs

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OM nucleic - nucleic search, using sw model

Run on: December 1, 2004, 23:10:21 ; Search time 1445.02 Seconds
(without alignments)
8934.210 Million cell updates/sec

Title: US-09-989-293A-376_COPY_92_364

Perfect score: 273

Sequence: 1 atgacattttttctgtcact.....gtgtaagaaacacacttag 273

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Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

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2: gb_hg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	273	100.0	713	6	AX055452 Sequence
3	273	100.0	713	6	AX403489 Sequence
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5	273	100.0	713	9	AY358685
6	273	100.0	165414	9	AC024224
7	202.2	74.1	240864	2	AC006510
8	142	52.0	881	9	AF400602
9	140	51.3	625	9	AF400597
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26	76	27.8	735	10	AF534909
27	75.4	27.6	1329	10	BC027742
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83	36.6	13.4	276523	10	AC012382
84	36.6	13.4	281659	2	AC074159
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86	36.4	13.3	75935	2	AC022818
87	36.4	13.3	144454	9	AC009780
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89	36.2	13.3	134687	9	AL445259
90	36.2	13.3	172070	2	AC134951
91	36.2	13.3	183951	2	CR318651
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AC147693 Gorilla g

c 93	36.2	13.3	196212	2	EX942812	166	34.6	12.7	156895	9	AC013526	AC013526 Homo sapi
c 94	36.2	13.3	204839	2	AC144882	167	34.6	12.7	163785	2	AC011766	AC011766 Homo sapi
c 95	36.2	13.3	216043	2	CR450789	c 168	34.6	12.7	166518	9	AC0078986	AC0078986 Homo sapi
c 96	36.2	13.3	235174	5	AL844847	c 169	34.6	12.7	173604	9	AC022692	AC022692 Homo sapi
c 97	36	13.2	156961	9	AC015592	c 170	34.6	12.7	179558	2	AC119329	AC119329 Rattus no
c 98	36	13.2	168406	9	AP002886	c 171	34.6	12.7	189481	2	AC150741	AC150741 Zea mays
c 99	36	13.2	175142	10	AC116421	c 172	34.6	12.7	199662	5	EX119910	EX119910 Zebrafish
c 100	36	13.2	210797	2	AC107868	c 173	34.6	12.7	210310	2	AC102807	AC102807 Mus muscu
c 101	36	13.2	219337	2	AC109284	c 174	34.6	12.7	210869	9	GNS01DRE	AL117192 Human chr
c 102	36	13.2	212310	2	AC144946	c 175	34.6	12.7	210310	2	AC102807	AL929356 Plasmodi
c 103	36	13.2	226769	10	AC1113038	c 176	34.6	12.7	335050	3	PF2923356	G05532 human STS W
c 104	36	13.2	233343	2	AC106481	c 177	34.4	12.6	1083	9	AC130874	AK130874 Homo sapi
c 105	35.8	13.1	123817	10	EX001045	c 178	34.4	12.6	1083	9	AC130874	BC007912 Homo sapi
c 106	35.8	13.1	223154	2	AC106651	c 179	34.4	12.6	1886	9	BC007912	Sequence
c 107	35.8	13.1	223154	2	AC106651	c 180	34.4	12.6	1969	6	AX748222	AX748222 Sequence
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c 109	35.8	13.1	250500	2	AC098524	c 182	34.4	12.6	2182	9	AK095487	AK095487 Homo sapi
c 110	35.8	13.1	255144	2	AC1303091	c 183	34.4	12.6	2535	9	BC016880	BC016880 Homo sapi
c 111	35.6	13.0	35538	2	U88182	c 184	34.4	12.6	4045	6	AX740479	AX740479 Sequence
c 112	35.6	13.0	45049	2	AC099832	c 185	34.4	12.6	5083	9	AB058739	AB058739 Homo sapi
c 113	35.6	13.0	130916	9	AC107882	c 186	34.4	12.6	5482	6	BD183342	BD183342 Novel gen
c 114	35.6	13.0	133892	9	AC107886	c 187	34.4	12.6	6030	5	SC284628	SC284628 Zebrafish
c 115	35.6	13.0	155920	5	BC005182	c 188	34.4	12.6	94286	8	AC104705	AC104705 Oryza sat
c 116	35.6	13.0	181967	2	CR677513	c 189	34.4	12.6	94286	8	AC104705	AL132118 Human DNA
c 117	35.6	13.0	182314	10	AL935301	c 190	34.4	12.6	107629	9	HS0838N17	AL049539 Human DNA
c 118	35.6	13.0	184444	2	AC025065	c 191	34.4	12.6	111694	9	HS0838N17	AL130539 Oryza sat
c 119	35.6	13.0	185638	9	AC006210	c 192	34.4	12.6	123167	8	AC130599	AL130599 Oryza sat
c 120	35.6	13.0	190708	2	CR381533	c 193	34.4	12.6	123170	2	AL138792	AL141201 Rattus no
c 121	35.6	13.0	205796	10	AC118004	c 194	34.4	12.6	143752	5	CR450697	CR450697 Zebrafish
c 122	35.6	13.0	207478	2	CR376722	c 195	34.4	12.6	147323	10	AL731651	AL731651 Mouse DNA
c 123	35.6	13.0	211479	2	AC006756	c 196	34.4	12.6	162757	10	AL645473	AL645473 Mouse DNA
c 124	35.6	13.0	237544	2	AC0109858	c 197	34.4	12.6	162757	10	MMAJ2971	AY297131 Mus muscu
c 125	35.4	13.0	87575	8	AC011622	c 198	34.4	12.6	234411	10	MMAJ2971	AC11893 Rattus no
c 126	35.4	13.0	106930	2	AC138283	c 199	34.4	12.6	255875	2	AC111893	AC124233 Mus muscu
c 127	35.4	13.0	147635	2	AC139342	c 200	34.4	12.6	269784	10	AC118216	AC124233 Sequence
c 128	35.4	13.0	151553	5	AL139342	c 201	34.4	12.6	336951	6	AR347036	AR347036 Schistos
c 129	35.4	13.0	158018	5	AL139342	c 202	34.2	12.5	696	3	AY225190	AY225190 Schistos
c 130	35.4	13.0	162633	2	AC148483	c 203	34.2	12.5	1251	1	AY548796	AY548796 Enterococ
c 131	35.4	13.0	162633	2	AC148483	c 204	34.2	12.5	1989	1	CEFA42F12	268116 Caenorhabd
c 132	35.2	12.9	519	1	AY038590	c 205	34.2	12.5	21677	3	CEFA42F12	AL357337 Human DNA
c 133	35.2	12.9	1464	1	AY038590	c 206	34.2	12.5	60954	8	AY262686	AY262686 Glycine m
c 134	35.2	12.9	10418	1	AE002280	c 207	34.2	12.5	103334	8	AY262686	293020 Human DNA s
c 135	35.2	12.9	40368	2	AC149396	c 208	34.2	12.5	125686	9	HS030316	AC007460 Homo sapi
c 136	35.2	12.9	92347	5	EX001037	c 209	34.2	12.5	140834	2	AP004460	AP004460 Oryza sat
c 137	35.2	12.9	142807	9	HS33B19	c 210	34.2	12.5	148626	8	AP004460	EX005169 Zebrafish
c 138	35.2	12.9	156105	9	AC020977	c 211	34.2	12.5	169110	5	EX005169	EX005169 Zebrafish
c 139	35.2	12.9	161081	2	AC022997	c 212	34.2	12.5	171552	2	EX005207	EX005207 Danio rer
c 140	35.2	12.9	173993	9	AC009230	c 213	34.2	12.5	173669	2	AC017110	AC017110 Homo sapi
c 141	35.2	12.9	179328	5	EX004569	c 214	34.2	12.5	183499	2	AL607153	AL607153 Homo sapi
c 142	35.2	12.9	193547	9	AC024569	c 215	34.2	12.5	189593	2	CR387920	CR387920 Danio rer
c 143	35.2	12.9	207757	10	AC022368	c 216	34.2	12.5	194497	9	AC021887	AC021887 Homo sapi
c 144	35.2	12.9	234419	2	AC102672	c 217	34.2	12.5	204988	2	CR293501	CR293501 Danio rer
c 145	35.2	12.9	236235	2	AC102672	c 218	34.2	12.5	211515	9	AC144479	AC144479 Pan trogl
c 146	35.2	12.9	237526	2	AC107246	c 219	34.2	12.5	213535	6	AX197417	AX197417 Sequence
c 147	35.2	12.9	264205	10	AC121125	c 220	34.2	12.5	213535	6	AX197417	AX223856 Sequence
c 148	35.2	12.9	269800	2	AC109955	c 221	34.2	12.5	213535	6	AX223856	AE014826 Plasmodi
c 149	35	12.8	140797	2	AC118723	c 222	34.2	12.5	250663	3	AE014826	AC128887 Rattus no
c 150	35	12.8	163926	9	AL512639	c 223	34.2	12.5	250663	3	AE014826	AE016952 Enterococ
c 151	35	12.8	164774	9	AL512639	c 224	34.2	12.5	259850	1	AE016952	BC004655 Homo sapi
c 152	35	12.8	174577	2	EX942829	c 225	34	12.5	300029	1	AE016952	AL845554 Human DNA
c 153	35	12.8	245037	2	CR382298	c 226	34	12.5	4725	9	BC040525	CR354545 Human DNA
c 154	34.8	12.7	91600	9	AC095347	c 227	34	12.5	15377	9	AL845554	CR354545 Human DNA
c 155	34.8	12.7	100258	9	AC002462	c 228	34	12.5	56495	9	CR354545	AL935032 Human DNA
c 156	34.8	12.7	110000	2	AC110363	c 229	34	12.5	97157	3	AC025715	AC025715 Caenorhab
c 157	34.8	12.7	110000	2	AC110363	c 230	34	12.5	97157	3	AC025715	AC025715 Caenorhab
c 158	34.8	12.7	180619	10	AL929257	c 231	34	12.5	109682	2	BX120007	BX120007 Human DNA
c 159	34.8	12.7	193306	2	AC111114	c 232	34	12.5	122395	9	AC149027	AC149027 Alligator
c 160	34.6	12.7	24581	8	AB006701	c 233	34	12.5	128963	9	AC026745	AC026745 Homo sapi
c 161	34.6	12.7	84194	8	AB006701	c 234	34	12.5	129071	9	AC010266	AC010266 Homo sapi
c 162	34.6	12.7	121116	2	AC024661	c 235	34	12.5	134841	9	EX927235	EX927235 Human DNA
c 163	34.6	12.7	141048	2	AC007644	c 236	34	12.5	140040	6	AX328485	AX328485 Sequence
c 164	34.6	12.7	148491	10	AL845503	c 237	34	12.5	151517	9	AC146373	AC146373 Pan trogl
c 165	34.6	12.7	151094	2	AC011769	c 238	34	12.5	159998	2	AC063974	AC063974 Homo sapi

C 239	34	12.5	164988	2	AC0800070	AC0800070 Homo sapi	C 312	33.6	12.3	159822	9	AC148714	AC148714 Macaca mu
C 240	34	12.5	167032	9	AC097507	AC097507 Homo sapi	313	33.6	12.3	160623	9	AL670296	AL670296 Human DNA
C 241	34	12.5	170387	9	AL356776	AL356776 Human DNA	314	33.6	12.3	166904	9	AL627309	AL627309 Human DNA
C 242	34	12.5	172660	2	AC148298	AC148298 Pan trogl	315	33.6	12.3	169442	9	AC110766	AC110766 Homo sapi
C 243	34	12.5	174269	2	AC132961	AC132961 Rattus no	316	33.6	12.3	170266	10	AC121900	AC121900 Mus muscu
C 244	34	12.5	177720	9	AC019193	AC019193 Homo sapi	317	33.6	12.3	179567	9	AL669831	AL669831 Human DNA
C 245	34	12.5	187182	2	AC117332	AC117332 Rattus no	318	33.6	12.3	184490	2	AC102150	AC102150 Mus muscu
C 246	34	12.5	205886	9	AC012504	AC012504 Homo sapi	319	33.6	12.3	184503	9	AC079305	AC079305 Homo sapi
C 247	34	12.5	206887	2	AC134007	AC134007 Rattus no	320	33.6	12.3	184644	9	AC138393	AC138393 Homo sapi
C 248	34	12.5	208921	10	AC134546	AC134546 Mus muscu	321	33.6	12.3	185134	2	AC002787	AC002787 Homo sapi
C 249	34	12.5	215948	2	CR383665	CR383665 Danio rer	322	33.6	12.3	188534	2	AC022913	AC022913 Homo sapi
C 250	34	12.5	217068	2	AC079434	AC079434 Mus muscu	323	33.6	12.3	188660	2	AC102327	AC102327 Mus muscu
C 251	34	12.5	248291	2	AC096243	AC096243 Rattus no	324	33.6	12.3	189411	9	AC096542	AC096542 Homo sapi
C 252	34	12.5	259970	2	AC106985	AC106985 Rattus no	325	33.6	12.3	189635	9	AP003082	AP003082 Homo sapi
C 253	34	12.5	324664	2	AC120818	AC120818 Rattus no	326	33.6	12.3	193689	2	AC066603	AC066603 Homo sapi
C 254	34	12.5	349402	1	EX842644	EX842644 Mycoplasma	327	33.6	12.3	194091	2	AC150448	AC150448 Pan trogl
C 255	33.8	12.4	1020	8	SSU30368	SSU30368 Sarcodictyote	328	33.6	12.3	194879	9	AC069287	AC069287 Homo sapi
C 256	33.8	12.4	2265	3	AB122064	AB122064 Crassostre	329	33.6	12.3	204343	2	AL359496	AL359496 Homo sapi
C 257	33.8	12.4	5144	8	AF237670	AF237670 Arabidops	330	33.6	12.3	210282	2	AP001274	AP001274 Homo sapi
C 258	33.8	12.4	93795	9	AB025611	AB025611 Arabidops	331	33.6	12.3	210582	2	AC148307	AC148307 Pan trogl
C 259	33.8	12.4	109972	9	AC110300	AC110300 Homo sapi	332	33.6	12.3	214952	2	AC145493	AC145493 Pan trogl
C 260	33.8	12.4	111882	3	AC115612	AC115612 Dictyoste	333	33.6	12.3	216012	2	AC130290	AC130290 Homo sapi
C 261	33.8	12.4	140602	9	AC012669	AC012669 Homo sapi	334	33.6	12.3	222817	2	AC137185	AC137185 Rattus no
C 262	33.8	12.4	143921	2	AC104080	AC104080 Homo sapi	335	33.6	12.3	226913	2	AL161615	AL161615 Homo sapi
C 263	33.8	12.4	164569	2	CR391967	CR391967 Danio rer	336	33.6	12.3	241471	2	AC114047	AC114047 Rattus no
C 264	33.8	12.4	168654	2	EX927204	EX927204 Danio rer	337	33.6	12.3	243910	2	AC096208	AC096208 Rattus no
C 265	33.8	12.4	168835	9	HS65218	HS65218 Human DNA	338	33.6	12.3	249274	2	AC123229	AC123229 Rattus no
C 266	33.8	12.4	172263	2	AC019035	AC019035 Homo sapi	339	33.6	12.3	253342	2	AC097968	AC097968 Rattus no
C 267	33.8	12.4	172263	2	AC019035	AC019035 Homo sapi	340	33.6	12.3	289251	2	AC114658	AC114658 Rattus no
C 268	33.8	12.4	180409	9	AL844742	AL844742 Homo sapi	341	33.4	12.2	999	3	AF517843	AF517843 Schistosoma
C 269	33.8	12.4	183256	10	AL844900	AL844900 Mouse DNA	342	33.4	12.2	1413	1	AB101201	AB101201 Acinetoba
C 270	33.8	12.4	188933	2	AC142251	AC142251 Mus muscu	343	33.4	12.2	1990	6	AX747578	AX747578 Sequence
C 271	33.8	12.4	191669	10	AL118020	AL118020 Mus muscu	344	33.4	12.2	1990	6	AX747578	AX747578 Sequence
C 272	33.8	12.4	209730	2	AL844860	AL844860 Mus muscu	345	33.4	12.2	1990	6	AX747578	AX747578 Sequence
C 273	33.8	12.4	225483	2	AC106205	AC106205 Rattus no	346	33.4	12.2	2502	2	AC019608	AC019608 Drosophila
C 274	33.8	12.4	227172	2	AC117605	AC117605 Mus muscu	347	33.4	12.2	64986	9	AL499610	AL499610 Human DNA
C 275	33.8	12.4	235755	2	AC108314	AC108314 Rattus no	348	33.4	12.2	78245	9	AC127897	AC127897 Homo sapi
C 276	33.8	12.4	242185	2	AC121187	AC121187 Rattus no	349	33.4	12.2	82047	3	CEY67A10A	CEY67A10A Caenorhab
C 277	33.8	12.4	243602	2	AC113642	AC113642 Rattus no	350	33.4	12.2	129307	10	AL627432	AL627432 Mouse DNA
C 278	33.8	12.4	252818	2	AC109196	AC109196 Mus muscu	351	33.4	12.2	130586	2	AC073238	AC073238 Homo sapi
C 279	33.8	12.4	271039	2	AC095175	AC095175 Rattus no	352	33.4	12.2	133157	9	AC109351	AC109351 Homo sapi
C 280	33.8	12.4	275200	10	AC116392	AC116392 Mus muscu	353	33.4	12.2	133790	8	AC116367	AC116367 Oryza sat
C 281	33.8	12.4	321328	2	AC120904	AC120904 Rattus no	354	33.4	12.2	134796	2	AC124114	AC124114 Mus muscu
C 282	33.6	12.3	321	6	AX310956	AX310956 Sequence	355	33.4	12.2	145105	2	AC018432	AC018432 Homo sapi
C 283	33.6	12.3	576	11	G95885	G95885 S210P6012PG	356	33.4	12.2	149617	2	AC068052	AC068052 Homo sapi
C 284	33.6	12.3	9646	6	AX346591	AX346591 Sequence	357	33.4	12.2	150634	2	AC113371	AC113371 Homo sapi
C 285	33.6	12.3	18218	6	AX346591	AX346591 Sequence	358	33.4	12.2	154994	9	AC099755	AC099755 Homo sapi
C 286	33.6	12.3	29436	9	AC137809	AC137809 Homo sapi	359	33.4	12.2	164473	9	AC109471	AC109471 Homo sapi
C 287	33.6	12.3	29436	9	AC137933	AC137933 Homo sapi	360	33.4	12.2	170817	9	AL513166	AL513166 Human DNA
C 288	33.6	12.3	39524	9	AC092299	AC092299 Homo sapi	361	33.4	12.2	170817	9	AL513166	AL513166 Human DNA
C 289	33.6	12.3	40302	9	AP006222	AP006222 Homo sapi	362	33.4	12.2	174652	2	AC023468	AC023468 Homo sapi
C 290	33.6	12.3	42640	9	AC138035	AC138035 Homo sapi	363	33.4	12.2	174652	2	AC024630	AC024630 Homo sapi
C 291	33.6	12.3	44419	9	AC138030	AC138030 Homo sapi	364	33.4	12.2	183498	5	EX072578	EX072578 Zebrafish
C 292	33.6	12.3	45470	9	AC097647	AC097647 Homo sapi	365	33.4	12.2	183635	9	AC055846	AC055846 Homo sapi
C 293	33.6	12.3	60102	2	AC137899	AC137899 Homo sapi	366	33.4	12.2	188797	9	AC150210	AC150210 Pan trogl
C 294	33.6	12.3	73353	2	AC101422	AC101422 Mus muscu	367	33.4	12.2	190773	9	AC018513	AC018513 Homo sapi
C 295	33.6	12.3	82139	3	AC115684	AC115684 Dictyoste	368	33.4	12.2	198194	2	AC142191	AC142191 Mus muscu
C 296	33.6	12.3	86701	9	AL353654	AL353654 Human DNA	369	33.4	12.2	200000	9	AB019437	AB019437 Homo sapi
C 297	33.6	12.3	99182	9	AC115287	AC115287 Homo sapi	370	33.4	12.2	200859	2	AC118255	AC118255 Mus muscu
C 298	33.6	12.3	113820	9	HS191N21	HS191N21 Human DNA	371	33.4	12.2	205512	2	AC148907	AC148907 Orolemur
C 299	33.6	12.3	120000	9	AC004842	AC004842 Homo sapi	372	33.4	12.2	219662	2	AC120368	AC120368 Mus muscu
C 300	33.6	12.3	120139	2	AC131281	AC131281 Homo sapi	373	33.4	12.2	231197	2	AC128935	AC128935 Rattus no
C 301	33.6	12.3	121390	2	AC138985	AC138985 Homo sapi	374	33.4	12.2	245217	2	AC110848	AC110848 Rattus no
C 302	33.6	12.3	122153	9	AC092941	AC092941 Homo sapi	375	33.4	12.2	247183	2	AC135481	AC135481 Rattus no
C 303	33.6	12.3	128374	9	AL929347	AL929347 Human DNA	376	33.4	12.2	269132	2	AC118381	AC118381 Rattus no
C 304	33.6	12.3	131234	9	HS172K2	HS172K2 Human DNA	377	33.4	12.2	277481	2	AC118399	AC118399 Rattus no
C 305	33.6	12.3	138251	9	AC004908	AC004908 Homo sapi	378	33.4	12.2	278310	2	AC069592	AC069592 Homo sapi
C 306	33.6	12.3	144165	9	AC002127	AC002127 Homo sapi	379	33.4	12.2	297900	2	AC006704	AC006704 Caenorhab
C 307	33.6	12.3	148322	5	EX072568	EX072568 Zebrafish	380	33.2	12.2	659	11	BV053084	BV053084 S212P6030
C 308	33.6	12.3	150660	10	AC115022	AC115022 Mus muscu	381	33.2	12.2	758	3	AB032460	AB032460 Drosophila
C 309	33.6	12.3	150642	9	AC136309	AC136309 Homo sapi	382	33.2	12.2	800	11	BV059985	BV059985 S212P6368
C 310	33.6	12.3	152802	9	AC110274	AC110274 Homo sapi	383	33.2	12.2	1078	3	AV368922	AV368922 Aulacidea
C 311	33.6	12.3	153649	9	AL732372	AL732372 Human DNA	384	33.2	12.2	1380	5	AF195051	AF195051 Danio rer
										1383	5	BC056700	BC056700 Danio rer

385	33.2	12.2	1440	5	BC067162	BC067162 Danio rer	c 458	33	12.1	166553	2	AL844523	AL844523 Homo sapi
386	33.2	12.2	2114	10	D4519981	D45199 Rattus norv	459	33	12.1	167881	8	AP004330	AP004330 Oryza sat
387	33.2	12.2	20417	1	AY517480	AY517480 Sulfolobu	460	33	12.1	169699	9	AC110275	AC110275 Homo sapi
388	33.2	12.2	40368	2	AC149396	AC149396 Phakopso	461	33	12.1	170195	9	AC025452	AC025452 Homo sapi
389	33.2	12.2	57497	9	AL592206	AL592206 Human DNA	462	33	12.1	173347	2	AC136808	AC136808 Rattus no
390	33.2	12.2	65531	2	AC101121	AC101121 Mus muscu	463	33	12.1	174591	9	AC109335	AC109335 Homo sapi
391	33.2	12.2	102703	9	AC004910	AC004910 Homo sapi	c 464	33	12.1	174768	2	AC079191	AC079191 Homo sapi
392	33.2	12.2	103223	8	AC007153	AC007153 Arabidops	465	33	12.1	175167	2	BX950226	BX950226 Danio rer
393	33.2	12.2	127380	10	AC125113	AC125113 Mus muscu	466	33	12.1	175331	2	AC150806	AC150806 Callithri
394	33.2	12.2	128785	9	AC125113	AC125113 Mus muscu	c 467	33	12.1	175331	2	AC110198	AC110198 Mus muscu
395	33.2	12.2	132352	8	AP005287	AP005287 Oryza sat	468	33	12.1	179554	2	AC073268	AC073268 Homo sapi
396	33.2	12.2	133606	2	AC142012	AC142012 Rattus no	469	33	12.1	183546	10	AC140395	AC140395 Mus muscu
397	33.2	12.2	148498	9	AP003473	AP003473 Homo sapi	470	33	12.1	184346	10	AC122283	AC122283 Mus muscu
398	33.2	12.2	159552	2	AC090623	AC090623 Homo sapi	c 471	33	12.1	184346	10	AC011721	AC011721 Homo sapi
399	33.2	12.2	159758	9	AP005356	AP005356 Homo sapi	c 472	33	12.1	184511	2	AC011721	AC011721 Homo sapi
400	33.2	12.2	160019	9	AC020654	AC020654 Homo sapi	c 473	33	12.1	187866	2	BX936363	BX936363 Danio rer
401	33.2	12.2	161940	10	AL929117	AL929117 Mouse DNA	c 474	33	12.1	190867	9	AC145922	AC145922 Pan trogl
402	33.2	12.2	162905	10	AC129318	AC129318 Mus muscu	475	33	12.1	196119	10	AC118223	AC118223 Mus muscu
403	33.2	12.2	163420	2	AC012576	AC012576 Homo sapi	c 476	33	12.1	196840	2	CR626942	CR626942 Danio rer
404	33.2	12.2	164170	10	AC101994	AC101994 Mus muscu	c 477	33	12.1	199306	10	AL672062	AL672062 Mouse DNA
405	33.2	12.2	165318	2	AC016051	AC016051 Homo sapi	c 478	33	12.1	203724	2	AC105072	AC105072 Mus muscu
406	33.2	12.2	167778	2	AC083936	AC083936 Homo sapi	c 479	33	12.1	203724	2	AC105072	AC105072 Mus muscu
407	33.2	12.2	171163	2	BX547932	BX547932 Danio rer	c 480	33	12.1	204520	10	AC129181	AC129181 Mus muscu
408	33.2	12.2	172539	2	AC110523	AC110523 Mus muscu	481	33	12.1	205170	2	AC113482	AC113482 Mus muscu
409	33.2	12.2	175047	2	AC116855	AC116855 Mus muscu	c 482	33	12.1	205255	2	AC113482	AC113482 Mus muscu
410	33.2	12.2	175998	10	BX005263	BX005263 Mouse DNA	c 483	33	12.1	205255	2	AC141909	AC141909 Rattus no
411	33.2	12.2	185417	9	AC012313	AC012313 Homo sapi	c 484	33	12.1	205255	2	AC141909	AC141909 Rattus no
412	33.2	12.2	191304	5	AL928675	AL928675 Zebrafish	c 485	33	12.1	205255	2	AC141909	AC141909 Rattus no
413	33.2	12.2	203639	10	AC113011	AC113011 Mus muscu	c 486	33	12.1	205255	2	AC141909	AC141909 Rattus no
414	33.2	12.2	210962	10	AC113011	AC113011 Mus muscu	c 487	33	12.1	205255	2	AC141909	AC141909 Rattus no
415	33.2	12.2	212338	2	AC103946	AC103946 Mus muscu	c 488	33	12.1	205255	2	AC141909	AC141909 Rattus no
416	33.2	12.2	213565	2	AC103946	AC103946 Mus muscu	c 489	33	12.1	205255	2	AC141909	AC141909 Rattus no
417	33.2	12.2	213677	2	AC146899	AC146899 Papio ham	c 490	33	12.1	205255	2	AC141909	AC141909 Rattus no
418	33.2	12.2	223478	2	AC106224	AC106224 Rattus no	c 491	33	12.1	205255	2	AC141909	AC141909 Rattus no
419	33.2	12.2	224649	2	AC111972	AC111972 Mus muscu	c 492	33	12.1	205255	2	AC141909	AC141909 Rattus no
420	33.2	12.2	226460	2	AC117652	AC117652 Mus muscu	c 493	33	12.1	205255	2	AC141909	AC141909 Rattus no
421	33.2	12.2	230936	2	AC099285	AC099285 Rattus no	c 494	33	12.1	205255	2	AC141909	AC141909 Rattus no
422	33.2	12.2	231639	2	AC095118	AC095118 Rattus no	495	32.8	12.0	435	6	CO435435	CO435435 Sequence
423	33.2	12.2	233071	2	CR457455	CR457455 Danio rer	496	32.8	12.0	914	8	OAD582290	OAD582290 Oxalis ad
424	33.2	12.2	235574	2	AC127657	AC127657 Rattus no	497	32.8	12.0	2419	3	TTTH508395	TTTH508395 Tetrahyme
425	33.2	12.2	245892	2	AC096984	AC096984 Rattus no	c 498	32.8	12.0	9832	6	AX345559	AX345559 Sequence
426	33.2	12.2	247017	2	AC110624	AC110624 Rattus no	c 499	32.8	12.0	42165	2	AX345559	AX345559 Sequence
427	33.2	12.2	252563	2	AC094054	AC094054 Rattus no	500	32.8	12.0	56974	4	CR388000	CR388000 Wallaby D
428	33.2	12.2	261134	2	CR318600	CR318600 Danio rer	c 501	32.8	12.0	56974	4	CR388000	CR388000 Wallaby D
429	33.2	12.2	261934	5	BX664745	BX664745 Zebrafish	c 502	32.8	12.0	56974	4	CR388000	CR388000 Wallaby D
430	33.2	12.2	319012	2	AC108717	AC108717 Homo sapi	c 503	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
431	33.2	12.2	324981	2	AC124889	AC124889 Rattus no	c 504	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
432	33	12.1	1448	10	AY156921	AY156921 Rattus no	c 505	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
433	33	12.1	1448	10	AY156921	AY156921 Rattus no	c 506	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
434	33	12.1	2757	9	BC003622	BC003622 Homo sapi	c 507	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
435	33	12.1	2757	9	BC007428	BC007428 Homo sapi	c 508	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
436	33	12.1	2916	9	AY129028	AY129028 Homo sapi	c 509	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
437	33	12.1	5653	1	CYT1431	D50600 Cytophaga s	c 510	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
438	33	12.1	66596	9	AC108801	AC108801 Mus muscu	c 511	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
439	33	12.1	70655	9	AC112649	AC112649 Homo sapi	c 512	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
440	33	12.1	74091	2	AC108783	AC108783 Mus muscu	c 513	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
441	33	12.1	74673	9	AC005683	AC005683 Homo sapi	c 514	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
442	33	12.1	89813	10	AL928720	AL928720 Mouse DNA	c 515	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
443	33	12.1	90594	2	AC116326	AC116326 Mus muscu	c 516	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
444	33	12.1	90594	2	AC116326	AC116326 Mus muscu	c 517	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
445	33	12.1	110000	2	AC087331_1	AC087331_1 Arabidops	c 518	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
446	33	12.1	110000	2	AC087331_2	AC087331_2 Arabidops	c 519	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
447	33	12.1	110000	14	AX318871_0	AX318871_0 Canarypox	c 520	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
448	33	12.1	117495	2	AC141989	AC141989 Rattus no	c 521	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
449	33	12.1	133120	9	HS933P23	HS933P23 Human DNA s	c 522	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
450	33	12.1	133934	8	AP003272	AP003272 Oryza sat	c 523	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
451	33	12.1	143266	2	AC067790	AC067790 Homo sapi	c 524	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
452	33	12.1	147364	9	AC110998	AC110998 Homo sapi	c 525	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
453	33	12.1	148835	9	AC011225	AC011225 Homo sapi	c 526	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
454	33	12.1	149125	2	AC069401	AC069401 Homo sapi	c 527	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
455	33	12.1	156867	2	AC027494	AC027494 Homo sapi	c 528	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
456	33	12.1	158741	9	AC091905	AC091905 Homo sapi	c 529	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
457	33	12.1	158885	9	CNS01DWT	AL138498 Human chr	c 530	32.8	12.0	110000	2	AX004762_3	AX004762_3 Mus muscu
						AC146203 Pan trogl							

C 531	32.8	12.0	207324	2	AC111759	AC111759 Rattus no	604	32.6	11.9	279539	2	AC111484	AC111484 Rattus no
C 532	32.8	12.0	210624	2	AC102565	Mus muscu	C 605	32.6	11.9	291147	2	AC094912	AC094912 Rattus no
C 533	32.8	12.0	214340	2	AC130012	Rattus no	C 606	32.6	11.9	346553	2	AC102164	Mus muscu
C 534	32.8	12.0	216044	10	AC114824	AC114824 Mus muscu	C 607	32.6	11.9	346970	2	BX510643	Danio rer
C 535	32.8	12.0	217400	2	BX323544	Danio rer	C 608	32.4	11.9	427	6	CQ669962	Sequence
C 536	32.8	12.0	230702	2	AC102235	Mus muscu	C 609	32.4	11.9	5482	5	BC074354	Sequence
C 537	32.8	12.0	237094	2	AC116661	Mus muscu	C 610	32.4	11.9	7218	6	I66494	Sequence
C 538	32.8	12.0	245820	2	AC106477	Rattus no	C 611	32.4	11.9	56128	9	AC005349	Homo sapi
C 539	32.8	12.0	249433	2	AC051620	Mus muscu	C 612	32.4	11.9	69709	3	CEY6B3B	Homo sapi
C 540	32.8	12.0	253649	2	AC106142	Rattus no	C 613	32.4	11.9	76287	9	AL645617	Human DNA
C 541	32.8	12.0	257109	3	AC118963	Dictyoste	C 614	32.4	11.9	84193	9	AL163538	Human DNA
C 542	32.8	12.0	257109	3	AC118963	Dictyoste	C 615	32.4	11.9	86212	8	AB010074	Arabidops
C 543	32.8	12.0	275702	2	AC125862	Rattus no	C 616	32.4	11.9	92227	9	AC097517	Homo sapi
C 544	32.8	12.0	326728	2	AC110313	Rattus no	C 617	32.4	11.9	95594	9	HS1186N24	Human DNA
C 545	32.8	12.0	335799	2	BX005139	Mus muscu	C 618	32.4	11.9	95612	8	AC007661	Arabidops
C 546	32.6	11.9	400	11	G13696	GL3696 human STS	C 619	32.4	11.9	97978	8	AL513285	Human DNA
C 547	32.6	11.9	830	11	BV058048	BV058048 S212P6013	C 620	32.4	11.9	104406	2	AC136810	Rattus no
C 548	32.6	11.9	1078	3	HY368925	Timaspiis	C 621	32.4	11.9	108125	9	AC093122	Homo sapi
C 549	32.6	11.9	41122	9	HSAC000109	AC000109 Human Cos	C 622	32.4	11.9	110000	1	AE017355	Continuation (7 of
C 550	32.6	11.9	42175	2	CR556698	Homo sapi	C 623	32.4	11.9	110000	2	AC129052	Continuation (3 of
C 551	32.6	11.9	45508	9	HSAC000110	AC000110 Human Cos	C 624	32.4	11.9	110000	2	EX890561	Continuation (4 of
C 552	32.6	11.9	55016	9	AC149643	AC149643 Homo sapi	C 625	32.4	11.9	110000	2	AC093122	Continuation (5 of
C 553	32.6	11.9	82604	9	AL500522	AL500522 Human DNA	C 626	32.4	11.9	110000	3	AC116984	Dictyoste
C 554	32.6	11.9	93925	9	AC090846	AC090846 Homo sapi	C 627	32.4	11.9	110000	8	CR382136	Continuation (13 o
C 555	32.6	11.9	107916	8	AP005569	AP005569 Oryza sat	C 628	32.4	11.9	111078	9	AC093892	Homo sapi
C 556	32.6	11.9	110000	2	AC102011	Continuation (3 of	C 629	32.4	11.9	111078	9	AC093892	Homo sapi
C 557	32.6	11.9	110000	2	AC107636	Continuation (3 of	C 630	32.4	11.9	114797	5	BX322797	Continuation (3 of
C 558	32.6	11.9	110000	2	CR555291	Danio rer	C 631	32.4	11.9	115597	2	AC136166	Rattus no
C 559	32.6	11.9	126228	9	AL513211	AL513211 Human DNA	C 632	32.4	11.9	119974	9	AC018763	Homo sapi
C 560	32.6	11.9	136362	10	AC127237	AC127237 Mus muscu	C 633	32.4	11.9	128976	10	AL837522	Mouse DNA
C 561	32.6	11.9	141796	9	AC010819	AC010819 Homo sapi	C 634	32.4	11.9	131144	10	AL645569	Mouse DNA
C 562	32.6	11.9	143799	9	AC011059	AC011059 Homo sapi	C 635	32.4	11.9	132728	2	AC099411	Felis cat
C 563	32.6	11.9	145437	2	AC009697	AC009697 Homo sapi	C 636	32.4	11.9	134206	2	AC099752	Felis cat
C 564	32.6	11.9	151448	2	CR547121	CR547121 Danio rer	C 637	32.4	11.9	135299	9	AC091857	Homo sapi
C 565	32.6	11.9	164038	2	AC150011	AC150011 Callithrix	C 638	32.4	11.9	135762	2	AC139785	Homo sapi
C 566	32.6	11.9	166387	2	AC145234	AC145234 Homo sapi	C 639	32.4	11.9	140241	9	AC079355	Homo sapi
C 567	32.6	11.9	167635	5	AL645789	AL645789 Zebrafish	C 640	32.4	11.9	143517	10	AL732418	Mouse DNA
C 568	32.6	11.9	172286	10	AL928962	AL928962 Mouse DNA	C 641	32.4	11.9	144041	2	AP001766	Homo sapi
C 569	32.6	11.9	172587	5	BX005125	BX005125 Zebrafish	C 642	32.4	11.9	151450	9	AC108679	Homo sapi
C 570	32.6	11.9	172732	9	AC105064	AC105064 Mus muscu	C 643	32.4	11.9	156312	9	AC138470	Homo sapi
C 571	32.6	11.9	172932	9	CNS01RH9	AL161665 Human chr	C 644	32.4	11.9	156321	9	AC074331	Homo sapi
C 572	32.6	11.9	173023	9	AL354898	AL354898 Human DNA	C 645	32.4	11.9	157224	2	AC105701	Rattus no
C 573	32.6	11.9	173094	2	AL603629	AL603629 Homo sapi	C 646	32.4	11.9	157224	9	AP005357	Homo sapi
C 574	32.6	11.9	173940	9	AC021180	AC021180 Homo sapi	C 647	32.4	11.9	158004	9	AC087319	Homo sapi
C 575	32.6	11.9	174140	5	AC012379	AC012379 Homo sapi	C 648	32.4	11.9	162750	9	AL355365	Human DNA
C 576	32.6	11.9	174182	5	BX323465	BX323465 Zebrafish	C 649	32.4	11.9	163772	2	AC079985	Homo sapi
C 577	32.6	11.9	174905	8	AP005789	AP005789 Oryza sat	C 650	32.4	11.9	166743	10	AC127226	Mus muscu
C 578	32.6	11.9	176503	9	AL512604	AL512604 Human DNA	C 651	32.4	11.9	166790	2	AC102293	Mus muscu
C 579	32.6	11.9	181682	2	AC090322	AC090322 Homo sapi	C 652	32.4	11.9	166804	8	OSJN00077	Oryza sat
C 580	32.6	11.9	183593	2	AP001639	AP001639 Homo sapi	C 653	32.4	11.9	170861	2	AC025698	Homo sapi
C 581	32.6	11.9	191096	9	AC008834	AC008834 Homo sapi	C 654	32.4	11.9	171965	2	AC027507	Homo sapi
C 582	32.6	11.9	191923	5	AC109480	AC109480 Homo sapi	C 655	32.4	11.9	177312	9	AC079801	Homo sapi
C 583	32.6	11.9	192205	5	AC145954	AC145954 Gallus ga	C 656	32.4	11.9	179036	2	BX294164	Danio rer
C 584	32.6	11.9	196712	5	BX323818	BX323818 Zebrafish	C 657	32.4	11.9	181265	2	AC019356	Homo sapi
C 585	32.6	11.9	197391	2	CR897749	CR897749 Danio rer	C 658	32.4	11.9	182547	9	AC146141	Pan trogl
C 586	32.6	11.9	198627	5	AL845168	AL845168 Zebrafish	C 659	32.4	11.9	183298	2	AC01809	Homo sapi
C 587	32.6	11.9	205646	9	AC062004	AC062004 Homo sapi	C 660	32.4	11.9	184646	2	EX936405	Mus muscu
C 588	32.6	11.9	206860	2	AC102884	AC102884 Homo sapi	C 661	32.4	11.9	185802	2	AC147846	Ocolemur
C 589	32.6	11.9	208106	10	AL831734	AL831734 Mouse DNA	C 662	32.4	11.9	187549	2	CR405687	Danio rer
C 590	32.6	11.9	219884	2	AC094517	AC094517 Rattus no	C 663	32.4	11.9	189891	2	AC141369	Rattus no
C 591	32.6	11.9	227936	2	AC119370	AC119370 Rattus no	C 664	32.4	11.9	191744	2	AC044865	Homo sapi
C 592	32.6	11.9	230218	2	AC094458	AC094458 Rattus no	C 665	32.4	11.9	191918	2	AC026484	Homo sapi
C 593	32.6	11.9	232619	2	AC128426	AC128426 Rattus no	C 666	32.4	11.9	192281	2	AC130708	Homo sapi
C 594	32.6	11.9	235317	2	AC121371	AC121371 Rattus no	C 667	32.4	11.9	193708	2	AC005035	Homo sapi
C 595	32.6	11.9	235440	2	AC117024	AC117024 Rattus no	C 668	32.4	11.9	194366	5	AL954179	Zebrafish
C 596	32.6	11.9	237927	2	AC130252	AC130252 Rattus no	C 669	32.4	11.9	196373	2	AC141648	Rattus no
C 597	32.6	11.9	241571	2	AC094827	AC094827 Rattus no	C 670	32.4	11.9	197371	2	AL355524	Homo sapi
C 598	32.6	11.9	248110	2	AC094827	AC094827 Rattus no	C 671	32.4	11.9	197821	2	AC116429	Homo sapi
C 599	32.6	11.9	250804	2	AC097842	AC097842 Rattus no	C 672	32.4	11.9	200219	2	AC117312	Rattus no
C 600	32.6	11.9	253510	2	AC096968	AC096968 Rattus no	C 673	32.4	11.9	208344	10	AC125070	Homo sapi
C 601	32.6	11.9	255891	2	AC094566	AC094566 Rattus no	C 674	32.4	11.9	211395	2	AC137779	Homo sapi
C 602	32.6	11.9	265040	2	AC11525	AC11525 Rattus no	C 675	32.4	11.9	211652	9	AP001838	Homo sapi
C 603	32.6	11.9	269376	2	AC135203	AC135203 Rattus no	C 676	32.4	11.9	212282	10	AC110499	Mus muscu

677	32.4	11.9	213599	2	AC140764	Rattus no	AC140764	Rattus no	750	32.2	11.8	190866	3	AC007824	Drosophil
678	32.4	11.9	216152	2	AC101858	Mus muscu	AC101858	Mus muscu	751	32.2	11.8	191353	2	AC090320	Homo sapi
679	32.4	11.9	216381	2	AC113714	Rattus no	AC113714	Rattus no	752	32.2	11.8	191854	2	AC141402	Homo sapi
680	32.4	11.9	220320	2	AC134121	Rattus no	AC134121	Rattus no	753	32.2	11.8	193304	2	AC109370	Rattus no
681	32.4	11.9	220428	2	AC122586	Rattus no	AC122586	Rattus no	754	32.2	11.8	193304	2	AC121898	Mus muscu
682	32.4	11.9	223467	2	AC095643	Rattus no	AC095643	Rattus no	755	32.2	11.8	193708	9	AC136428	Homo sapi
683	32.4	11.9	227763	2	AC108534	Rattus no	AC108534	Rattus no	756	32.2	11.8	195739	10	AC124519	Mus muscu
684	32.4	11.9	228976	2	AC099218	Rattus no	AC099218	Rattus no	757	32.2	11.8	198786	9	AC092098	Homo sapi
685	32.4	11.9	229306	2	AC114032	Rattus no	AC114032	Rattus no	758	32.2	11.8	206536	2	AC145310	Homo sapi
686	32.4	11.9	230338	2	AC114347	Rattus no	AC114347	Rattus no	759	32.2	11.8	207450	2	AC133253	Homo sapi
687	32.4	11.9	230568	2	AC113731	Rattus no	AC113731	Rattus no	760	32.2	11.8	211018	2	AC140879	Homo sapi
688	32.4	11.9	230668	2	AC113731	Rattus no	AC113731	Rattus no	761	32.2	11.8	213753	2	AC110715	Drosophil
689	32.4	11.9	231612	2	AC126903	Rattus no	AC126903	Rattus no	762	32.2	11.8	220035	3	AE003716	Drosophil
690	32.4	11.9	231612	2	AC130088	Rattus no	AC130088	Rattus no	763	32.2	11.8	224003	2	AC111688	Rattus no
691	32.4	11.9	231612	2	AC094419	Rattus no	AC094419	Rattus no	764	32.2	11.8	231967	2	AC111688	Rattus no
692	32.4	11.9	233628	10	AC091683	Mus muscu	AC091683	Mus muscu	765	32.2	11.8	233077	2	AC096835	Rattus no
693	32.4	11.9	233628	10	AC112572	Rattus no	AC112572	Rattus no	766	32.2	11.8	234138	2	AC111988	Rattus no
694	32.4	11.9	241557	2	AC098000	Rattus no	AC098000	Rattus no	767	32.2	11.8	235276	2	AC137397	Rattus no
695	32.4	11.9	241557	2	AC120235	Rattus no	AC120235	Rattus no	768	32.2	11.8	235897	2	AC095685	Rattus no
696	32.4	11.9	243360	2	AC109684	Rattus no	AC109684	Rattus no	769	32.2	11.8	239424	2	AC118504	Rattus no
697	32.4	11.9	243638	2	CR456621	Danio rer	CR456621	Danio rer	770	32.2	11.8	241865	2	AC118396	Zebrafish
698	32.4	11.9	244676	2	AC135003	Rattus no	AC135003	Rattus no	771	32.2	11.8	243759	5	AL928866	Zebrafish
699	32.4	11.9	245853	2	AC131862	Rattus no	AC131862	Rattus no	772	32.2	11.8	250885	2	AC113161	Rattus no
700	32.4	11.9	249680	2	AC094431	Rattus no	AC094431	Rattus no	773	32.2	11.8	251806	2	AC096305	Rattus no
701	32.4	11.9	252367	2	AC099001	Rattus no	AC099001	Rattus no	774	32.2	11.8	252679	2	AC118394	Rattus no
702	32.4	11.9	262268	2	AC136923	Mus muscu	AC136923	Mus muscu	775	32.2	11.8	253176	2	AC094477	Rattus no
703	32.4	11.9	265092	2	AC126568	Rattus no	AC126568	Rattus no	776	32.2	11.8	254116	2	AC118902	Rattus no
704	32.4	11.9	267077	2	AC106340	Rattus no	AC106340	Rattus no	777	32.2	11.8	258265	2	AC120472	Rattus no
705	32.4	11.9	267559	2	AC127644	Rattus no	AC127644	Rattus no	778	32.2	11.8	261088	2	AC131166	Rattus no
706	32.4	11.9	269832	2	AC112751	Rattus no	AC112751	Rattus no	779	32.2	11.8	261929	2	CR382370	Danio rer
707	32.4	11.9	269956	2	AC094994	Rattus no	AC094994	Rattus no	780	32.2	11.8	265699	5	AX088533	Zebrafish
708	32.4	11.9	284507	2	AC096470	Rattus no	AC096470	Rattus no	781	32.2	11.8	267191	2	AC132043	Rattus no
709	32.4	11.9	302156	3	AC116977	Rattus no	AC116977	Rattus no	782	32.2	11.8	276285	2	AC094113	Rattus no
710	32.4	11.9	316119	2	AC119083	Rattus no	AC119083	Rattus no	783	32.2	11.8	283903	2	AC094113	Rattus no
711	32.2	11.8	331195	2	AC117292	Rattus no	AC117292	Rattus no	784	32.2	11.8	292345	2	AC133617	Rattus no
712	32.2	11.8	331195	2	AC117292	Rattus no	AC117292	Rattus no	785	32.2	11.8	304341	1	AE017163	Prochloro
713	32.2	11.8	331195	2	AC117292	Rattus no	AC117292	Rattus no	786	32.2	11.8	304341	1	AE017163	Prochloro
714	32.2	11.8	36188	3	AC116922	Dictyoste	AC116922	Dictyoste	787	32.2	11.8	304341	1	AE017163	Prochloro
715	32.2	11.8	41469	2	AC140812	4	AC140812	4	788	32.2	11.7	366	6	CO474577	Sequence
716	32.2	11.8	66674	2	AC131289	Homo sapi	AC131289	Homo sapi	789	32.2	11.7	366	6	CO474577	Sequence
717	32.2	11.8	97308	2	AC013925	Drosophil	AC013925	Drosophil	790	32.2	11.7	1325	6	CO717251	Sequence
718	32.2	11.8	98347	2	AL513203	Mus muscu	AL513203	Mus muscu	791	32.2	11.7	1931	6	AF237982	Sequence
719	32.2	11.8	100190	2	AL391257	Homo sapi	AL391257	Homo sapi	792	32.2	11.7	2129	9	AF237982	Homo sapi
720	32.2	11.8	105320	3	AC116920	Dictyoste	AC116920	Dictyoste	793	32.2	11.7	2209	9	BC010358	Homo sapi
721	32.2	11.8	126391	9	AC007243	Homo sapi	AC007243	Homo sapi	794	32.2	11.7	3294	10	BC031171	Mus muscu
722	32.2	11.8	127370	9	AL451044	Human DNA	AL451044	Human DNA	795	32.2	11.7	3456	6	CO842456	Sequence
723	32.2	11.8	135630	10	AL928595	Mouse DNA	AL928595	Mouse DNA	796	32.2	11.7	3456	6	CO842456	Sequence
724	32.2	11.8	138308	2	AC145287	Homo sapi	AC145287	Homo sapi	797	32.2	11.7	14869	1	AE000721	Homo sapi
725	32.2	11.8	148008	9	AC092004	Bos tauru	AC092004	Bos tauru	798	32.2	11.7	30014	4	AY152832	Pellis cat
726	32.2	11.8	160707	2	AC044899	Homo sapi	AC044899	Homo sapi	799	32.2	11.7	49995	2	AC011335	Homo sapi
727	32.2	11.8	166333	10	AL513470	Mouse DNA	AL513470	Mouse DNA	800	32.2	11.7	56007	2	AC100073	Mus muscu
728	32.2	11.8	167545	2	AC138799	Homo sapi	AC138799	Homo sapi	801	32.2	11.7	70360	2	AC101122	Mus muscu
729	32.2	11.8	170935	2	AC092008	Bos tauru	AC092008	Bos tauru	802	32.2	11.7	75021	2	AC124656	Homo sapi
730	32.2	11.8	172419	9	AC098858	Homo sapi	AC098858	Homo sapi	803	32.2	11.7	77139	2	AC008466	Homo sapi
731	32.2	11.8	172674	3	AC007807	Drosophil	AC007807	Drosophil	804	32.2	11.7	78139	2	AP000449	Homo sapi
732	32.2	11.8	173206	9	AC141248	Homo sapi	AC141248	Homo sapi	805	32.2	11.7	86523	8	AC084419	Caenorhab
733	32.2	11.8	174326	2	CR361546	Danio rer	CR361546	Danio rer	806	32.2	11.7	106329	3	AC004411	Arabidops
734	32.2	11.8	174651	2	CR361546	Danio rer	CR361546	Danio rer	807	32.2	11.7	107343	5	AL954693	Zebrafish
735	32.2	11.8	180384	10	AC131339	Mus muscu	AC131339	Mus muscu	808	32.2	11.7	107912	2	AC133569	Homo sapi
736	32.2	11.8	180542	2	BX927066	Danio rer	BX927066	Danio rer	809	32.2	11.7	110000	2	AC117114	4
737	32.2	11.8	181036	9	AC087683	Homo sapi	AC087683	Homo sapi	810	32.2	11.7	113686	9	AC060834	Homo sapi
738	32.2	11.8	182002	2	AC142090	Takifugu	AC142090	Takifugu	811	32.2	11.7	115399	2	AP004322	Oryza sat
739	32.2	11.8	182748	5	AL935165	Zebrafish	AL935165	Zebrafish	812	32.2	11.7	115498	9	AL356255	Human DNA
740	32.2	11.8	183375	2	AC150471	Macropus	AC150471	Macropus	813	32.2	11.7	116139	2	BL3664701	Homo sapi
741	32.2	11.8	183958	5	AL772189	Zebrafish	AL772189	Zebrafish	814	32.2	11.7	117000	10	AC087871	Genomic s
742	32.2	11.8	184182	2	AC129405	Rattus no	AC129405	Rattus no	815	32.2	11.7	120849	2	AC087148	Mus muscu
743	32.2	11.8	185187	9	AC141272	Homo sapi	AC141272	Homo sapi	816	32.2	11.7	128928	9	AC068658	Homo sapi
744	32.2	11.8	185268	10	AC122458	Mus muscu	AC122458	Mus muscu	817	32.2	11.7	133487	2	AC024241	Homo sapi
745	32.2	11.8	185342	2	CR387989	Danio rer	CR387989	Danio rer	818	32.2	11.7	133952	2	CR450765	Danio rer
746	32.2	11.8	186807	10	AC121592	Mus muscu	AC121592	Mus muscu	819	32.2	11.7	134701	5	AX255885	Zebrafish
747	32.2	11.8	186890	9	AC141587	Homo sapi	AC141587	Homo sapi	820	32.2	11.7	138102	10	AC099575	Mus muscu
748	32.2	11.8	188148	2	AC036220	Homo sapi	AC036220	Homo sapi	821	32.2	11.7	141214	4	AY152830	Felis cat
749	32.2	11.8	188406	9	AC140658	Homo sapi	AC140658	Homo sapi	822	32.2	11.7	141705	5	AX571715	Zebrafish
									823	32.2	11.7	145918	9	AC034229	Homo sapi

C 823	32	11.7	147724	8	AP003525	Oryza sat	C 896	32	11.7	270216	2	AC112038	AC112038 Rattus no
C 824	32	11.7	149122	5	AL954322	Zebrafish	897	32	11.7	281307	2	AC106352	AC106352 Rattus no
C 825	32	11.7	151757	4	AC150635	Bos taurus	898	32	11.7	294817	2	AC114626	AC114626 Mus muscu
C 826	32	11.7	152086	2	AC121444	Rattus no	C 899	32	11.7	299308	2	AC006898	AC006898 Caenorhab
C 827	32	11.7	153066	2	CR559943	Danio rer	C 900	32	11.7	299820	2	AC006803	AC006803 Caenorhab
C 828	32	11.7	154104	2	AC129073	Felis cat	C 901	32	11.7	299820	2	AC006871	AC006871 Caenorhab
C 829	32	11.7	155363	5	EX088582	Zebrafish	C 902	32	11.7	301030	1	AE016930	AE016930 Bacteroid
C 830	32	11.7	157208	9	AC113409	AC086582	C 903	32	11.7	302568	2	AC127044	AC127044 Rattus no
C 831	32	11.7	157435	9	HS50024	AC113409	C 904	31.8	11.6	337	6	CQ672641	CQ672641 Sequence
C 832	32	11.7	160705	2	AC130060	AL034380	C 905	31.8	11.6	506	6	AX396801	AX396801 Sequence
C 833	32	11.7	161261	9	AC141070	AC130060	C 906	31.8	11.6	713	6	AX381927	AX381927 Sequence
C 834	32	11.7	162329	10	AC140799	AC140799	C 907	31.8	11.6	773	8	TRADH1PRB	229507 Trifolium r
C 835	32	11.7	162546	2	AC141376	AC141376	C 908	31.8	11.6	773	8	AX780655	AX780655 Sequence
C 836	32	11.7	163413	2	AC118693	AC118693	C 909	31.8	11.6	983	6	AF289489	AF289489 Homo sapi
C 837	32	11.7	163547	10	AL928788	AL928788	C 910	31.8	11.6	2680	9	BC252336	BC252336 Homo sapi
C 838	32	11.7	166928	9	AC114938	AC114938	C 911	31.8	11.6	2761	9	BF202523	BF202523 Homo sapi
C 839	32	11.7	167039	2	AC112923	AC114938	C 912	31.8	11.6	8478	6	ARI73058	ARI73058 Sequence
C 840	32	11.7	168683	2	AC112923	AC114938	C 913	31.8	11.6	10153	1	BSU51868	BSU51868 Sequence
C 841	32	11.7	169699	2	AC101657	AC101657	C 914	31.8	11.6	12940	8	AY299396	AY299396 Pisum sat
C 842	32	11.7	171037	5	EX005228	AC101657	C 915	31.8	11.6	27394	3	CEB32B6	CEB32B6 Sequence
C 843	32	11.7	173519	2	AC145860	AC101657	C 916	31.8	11.6	43742	10	AL844485	AL844485 Mouse DNA
C 844	32	11.7	173617	5	AC145860	AC101657	C 917	31.8	11.6	53369	9	AP002404	AP002404 Homo sapi
C 845	32	11.7	174685	2	AC148563	AC148563	C 918	31.8	11.6	72832	8	AC074228	AC074228 Arabidops
C 846	32	11.7	175555	2	CR387982	CR387982	C 919	31.8	11.6	80664	2	AC027265	AC027265 Homo sapi
C 847	32	11.7	175583	9	AL590502	AL590502	C 920	31.8	11.6	82875	9	AC123024	AC123024 Homo sapi
C 848	32	11.7	177655	2	AC145232	AC145232	C 921	31.8	11.6	89119	9	AC123025	AC123025 Homo sapi
C 849	32	11.7	179899	2	AC116736	AC116736	C 922	31.8	11.6	90373	3	ATF8F16	ATF8F16 Dictyoste
C 850	32	11.7	182182	5	EX890617	EX890617	C 923	31.8	11.6	96416	9	AC112720	AC112720 Homo sapi
C 851	32	11.7	182428	2	EX957249	EX957249	C 924	31.8	11.6	101522	2	AC106166	Continuation (6 of
C 852	32	11.7	183245	8	AP003458	AP003458	C 925	31.8	11.6	108987	8	AP004511	AP004511 Lotus cor
C 853	32	11.7	184730	2	AC118631	AC118631	C 926	31.8	11.6	110000	1	BX908798	Continuation (18 o
C 854	32	11.7	185339	9	AC141293	AC1122483	C 927	31.8	11.6	119481	9	AC019048	Continuation (18 o
C 855	32	11.7	185388	10	AC122483	AC122483	C 928	31.8	11.6	122629	9	HS653H13	AC1031466 Homo sapi
C 856	32	11.7	186141	9	AC004988	AC004988	C 929	31.8	11.6	125377	2	AC118135	AC1031466 Homo sapi
C 857	32	11.7	186251	2	AC139807	AC139807	C 930	31.8	11.6	126392	9	CR626894	CR626894 Human DNA
C 858	32	11.7	186473	2	AC051660	AC051660	C 931	31.8	11.6	126600	2	AP006544	AP006544 Homo sapi
C 859	32	11.7	186583	10	AC107669	AC107669	C 932	31.8	11.6	127372	2	AC068172	AC068172 Homo sapi
C 860	32	11.7	186769	2	AC090591	AC090591	C 933	31.8	11.6	127653	9	AL353135	AL353135 Human DNA
C 861	32	11.7	186930	2	AC135873	AC135873	C 934	31.8	11.6	131101	9	AC144532	AC144532 Homo sapi
C 862	32	11.7	187934	9	AP003068	AP003068	C 935	31.8	11.6	134960	2	AP002337	AP002337 Homo sapi
C 863	32	11.7	191376	2	AC138945	AC138945	C 936	31.8	11.6	135637	9	AP003400	AP003400 Homo sapi
C 864	32	11.7	194561	2	CR450706	CR450706	C 937	31.8	11.6	135698	2	AL365218	AL365218 Homo sapi
C 865	32	11.7	194770	2	AC149064	AC149064	C 938	31.8	11.6	135964	9	AC005914	AC005914 Homo sapi
C 866	32	11.7	194785	2	AC136047	AC136047	C 939	31.8	11.6	136474	2	AC036230	AC036230 Homo sapi
C 867	32	11.7	196550	9	AC137800	AC137800	C 940	31.8	11.6	137233	2	AC090271	AC090271 Homo sapi
C 868	32	11.7	203418	2	AC063958	AC063958	C 941	31.8	11.6	139693	8	AC123521	AC123521 Oryza sat
C 869	32	11.7	203519	10	AC112258	AC112258	C 942	31.8	11.6	146666	9	AL160287	AL160287 Human DNA
C 870	32	11.7	204498	5	AL831791	AL831791	C 943	31.8	11.6	145340	9	AL136525	AL136525 Human DNA
C 871	32	11.7	207702	10	AC060781	AC060781	C 944	31.8	11.6	145340	9	AL141842	AC141842 Apis mell
C 872	32	11.7	208106	10	AC102225	AC102225	C 945	31.8	11.6	146954	8	AP004635	AP004635 Oryza sat
C 873	32	11.7	212159	2	AC101877	AC101877	C 946	31.8	11.6	152115	2	AC149042	AC149042 Gasterost
C 874	32	11.7	215359	9	AC012495	AC012495	C 947	31.8	11.6	153185	2	AC073228	AC073228 Homo sapi
C 875	32	11.7	216143	3	AC084197	AC084197	C 948	31.8	11.6	155588	2	AC136265	AC136265 Rattus no
C 876	32	11.7	220387	2	AC145279	AC145279	C 949	31.8	11.6	156754	9	AC021055	AC021055 Homo sapi
C 877	32	11.7	221001	10	AC109271	AC109271	C 950	31.8	11.6	157064	9	AL512884	AL512884 Human DNA
C 878	32	11.7	222634	10	AC131866	AC131866	C 951	31.8	11.6	157221	9	AC008376	AC008376 Homo sapi
C 879	32	11.7	222965	2	AC096522	AC096522	C 952	31.8	11.6	157918	2	AC024252	AC024252 Homo sapi
C 880	32	11.7	226926	10	AC122287	AC122287	C 953	31.8	11.6	158404	9	AC090094	AC090094 Homo sapi
C 881	32	11.7	227582	2	EX324177	EX324177	C 954	31.8	11.6	158401	9	AL158063	AL158063 Human DNA
C 882	32	11.7	232413	2	AC117096	AC117096	C 955	31.8	11.6	158481	9	AC007751	AC007751 Homo sapi
C 883	32	11.7	236182	10	AC111140	AC111140	C 956	31.8	11.6	158963	9	AC108457	AC108457 Homo sapi
C 884	32	11.7	236334	2	AC097363	AC097363	C 957	31.8	11.6	160822	9	AL935188	AL935188 Zebrafish
C 885	32	11.7	237027	2	AC122580	AC122580	C 958	31.8	11.6	160946	5	AL935188	AL935188 Zebrafish
C 886	32	11.7	237541	2	AC112564	AC112564	C 959	31.8	11.6	161874	9	AC079864	AC079864 Homo sapi
C 887	32	11.7	239185	2	AC124034	AC124034	C 960	31.8	11.6	162020	2	AC009864	AC009864 Homo sapi
C 888	32	11.7	242339	2	AC006880	AC006880	C 961	31.8	11.6	163114	9	AC096886	AC096886 Homo sapi
C 889	32	11.7	244845	2	AC105622	AC105622	C 962	31.8	11.6	163317	9	AC096564	AC096564 Homo sapi
C 890	32	11.7	246370	2	AC107575	AC107575	C 963	31.8	11.6	163380	2	AC113379	AC113379 Homo sapi
C 891	32	11.7	248500	2	AC104400	AC104400	C 964	31.8	11.6	163443	2	AC103218	AC103218 Rattus no
C 892	32	11.7	250096	10	AC107773	AC107773	C 965	31.8	11.6	165075	2	AC148584	AC148584 Gasterost
C 893	32	11.7	250257	2	AC097828	AC097828	C 966	31.8	11.6	165200	5	EX323079	EX323079 Zebrafish
C 894	32	11.7	254884	2	AC098430	AC098430	C 967	31.8	11.6	167409	2	AC073374	AC073374 Homo sapi
C 895	32	11.7	258426	2	AC105645	AC105645	C 968	31.8	11.6	167764	2	AC073870	AC073870 Homo sapi
							968	31.8	11.6	168425	2	AC012198	AC012198 Homo sapi

c 969	31.8	11.6	169177	2	AC023397	Homo sapi	AC023397 Homo sapi
c 970	31.8	11.6	171054	10	AC116590	Mus muscu	AC116590 Mus muscu
c 971	31.8	11.6	172706	2	AL391135	Homo sapi	AL391135 Homo sapi
c 972	31.8	11.6	173389	9	CNS05TCM	Human chr	AL355103 Human chr
c 973	31.8	11.6	173675	2	AC112969	Mus muscu	AC112969 Mus muscu
c 974	31.8	11.6	174383	5	AL929216	Zebrafish	AL929216 Zebrafish
c 975	31.8	11.6	174525	2	AC067763	Homo sapi	AC067763 Homo sapi
c 976	31.8	11.6	175066	9	AC005900	Homo sapi	AC005900 Homo sapi
c 977	31.8	11.6	176761	9	AC124608	Homo sapi	AC124608 Homo sapi
c 978	31.8	11.6	177872	10	AC093371	Genomic B	AC093371 Genomic B
c 979	31.8	11.6	177951	2	AC074383	Homo sapi	AC074383 Homo sapi
c 980	31.8	11.6	178000	8	AC123522	Oryza sat	AC123522 Oryza sat
c 981	31.8	11.6	178066	9	AC087641	Homo sapi	AC087641 Homo sapi
c 982	31.8	11.6	178653	2	AC090088	Homo sapi	AC090088 Homo sapi
c 983	31.8	11.6	178982	9	AP001591	Homo sapi	AP001591 Homo sapi
c 984	31.8	11.6	179483	9	AC019230	Homo sapi	AC019230 Homo sapi
c 985	31.8	11.6	180318	2	AC123674	Mus muscu	AC123674 Mus muscu
c 986	31.8	11.6	180355	8	AP005504	Oryza sat	AP005504 Oryza sat
c 987	31.8	11.6	181442	2	AC134875	Homo sapi	AC134875 Homo sapi
c 988	31.8	11.6	183727	2	AC117802	Mus muscu	AC117802 Mus muscu
c 989	31.8	11.6	184057	9	AP000753	Homo sapi	AP000753 Homo sapi
c 990	31.8	11.6	184059	2	AC090382	Homo sapi	AC090382 Homo sapi
c 991	31.8	11.6	185018	9	AC110614	Homo sapi	AC110614 Homo sapi
c 992	31.8	11.6	185524	2	AC132522	Rattus no	AC132522 Rattus no
c 993	31.8	11.6	185972	2	AC069355	Homo sapi	AC069355 Homo sapi
c 994	31.8	11.6	186271	10	AC135236	Mus muscu	AC135236 Mus muscu
c 995	31.8	11.6	186676	9	AC067881	Homo sapi	AC067881 Homo sapi
c 996	31.8	11.6	187234	2	AC114142	Rattus no	AC114142 Rattus no
c 997	31.8	11.6	188256	2	AP001927	Homo sapi	AP001927 Homo sapi
c 998	31.8	11.6	189145	10	AC101713	Mus muscu	AC101713 Mus muscu
c 999	31.8	11.6	190657	2	AC011129	Homo sapi	AC011129 Homo sapi
1000	31.8	11.6	191752	9	BC322613	Human DNA	BC322613 Human DNA
1001	31.8	11.6	193116	10	BX005100	Mouse DNA	BX005100 Mouse DNA
c1002	31.8	11.6	194472	2	AC102117	Mus muscu	AC102117 Mus muscu
c1003	31.8	11.6	194510	2	BC324111	Danio rer	BC324111 Danio rer
1004	31.8	11.6	194816	2	AC130765	Rattus no	AC130765 Rattus no
c1005	31.8	11.6	194920	8	ATCHRIV74	Arabidops	AL161578 Arabidops
1006	31.8	11.6	195231	9	AC117465	Homo sapi	AC117465 Homo sapi
c1007	31.8	11.6	195519	10	AL672297	Mouse DNA	AL672297 Mouse DNA
c1008	31.8	11.6	198132	10	AC147246	Mus muscu	AC147246 Mus muscu
1009	31.8	11.6	199922	1	BSUB0016	Bacillus su	Z99119 Bacillus su
c1010	31.8	11.6	200329	10	AC078911	Mus muscu	AC078911 Mus muscu
c1011	31.8	11.6	203700	2	AC141140	Rattus no	AC141140 Rattus no
c1012	31.8	11.6	204720	2	BC537123	Danio rer	BC537123 Danio rer
c1013	31.8	11.6	207083	2	AC055797	Homo sapi	AC055797 Homo sapi
1014	31.8	11.6	208501	2	CR376783	Danio rer	CR376783 Danio rer
c1015	31.8	11.6	208614	10	AL807380	Mouse DNA	AL807380 Mouse DNA
c1016	31.8	11.6	219400	2	AC103300	Rattus no	AC103300 Rattus no
c1017	31.8	11.6	220060	1	AF008220	Bacillus	AF008220 Bacillus
1018	31.8	11.6	221471	2	AC122645	Rattus no	AC122645 Rattus no
1019	31.8	11.6	223501	2	AC116674	Mus muscu	AC116674 Mus muscu
1020	31.8	11.6	224321	2	AC073311	Homo sapi	AC073311 Homo sapi
1021	31.8	11.6	224468	2	AL596455	Mus muscu	AL596455 Mus muscu
1022	31.8	11.6	224645	2	AC094037	Rattus no	AC094037 Rattus no
1023	31.8	11.6	224645	2	AC134244	Mus muscu	AC134244 Mus muscu
c1024	31.8	11.6	226067	2	AC138358	Mus muscu	AC138358 Mus muscu
c1025	31.8	11.6	226685	5	BX072537	Zebrafish	BX072537 Zebrafish
c1026	31.8	11.6	228633	5	BX49600	Zebrafish	BX49600 Zebrafish
c1027	31.8	11.6	228730	2	AC096117	Rattus no	AC096117 Rattus no
c1028	31.8	11.6	229277	2	AC127672	Rattus no	AC127672 Rattus no
1029	31.8	11.6	230329	2	AC142070	Rattus no	AC142070 Rattus no
c1030	31.8	11.6	230669	2	AC101989	Mus muscu	AC101989 Mus muscu
c1031	31.8	11.6	232847	2	AC099614	Mus muscu	AC099614 Mus muscu
1032	31.8	11.6	233777	10	AC100043	Mus muscu	AC100043 Mus muscu
c1033	31.8	11.6	237108	2	AC127613	Rattus no	AC127613 Rattus no
1034	31.8	11.6	237293	2	AC105553	Rattus no	AC105553 Rattus no
c1035	31.8	11.6	238751	2	AC095116	Rattus no	AC095116 Rattus no
c1036	31.8	11.6	247007	2	AC113986	Mus muscu	AC113986 Mus muscu
c1037	31.8	11.6	248293	2	AC094985	Rattus no	AC094985 Rattus no
c1038	31.8	11.6	252370	2	AC098545	Rattus no	AC098545 Rattus no
1039	31.8	11.6	253621	2	AC105539	Rattus no	AC105539 Rattus no
1040	31.8	11.6	257094	2	AC113772	Rattus no	AC113772 Rattus no
1041	31.8	11.6	265402	2	AC149060	Mus muscu	AC149060 Mus muscu
1042	31.8	11.6	266775	2	AC129793	Rattus no	AC129793 Rattus no
c1043	31.8	11.6	275862	2	AC112376	Rattus no	AC112376 Rattus no
c1044	31.8	11.6	283873	2	AC097216	Rattus no	AC097216 Rattus no
c1045	31.8	11.6	339485	8	AF172282	Oryza sat	AF172282 Oryza sat
c1046	31.6	11.6	299	6	AR355053	Sequence	AR355053 Sequence
c1047	31.6	11.6	813	11	CNS06JPD4	U401438 T7 end of	U401438 T7 end of
c1048	31.6	11.6	1664	1	AF194946	Escherich	AF194946 Escherich
c1049	31.6	11.6	1665	1	AY250001	AY250001 Escherich	AY250001 Escherich
c1050	31.6	11.6	2526	5	XHCFYN	X54971 Xiphophorus	X54971 Xiphophorus
c1051	31.6	11.6	2951	8	ATU35049	U35049 Arabidopsis	U35049 Arabidopsis
c1052	31.6	11.6	5539	8	AX281516	Sequence	AX281516 Sequence
c1053	31.6	11.6	14307	6	AX345630	Sequence	AX345630 Sequence
c1054	31.6	11.6	29290	3	CEY60A9A	AX110495 Caenorhab	AX110495 Caenorhab
c1055	31.6	11.6	36148	3	AC116100	Dictyoste	AC116100 Dictyoste
c1056	31.6	11.6	54060	2	AC068819	Homo sapi	AC068819 Homo sapi
c1057	31.6	11.6	71287	2	AC014345	Drosophil	AC014345 Drosophil
c1058	31.6	11.6	95739	2	AP004644	Oryza sat	AP004644 Oryza sat
c1059	31.6	11.6	98398	2	AC149207	Medicago	AC149207 Medicago
c1060	31.6	11.6	101220	8	AC118284	AC118284 Oryza sat	AC118284 Oryza sat
c1061	31.6	11.6	106482	10	AC007585	Mus muscu	AC007585 Mus muscu
c1062	31.6	11.6	110000	2	AC102011	Mus muscu	AC102011 Mus muscu
c1063	31.6	11.6	110000	2	AC114905	Mus muscu	AC114905 Mus muscu
c1064	31.6	11.6	110297	9	AC008928	Homo sapi	AC008928 Homo sapi
c1065	31.6	11.6	114144	9	AL556240	Human DNA	AL556240 Human DNA
c1066	31.6	11.6	114787	10	AL646048	Mouse DNA	AL646048 Mouse DNA
c1067	31.6	11.6	117222	2	AC119167	Mus muscu	AC119167 Mus muscu
c1068	31.6	11.6	117487	2	AP002335	Homo sapi	AP002335 Homo sapi
c1069	31.6	11.6	124148	10	AC134433	Mus muscu	AC134433 Mus muscu
c1070	31.6	11.6	125893	8	AC124960	Medicago	AC124960 Medicago
c1071	31.6	11.6	126154	10	AL935159	Mouse DNA	AL935159 Mouse DNA
c1072	31.6	11.6	129921	8	AC146568	Medicago	AC146568 Medicago
c1073	31.6	11.6	130618	8	OSJN00103	Oryza sat	AL606655 Oryza sat
c1074	31.6	11.6	131286	4	AB053451	Sus scrof	AB053451 Sus scrof
c1075	31.6	11.6	131743	8	AB004561	Arabidops	AC004561 Arabidops
c1076	31.6	11.6	132490	10	AC116841	Mus muscu	AC116841 Mus muscu
c1077	31.6	11.6	134472	9	AC148717	Macaca mu	AC148717 Macaca mu
c1078	31.6	11.6	134714	10	AC119168	Mus muscu	AC119168 Mus muscu
c1079	31.6	11.6	134780	9	HS45F6	Human DNA	AL93168 Mus muscu
c1080	31.6	11.6	134837	5	BX510372	Zebrafish	BX510372 Zebrafish
c1081	31.6	11.6	137457	8	AP005687	Oryza sat	AP005687 Oryza sat
c1082	31.6	11.6	138489	2	AC010835	Homo sapi	AC010835 Homo sapi
c1083	31.6	11.6	138843	8	AP004657	Oryza sat	AP004657 Oryza sat
c1084	31.6	11.6	143498	9	AP0105391	Homo sapi	AP0105391 Homo sapi
c1085	31.6	11.6	143621	9	AP001883	Homo sapi	AP001883 Homo sapi
c1086	31.6	11.6	143786	3	AC024859	Caenorhab	AC024859 Caenorhab
c1087	31.6	11.6	144024	2	CR388171	Danio rer	CR388171 Danio rer
c1088	31.6	11.6	144131	10	AC110822	Mus muscu	AC110822 Mus muscu
c1089	31.6	11.6	145596	8	AP005876	Oryza sat	AP005876 Oryza sat
c1090	31.6	11.6	148120	9	AC090051	Homo sapi	AC090051 Homo sapi
c1091	31.6	11.6	148476	2	AC118826	Rattus no	AC118826 Rattus no
c1092	31.6	11.6	148883	2	AC147911	Xenopus t	AC147911 Xenopus t
c1093	31.6	11.6	151453	9	AC091888	Homo sapi	AC091888 Homo sapi
c1094	31.6	11.6	151694	10	AC119328	Mus muscu	AC119328 Mus muscu
c1095	31.6	11.6	154071	3	AC115598	Dictyoste	AC115598 Dictyoste
c1096	31.6	11.6	154753	2	AC020605	Homo sapi	AC020605 Homo sapi
c1097	31.6	11.6	155376	9	AC027026	Homo sapi	AC027026 Homo sapi
c1098	31.6	11.6	156186	2	AC036150	Homo sapi	AC036150 Homo sapi
c1099	31.6	11.6	156279	2	AC136205	Sus scrof	AC136205 Sus scrof
c1100	31.6	11.6	157099	9	AC002451	Homo sapi	AC002451 Homo sapi
c1101	31.6	11.6	159361	10	AC125130	Mus muscu	AC125130 Mus muscu
c1102	31.6	11.6	159579	2	AC120928	Rattus no	AC120928 Rattus no
c1103	31.6	11.6	160094	5	BX855617	Zebrafish	BX855617 Zebrafish
c1104	31.6	11.6	160615	10	AL672023	Mouse DNA	AL672023 Mouse DNA
c1105	31.6	11.6	160687	9	AC004957	Homo sapi	AC004957 Homo sapi
c1106	31.6	11.6	161671	2	AC018369	Homo sapi	AC018369 Homo sapi
c1107	31.6	11.6	161731	9	AC107021	Homo sapi	AC107021 Homo sapi
c1108	31.6	11.6	164470	9	AC012346	Homo sapi	AC012346 Homo sapi
c1109	31.6	11.6	164857	5	BX248312	Zebrafish	BX248312 Zebrafish
c1110	31.6	11.6	166009	10	AC123035	Mus muscu	AC123035 Mus muscu
c1111	31.6	11.6	166339	9	AC092673	Homo sapi	AC092673 Homo sapi
c1112	31.6	11.6	166928	2	AC110905	Mus muscu	AC110905 Mus muscu
c1113	31.6	11.6	167009	5	BX072530	Zebrafish	BX072530 Zebrafish
c1114	31.6	11.6	167727	9	AC016845	Homo sapi	AC016845 Homo sapi

1115	31.6	11.6	170264	5	BX120013	BX120013 Zebrafish	cl188	31.6	11.6	237228	2	AC136130	AC136130 Rattus no
1116	31.6	11.6	170447	2	AC120610	AC120610 Rattus no	cl189	31.6	11.6	239162	2	AC094172	AC094172 Rattus no
1117	31.6	11.6	172263	2	AC119280	AC119280 Mus muscu	cl190	31.6	11.6	241778	2	AC106151	AC106151 Rattus no
1118	31.6	11.6	173937	5	AL928976	AL928976 Zebrafish	1191	31.6	11.6	244341	2	AC108226	AC108226 Rattus no
1119	31.6	11.6	175570	10	AL844893	AL844893 Mouse DNA	1192	31.6	11.6	246177	10	AC132957	AC132957 Mus muscu
1120	31.6	11.6	176258	10	AC147624	AC147624 Mus muscu	1193	31.6	11.6	247655	10	AC145549	AC145549 Mus muscu
1121	31.6	11.6	176638	2	AC102137	AC102137 Mus muscu	cl194	31.6	11.6	249995	3	AE014840	AE014840 Plasmodi
1122	31.6	11.6	176876	10	AC147238	AC147238 Mus muscu	cl195	31.6	11.6	251207	2	AC106955	AC106955 Rattus no
1123	31.6	11.6	177658	5	AL935269	AL935269 Zebrafish	cl196	31.6	11.6	252830	2	AC095714	AC095714 Rattus no
1124	31.6	11.6	177771	2	AC140905	AC140905 Homo sapi	cl197	31.6	11.6	253559	2	AC133708	AC133708 Rattus no
1125	31.6	11.6	178787	2	AC120499	AC120499 Papio ham	cl198	31.6	11.6	253617	2	AC123084	AC123084 Rattus no
1126	31.6	11.6	179374	3	AC009357	AC009357 Drosophil	cl199	31.6	11.6	253617	2	AC123084	AC123084 Rattus no
1127	31.6	11.6	180578	5	AL929493	AL929493 Zebrafish	cl200	31.6	11.6	254538	2	AC097032	AC097032 Rattus no
1128	31.6	11.6	180760	2	AC110532	AC110532 Mus muscu	1201	31.6	11.6	255426	2	BX469922	BX469922 Danio rer
1129	31.6	11.6	181197	5	BX005330	BX005330 Zebrafish	1202	31.6	11.6	256556	10	AC118613	AC118613 Mus muscu
1130	31.6	11.6	181518	2	AC141952	AC141952 Rattus no	1203	31.6	11.6	259160	2	AC114105	AC114105 Rattus no
1131	31.6	11.6	181633	3	AC008224	AC008224 Drosophil	1204	31.6	11.6	260636	2	AC121316	AC121316 Mus muscu
1132	31.6	11.6	181644	2	AC021202	AC021202 Homo sapi	1205	31.6	11.6	262268	2	AC126487	AC126487 Rattus no
1133	31.6	11.6	181731	9	AC090822	AC090822 Homo sapi	1206	31.6	11.6	262768	2	AC129379	AC129379 Rattus no
1134	31.6	11.6	181994	2	AC090822	AC090822 Homo sapi	1207	31.6	11.6	270264	2	AC103092	AC103092 Rattus no
1135	31.6	11.6	182261	2	AC115833	AC115833 Mus muscu	1208	31.6	11.6	271932	2	AC109948	AC109948 Rattus no
1136	31.6	11.6	182269	5	BX005483	BX005483 Zebrafish	1209	31.6	11.6	280176	2	AC095749	AC095749 Rattus no
1137	31.6	11.6	182479	2	AC141330	AC141330 Rattus no	1210	31.6	11.6	284640	2	AC103941	AC103941 Rattus no
1138	31.6	11.6	183082	2	AC090902	AC090902 Homo sapi	1211	31.6	11.6	298960	2	AC113105	AC113105 Mus muscu
1139	31.6	11.6	183298	5	BX469899	BX469899 Zebrafish	1212	31.6	11.6	298960	2	AC006896	AC006896 Caenorhab
1140	31.6	11.6	184184	5	AC016583	AC016583 Homo sapi	1213	31.6	11.6	305166	3	AE003601	AE003601 Drosophil
1141	31.6	11.6	184769	9	AC016583	AC016583 Homo sapi	1214	31.6	11.6	320168	2	AC133987	AC133987 Rattus no
1142	31.6	11.6	184925	2	AC027608	AC027608 Homo sapi	1215	31.6	11.6	342544	2	AC120678	AC120678 Rattus no
1143	31.6	11.6	185260	1	AC149084	AC149084 Homo sapi	1216	31.4	11.5	402	8	AB025777	AB025777 Eupenicil
1144	31.6	11.6	187401	8	AP005249	AP005249 Oryza sat	1217	31.4	11.5	844	11	BV061494	BV061494 S212P6641
1145	31.6	11.6	189178	10	AC130138	AC130138 Rattus no	1218	31.4	11.5	1318	9	AB03277503	AB03277503 Homo sapi
1146	31.6	11.6	189231	9	AC090138	AC090138 Homo sapi	1219	31.4	11.5	4978	10	BC061469	BC061469 Mus muscu
1147	31.6	11.6	192807	2	AC112073	AC112073 Rattus no	1220	31.4	11.5	6156	6	AX281194	AX281194 Sequence
1148	31.6	11.6	193914	10	AL645664	AL645664 Mouse DNA	1221	31.4	11.5	6156	6	AX356463	AX356463 Sequence
1149	31.6	11.6	194766	2	CR339055	CR339055 Danio rer	1222	31.4	11.5	8387	5	AF349437	AF349437 Danio rer
1150	31.6	11.6	194810	10	AC139318	AC139318 Mus muscu	1223	31.4	11.5	28000	8	SPBC13G1	SPBC13G1 Homo sapi
1151	31.6	11.6	196786	2	AC102636	AC102636 Mus muscu	1224	31.4	11.5	48645	9	AC005575	AC005575 Homo sapi
1152	31.6	11.6	197803	10	AC129541	AC129541 Mus muscu	1225	31.4	11.5	68862	2	AC101828	AC101828 Mus muscu
1153	31.6	11.6	198116	2	AC147351	AC147351 Xenopus t	1226	31.4	11.5	69518	9	AL359263	AL359263 Human DNA
1154	31.6	11.6	198383	10	AC132435	AC132435 Mus muscu	1227	31.4	11.5	73572	2	AC022928	AC022928 Homo sapi
1155	31.6	11.6	198489	5	AC100820	AC100820 Homo sapi	1228	31.4	11.5	78121	8	AT141722	AT141722 Apis mell
1156	31.6	11.6	199148	5	AC145945	AC145945 Gallus ga	1229	31.4	11.5	82316	8	ATT232K7	ATT232K7 Arabidops
1157	31.6	11.6	200617	5	BX569783	BX569783 Zebrafish	1230	31.4	11.5	95385	8	AC146650	AC146650 Medicago
1158	31.6	11.6	200790	10	AC100511	AC100511 Mus muscu	1231	31.4	11.5	95597	9	AC012555	AC012555 Homo sapi
1159	31.6	11.6	200823	2	AC009652	AC009652 Homo sapi	1232	31.4	11.5	95643	8	ATT6K21	ATT6K21 Arabidops
1160	31.6	11.6	201000	9	AC105150	AC105150 Homo sapi	1233	31.4	11.5	100326	10	AL669928	AL669928 Mouse DNA
1161	31.6	11.6	201018	2	CR388072	CR388072 Danio rer	1234	31.4	11.5	107027	8	ATF14L2	ATF14L2 Arabidops
1162	31.6	11.6	201174	10	AC113953	AC113953 Mus muscu	1235	31.4	11.5	109598	2	AC010461	AC010461 Homo sapi
1163	31.6	11.6	201700	2	AC110577	AC110577 Mus muscu	1236	31.4	11.5	110000	2	AC098262	AC098262 Rattus no
1164	31.6	11.6	201973	2	AC017049	AC017049 Homo sapi	1237	31.4	11.5	110000	2	AC099158-2	AC099158-2 Continuation (3 of
1165	31.6	11.6	201981	2	AC073640	AC073640 Homo sapi	1238	31.4	11.5	110000	3	AC148656-0	AC148656-0 Mus muscu
1166	31.6	11.6	202788	2	AC136457	AC136457 Mus muscu	1239	31.4	11.5	111620	10	AL671892	AL671892 Mouse DNA
1167	31.6	11.6	202997	2	AC137426	AC137426 Rattus no	1240	31.4	11.5	111620	9	AC005162	AC005162 Homo sapi
1168	31.6	11.6	203542	2	AC116273	AC116273 Rattus no	1241	31.4	11.5	116793	10	AC079990	AC079990 Rattus no
1169	31.6	11.6	203542	2	AC113586	AC113586 Mus muscu	1242	31.4	11.5	116800	9	AL391379	AL391379 Human DNA
1170	31.6	11.6	204291	10	AC090654	AC090654 Mus muscu	1243	31.4	11.5	120337	9	AL353717	AL353717 Human DNA
1171	31.6	11.6	204591	2	AC127404	AC127404 Rattus no	1244	31.4	11.5	120337	9	AC109443	AC109443 Homo sapi
1172	31.6	11.6	207555	2	AC118714	AC118714 Mus muscu	1245	31.4	11.5	124067	9	AP000435	AP000435 Homo sapi
1173	31.6	11.6	210089	10	AC139571	AC139571 Mus muscu	1246	31.4	11.5	126154	10	AL935159	AL935159 Mouse DNA
1174	31.6	11.6	211375	2	AC141149	AC141149 Rattus no	1247	31.4	11.5	127436	9	AC104459	AC104459 Homo sapi
1175	31.6	11.6	211487	2	AC147336	AC147336 Xenopus t	1248	31.4	11.5	129219	2	AC149731	AC149731 Bos tauru
1176	31.6	11.6	213606	2	AC023811	AC023811 Mus muscu	1249	31.4	11.5	133579	9	AL590244	AL590244 Human DNA
1177	31.6	11.6	214470	2	AC092252	AC092252 Mus muscu	1250	31.4	11.5	133579	9	AC137823	AC137823 Medicago
1178	31.6	11.6	216589	2	AC102572	AC102572 Mus muscu	1251	31.4	11.5	134391	2	AC141038	AC141038 Rattus no
1179	31.6	11.6	217477	2	AC032070	AC032070 Mus muscu	1252	31.4	11.5	137490	9	AC105273	AC105273 Homo sapi
1180	31.6	11.6	221533	2	BX890567	BX890567 Danio rer	1253	31.4	11.5	138485	2	AC124406	AC124406 Mus muscu
1181	31.6	11.6	221951	10	AC122857	AC122857 Mus muscu	1254	31.4	11.5	139401	2	AC132837	AC132837 Homo sapi
1182	31.6	11.6	222571	2	AC110338	AC110338 Rattus no	1255	31.4	11.5	139670	2	AC022650	AC022650 Homo sapi
1183	31.6	11.6	222692	2	AC126962	AC126962 Rattus no	1256	31.4	11.5	139973	2	AC126788	AC126788 Medicago
1184	31.6	11.6	222955	2	AC129430	AC129430 Rattus no	1257	31.4	11.5	141589	2	AC146829	AC146829 Carollia
1185	31.6	11.6	223932	2	AC134196	AC134196 Rattus no	1258	31.4	11.5	147557	2	AC079103	AC079103 Homo sapi
1186	31.6	11.6	225868	2	AC134766	AC134766 Rattus no	1259	31.4	11.5	149880	2	AL672300	AL672300 Mouse DNA
1187	31.6	11.6	227631	2	AC115692	AC115692 Mus muscu	1260	31.4	11.5	149991	10		
			234843	2	AC106580	AC106580 Rattus no							

c1261	31.4	11.5	150634	2	AC113371	AC113371 Homo sapi	c1334	31.4	11.5	216208	5	BX248122	Zebrafish
1262	31.4	11.5	151889	9	AC084250	AC084250 Homo sapi	c1335	31.4	11.5	217446	2	AC117665	Mus muscu
c1263	31.4	11.5	151959	2	AC021689	AC021689 Homo sapi	c1336	31.4	11.5	220618	2	AC131892	Atelerix
1264	31.4	11.5	155254	2	AC129952	AC129952 Mus muscu	1337	31.4	11.5	221951	10	AC122857	Mus muscu
1265	31.4	11.5	155300	2	AL929459	AL929459 Danio rer	c1338	31.4	11.5	228285	2	CR391925	Danio rer
1266	31.4	11.5	160327	4	AC149763	AC149763 Bos tauru	c1339	31.4	11.5	230018	2	AC106538	Rattus no
c1267	31.4	11.5	161920	9	AC025169	AC025169 Homo sapi	1340	31.4	11.5	231367	2	AC150501	Bos tauru
1268	31.4	11.5	161956	2	AC147019	AC147019 Pan trogl	c1341	31.4	11.5	231759	2	AC120707	Rattus no
c1269	31.4	11.5	162063	9	AC015553	AC015553 Homo sapi	1342	31.4	11.5	232195	2	AC106493	Zebrafish
1270	31.4	11.5	164473	9	AC109471	AC109471 Homo sapi	c1343	31.4	11.5	232304	5	BX322616	Zebrafish
1271	31.4	11.5	164953	9	AC016252	AC016252 Homo sapi	1344	31.4	11.5	234405	2	AC095507	Rattus no
1272	31.4	11.5	165021	2	AC026490	AC026490 Homo sapi	c1345	31.4	11.5	235666	2	AC094427	Rattus no
1273	31.4	11.5	165047	9	AC079835	AC079835 Homo sapi	c1346	31.4	11.5	236566	2	AC097686	Rattus no
1274	31.4	11.5	165295	2	AC068486	AC068486 Homo sapi	1347	31.4	11.5	237739	2	AC134520	Atelerix
1275	31.4	11.5	165928	2	AC150538	AC150538 Bos tauru	1348	31.4	11.5	241200	2	CR450844	Danio rer
c1276	31.4	11.5	166486	9	CNS01DWC	AL317100 Human chr	c1349	31.4	11.5	242642	2	AC115480	Rattus no
c1277	31.4	11.5	170186	2	AC027236	AC027236 Homo sapi	c1350	31.4	11.5	243674	2	AC098477	Rattus no
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ALIGNMENTS

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ACCESSION AR252626
VERSION AR252626.1 GI:27300534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 713)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 376 12-NOV-2002;
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ACCESSION AX055452
VERSION AX055452.1 GI:12228719
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 82 07-DEC-2000;
Genentech, Inc. (US)
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DEFINITION Sequence 473 from Patent WO0140466.
ACCESSION AX464340
VERSION AX464340.1 GI:21899186
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;
Genentech Inc. (US)
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ACCESSION AX403489
VERSION AX403489.1 GI:21436980
KEYWORDS
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrata,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0073454-A 376 07-DEC-2000;
Genentech Inc. (US)
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RESULT 4
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DEFINITION Sequence 473 from Patent WO0140466.
ACCESSION AX464340
VERSION AX464340.1 GI:21899186
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;
Genentech Inc. (US)
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 DEFINITION Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.
 ACCESSION AY358685
 VERSION AY358685.1 GI:37182491
 KEYWORDS FLJ_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 713)
 AUTHORS Clark H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,
 Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simons, L., Singh, J., Smith, V.,
 Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wilead, D., Woods, K.,
 Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
 Goddard, A., Wood, W.I. and Godowski, P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 713)
 AUTHORS Clark, H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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 Query Match 100.0%; Score 273; DB 9; Length 713;
 Best Local Similarity 100.0%; Pred. No. 2.6e-65;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGACATTTTCTGTCACATTTATTATTGTTGGTATGTAAGCTATTTGGAGATCAAT 60
 Db 92 ATGACATTTTCTGTCACATTTATTATTGTTGGTATGTAAGCTATTTGGAGATCAAT 151
 QY 61 TCAGGAGCAACACATTCGAGATGGCTACTTCTATCAAGAAATAAGAGACCCACAGT 120
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 Db 272 GGCAAGGGCATAGTTAAAGGACGGGAATCTTGACTCAAGAGGGTTAATTTCTTGGTGTGAA 331
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 Db 332 GCCTGGGCGAGGGGTGTTAAAGAAAACACTTAG 364

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 DEFINITION Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute
 Human BAC Library) complete sequence.
 ACCESSION AC024224
 VERSION AC024224.33 GI:21240476
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 165414)
 AUTHORS Murny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
 Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
 Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.P., Carter, M., Cavaros, S.R., Chacko, J., Chavez, D.,
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 Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S.,
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 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwundu, G.,
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 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I.,
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansy, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Umani, K., Vazquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczky, R., Woodden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R.,
 Weinstein, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 165414)
 Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One


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Db 117328 ATGACATTTTCTGTCACATATTATTATTTCTGGTATGTCAGCTATTTCGAGATCCAA 117269
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RESULT 7
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DEFINITION
Homo sapiens clone RP11-13C13, RP11-656E20, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
AC006510 AC006514
AC006510.8 GI:10122018
HTG: HTGS_PHASE1.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 240864)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,P.R., Allen,C.,
Alsbrooks,S.L., Amaraturge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
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Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Washington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
and Gibbs,R.
Direct Submission
TITLE
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Unpublished
2. (bases 1 to 240864)
Worley,K.C.
Direct Submission
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2000 this sequence version replaced gi:10086352.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: J-33
Center clone name: RP11-13C13, RP11-656E20
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 77% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71594 bases at least Q40
Consensus quality: 93014 bases at least Q30
Consensus quality: 110702 bases at least Q20
Estimated insert size: 229041; sum-of-contigs estimation
Estimated insert size: 331000; agarose-fp estimation
Quality coverage: 0.8x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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* 134783 134882: gap of unknown length
* 134883 163654: contig of 28772 bp in length
* 163655 163754: gap of unknown length
* 163755 185050: contig of 21296 bp in length
* 185051 194802: gap of unknown length
* 194803 194902: gap of unknown length
* 194903 202527: contig of 7625 bp in length
* 202528 202627: gap of unknown length
* 202628 208658: contig of 6031 bp in length
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* 221786 221885: gap of unknown length
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RESULT 10
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DEFINITION Novel membrane protein and DNA thereof.
ACCESSION E21012
VERSION E21012.1 GI:13023572
KEYWORDS JP 1999001497-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 741)
AUTHORS Shuji,H., Shoji,F., Kazunori,N. and Yasushi,A.
TITLE Novel membrane protein and DNA thereof
JOURNAL Patent: JP 1999001497-A 2 06-JAN-1999;
TAKEDA CHEM IND LTD
OS Unidentified
PN JP 1999001497-A/2
PD 06-JAN-1999
PF 13-JUN-1997 JP 1997156376
PR
PI SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, YASUSHI ARAHA PC
C07K14/47,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00, PC
A61K39/395,
PC A61K48/00,C07K16/28,C12N1/21,C12N15/09,C12P21/02,C12Q1/68, PC
G01N33/53//
PC (C12N1/21,C12R1:19),(C12N15/09,C12R1:91),A61K37/02,A61K37/02,
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Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCTATTGGAGATCCCAATTCAGGAGCAACACATTTGGAGATGGCTACTTTCTATCAAGA 102
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DEFINITION Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete cds, alternatively spliced.
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AF400595
VERSION AF400595.1 GI:15986699
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
MEDLINE 21570237
PubMed 11567029
REFERENCE 2 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
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ORIGIN
Query Match 51.3%; Score 140; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCTATTGGAGATCCCAATTCAGGAGCAACACATTTGGAGATGGCTACTTTCTATCAAGA 102
Db 202 GCTATTGGAGATCCCAATTCAGGAGCAACACATTTGGAGATGGCTACTTTCTATCAAGA 261
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RESULT 12
AY026769
LOCUS AY026769 744 bp mRNA linear PRI 05-OCT-2001
DEFINITION Homo sapiens lectin-like receptor 1 (DECTIN1) mRNA, complete cds.
ACCESSION AY026769
VERSION AY026769.2 GI:15967096
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
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AUTHORS Hermanz-Falcon, P., Arce, I., Roda-Navarro, P. and Fernandez-Ruiz, E.
 TITLE Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene expressed on dendritic cells
 JOURNAL Immunogenetics 53 (4), 288-295 (2001)
 MEDLINE 21383615
 PUBMED 11491532
 REFERENCE 2 (bases 1 to 744)
 AUTHORS Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.
 TITLE Direct Submission
 JOURNAL Submitted (01-FEB-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain
 REFERENCE 3 (bases 1 to 744)
 AUTHORS Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain
 REMARK Sequence update by submitter
 COMMENT On Oct 5, 2001 this sequence version replaced gi:14278818.
 FEATURES
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QY 163 AAAGCTGTCAAAACACACAGG 182
 Db 322 AAAGCTGTCAAAACACACAGG 341

RESULT 13
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 DEFINITION
 AF400601
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 787)
 Willmet, J.A., Gordon, S. and Brown, G.D.
 AUTHORS Characterization of the human beta -glucan receptor and its
 TITLE alternatively spliced isoforms

JOURNAL Chem. 276 (47), 43818-43823 (2001)
 MEDLINE 21570237
 PUBMED 11567029
 REFERENCE 2 (bases 1 to 787)
 AUTHORS Willmet, J.A., Gordon, S. and Brown, G.D.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology, Oxford University, South Parks Road, Oxford OX1 3RE, UK
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QY 43 GCTATTGGAGATCCAAATTCAGAGCAACACATTGGAGATGGCTACTTCTATCAAGA 102
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QY 163 AAAGCTGTCAAAACACACAGG 182
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RESULT 14
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 DEFINITION
 BD136999
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1018)
 Chalus, L., Quan, A., Bates, E.E.M., Gorman, D.M., Saeland, S.,
 Lebecque, S.J.E. and Jr, J.H.P.
 TITLE Isolated mammalian membrane protein gene and reagent relating
 JOURNAL Patent: JP 2002506645-A 3 05-MAR-2002;
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002506645-A/3
 PD 05-MAR-2002
 PF 16-MAR-1999 JP 2000536856
 PR 17-MAR-1998 US 09/040111
 PI LIONEL CHALUS, AHN QUAN, ELIZABETH ESTHER MARY BATES, DANIEL M
 PI GORMAN,
 PI SEM SAELEND, SERGE J E LEBECQUE, JOSEPH H PHILIPPS JR PC

C12N15/09,A61K31/70,A61K38/00,A61K39/395,A61K39/395,A61P35/00, PC
A61P37/02,
PC A61P43/00,C07K14/705,C07K16/28,C12N1/19,C12N1/21,C12N5/10, PC
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PC G01N33/68,C12N15/00,A61K37/02,C12N5/00
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RESULT 15
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DEFINITION Sequence 7 from Patent WO02077216.
ACCESSION AX664609
VERSION AX664609.1 GI:29164442
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
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AUTHORS de Martin,R., Hofer,E., Hofer-Warbinek,R., Kalthoff,F.S.,
Lipp,H.J., Mechtcheriakova,D., Schmid,J. and Sobanov,Y.
TITLE Ikk2 variant, dino gene, lectin-like receptor gene, and proteins
encoded thereby
JOURNAL Patent: WO 02077216-A 7 03-OCT-2002;
Novartis AG (CH); Novartis Erfindungen Verwaltungsgesellschaft
M.B.H. (AT)

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417 AATAAGAGAACACAGTCAACCCACACATCATCTTTTAGAAGACAGTGTGACTCCTACC 476
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Searched: 32822875 seqs, 18219865908 residues

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Minimum DB seq length: 0
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Listing first 1500 summaries

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8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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C 2	177.2	64.9	800 6 CB958894 AGENCOURT
C 3	138.4	50.7	659 4 B1018962 IL3-MT026
C 4	120.6	44.2	663 8 AZ121459 RPCI-23-3
C 5	120	44.0	673 1 AV721179 AV721179
C 6	104.8	38.4	582 6 CB420818 CB420818
C 7	73.8	27.0	855 4 B1107684 602891529
C 8	49.6	18.2	363 5 BY547544 BY547544
C 9	49.6	18.2	419 5 BY536666 BY536666
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C 13	39.2	14.4	602 1 AV996730 AV996730
C 14	39.2	14.4	703 5 BW404792 BW404792
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C 19	38	13.9	506 6 CB982629 CB982629
C 20	37.8	13.8	599 9 BX170171 Danio rer
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254	33.6	12.3	856	3	AK009298	AK009298 Mus_musc	327	33	12.1	571	9	CR328964	CR328964 Medicago
255	33.6	12.3	1057	3	BE299581	BE299581 600944106	328	33	12.1	573	6	CB101958	CB101958 kl75f12.y
256	33.6	12.3	1312	2	BG853945	BG853945 1024038E1	329	33	12.1	586	5	BW225512	BW225512 BW225512
257	33.6	12.3	1719	4	BG892618	BG892618 fq77b07.x	330	33	12.1	633	9	CG028766	CG028766 CHGAL95TF
258	33.4	12.2	290	4	BI318003	BI318003 fq73e01.x	331	33	12.1	643	9	CE212119	CE212119 tigr-gss-
259	33.4	12.2	290	4	BI318003	BI318003 fq73e01.x	332	33	12.1	646	5	BW091360	BW091360 BW091360
260	33.4	12.2	412	4	BI021259	BI021259 IL3-MT026	333	33	12.1	664	1	AV682787	AV682787 AV682787
261	33.4	12.2	448	4	BI707671	BI707671 fs36b06.x	334	33	12.1	717	7	CK476693	CK476693 AGENCOURT
262	33.4	12.2	448	4	BI708124	BI708124 fs42d03.x	335	33	12.1	755	5	BW094641	BW094641 BW094641
263	33.4	12.2	448	4	BI843541	BI843541 ft91a02.x	336	33	12.1	769	5	BW396094	BW396094 BW396094
264	33.4	12.2	448	4	BM081763	BM081763 fu94d02.x	337	33	12.1	771	5	BW146633	BW146633 BW146633
265	33.4	12.2	450	4	BI472675	BI472675 fs03b07.x	338	33	12.1	774	5	BW020922	BW020922 BW020922
266	33.4	12.2	462	6	CB319486	CB319486 AGENCOURT	339	33	12.1	791	1	AU139683	AU139683 AU139683
267	33.4	12.2	534	1	AJ790888	AJ790888 AJ790888	340	33	12.1	800	5	BW120032	BW120032 BW120032
268	33.4	12.2	542	8	BZ899565	BZ899565 CH240_16G	341	33	12.1	849	7	CK474760	CK474760 AGENCOURT
269	33.4	12.2	542	8	CF366273	CF366273 836974 MA	342	33	12.1	855	9	CR011771	CR011771 Forward s
270	33.4	12.2	653	7	CF366273	CF366273 836974 MA	343	33	12.1	873	9	CG943528	CG943528 MBEJTP46TF
271	33.4	12.2	736	9	BX228482	BX228482 Danilo rer	344	33	12.1	885	2	BF267595	BF267595 HV_Cea001
272	33.4	12.2	747	9	CL419625	CL419625 ZMMBBb043	345	33	12.1	885	8	BH134055	BH134055 ENTNA26TF
273	33.4	12.2	869	8	B2131232	B2131232 CH230-298	346	33	12.1	957	9	CNS04EGB	CNS04EGB Tetraodon
274	33.4	12.2	1067	9	AG029559	AG029559 Pan trogl	347	33	12.1	1101	9	CNS00B01	CNS00B01 Drosophila
275	33.2	12.2	236	4	BM574306	BM574306 fx84g01.y	348	33	12.1	2369	7	CR087716	CR087716 EC2BBA29A
276	33.2	12.2	374	5	AW403597	AW403597 BY403597	349	32.8	12.0	215	7	CNS00B01	CNS00B01 Mus muscu
277	33.2	12.2	449	2	AW145257	AW145257 ga31a10.y	350	32.8	12.0	336	9	CR087716	CR087716 EC2BBA29A
278	33.2	12.2	463	6	CD083579	CD083579 MA3-9999U	351	32.8	12.0	336	9	CR087716	CR087716 EC2BBA29A
279	33.2	12.2	532	6	CD083579	CD083579 MA3-9999U	352	32.8	12.0	341	2	AW205495	AW205495 UI-H-B12-
280	33.2	12.2	545	1	AV777351	AV777351 AV777351	353	32.8	12.0	341	2	AW205495	AW205495 UI-H-B12-
281	33.2	12.2	560	6	CA969192	CA969192 CcLX06a21	354	32.8	12.0	368	1	AA465529	AA465529 aa3c11.s
282	33.2	12.2	581	7	BN812950	BN812950 F906_0110	355	32.8	12.0	375	8	AQ632517	AQ632517 ROCI-11-4
283	33.2	12.2	587	2	AW561425	AW561425 ga80b12.y	356	32.8	12.0	384	8	B2514028	B2514028 BOMON56TF
284	33.2	12.2	621	9	CG794141	CG794141 AMGNNUC.y	357	32.8	12.0	393	1	AA827853	AA827853 od56e01.s
285	33.2	12.2	661	4	BJ164622	BJ164622 ZMMBBb031	358	32.8	12.0	398	1	AA737447	AA737447 oa49a06.s
286	33.2	12.2	730	7	CF348020	CF348020 AGENCOURT	359	32.8	12.0	418	7	Z699975	Z699975 AGESTSE2 A
287	33.2	12.2	739	9	CF348020	CF348020 AGENCOURT	360	32.8	12.0	429	9	CR493520	CR493520 Medicago
288	33.2	12.2	743	9	BX154154	BX154154 Danilo rer	361	32.8	12.0	449	2	BE671691	BE671691 7b60e10.x
289	33.2	12.2	752	7	CO808571	CO808571 AGENCOURT	362	32.8	12.0	479	8	AQ542164	AQ542164 ROCI-11-3
290	33.2	12.2	755	7	CF996512	CF996512 AGENCOURT	363	32.8	12.0	480	6	CD296558	CD296558 StrPu691.
291	33.2	12.2	771	7	CF996512	CF996512 AGENCOURT	364	32.8	12.0	485	2	BF446067	BF446067 hn72b04.x
292	33.2	12.2	776	7	CK029628	CK029628 AGENCOURT	365	32.8	12.0	514	2	BF446067	BF446067 hn72b04.x
293	33.2	12.2	777	9	BX190852	BX190852 Danilo rer	366	32.8	12.0	540	8	AZ034797	AZ034797 ROCI-23-3
294	33.2	12.2	780	7	CK029053	CK029053 AGENCOURT	367	32.8	12.0	603	5	BP771182	BP771182 BP771182
295	33.2	12.2	781	7	CK029053	CK029053 AGENCOURT	368	32.8	12.0	606	8	BH673639	BH673639 BOMOC91TF
296	33.2	12.2	788	7	CK028648	CK028648 AGENCOURT	369	32.8	12.0	610	9	CR483849	CR483849 Medicago
297	33.2	12.2	793	7	CK143019	CK143019 AGENCOURT	370	32.8	12.0	619	9	CC954543	CC954543 BOIFG30TF
298	33.2	12.2	794	7	CK143019	CK143019 AGENCOURT	371	32.8	12.0	632	9	CR479082	CR479082 Medicago
299	33.2	12.2	797	7	CK138880	CK138880 AGENCOURT	372	32.8	12.0	639	8	BH504987	BH504987 BOHBO44TF
300	33.2	12.2	798	7	CK138880	CK138880 AGENCOURT	373	32.8	12.0	640	8	BH580915	BH580915 BOGPA34TF
301	33.2	12.2	804	5	BW750202	BW750202 CH3#031.F	374	32.8	12.0	653	2	AW514783	AW514783 xu81g11.x
302	33.2	12.2	805	7	CK052438	CK052438 AGENCOURT	375	32.8	12.0	661	8	BZ502930	BZ502930 BONBW19TF
303	33.2	12.2	811	7	CK126517	CK126517 AGENCOURT	376	32.8	12.0	667	8	AG165116	AG165116 Pan trogl
304	33.2	12.2	818	6	CA473875	CA473875 AGENCOURT	377	32.8	12.0	689	8	AZ604530	AZ604530 IM0425K20
305	33.2	12.2	842	8	AZ204600	AZ204600 SP_0100.A	378	32.8	12.0	700	8	BH953056	BH953056 odh2Ba09.
306	33.2	12.2	848	8	BH136200	BH136200 ENTK89TR	379	32.8	12.0	701	5	BX310065	BX310065 odh2Ba09.
307	33.2	12.2	856	8	BH136200	BH136200 ENTK89TR	380	32.8	12.0	701	5	BX310065	BX310065 odh2Ba09.
308	33.2	12.2	858	9	CR001848	CR001848 Reverse s	381	32.8	12.0	702	9	BX125178	BX125178 Danilo rer
309	33.2	12.2	867	9	CL494991	CL494991 SAIL_603	382	32.8	12.0	714	9	CG923120	CG923120 BOND91TF
310	33.2	12.2	873	9	CL494991	CL494991 SAIL_603	383	32.8	12.0	714	9	CG923120	CG923120 BOND91TF
311	33.2	12.2	882	7	CNS19542	CNS19542 AGENCOURT	384	32.8	12.0	742	8	BZ059671	BZ059671 l1e5c12.
312	33.2	12.2	889	7	CNS19330	CNS19330 AGENCOURT	385	32.8	12.0	745	5	BX706222	BX706222 BX706222
313	33.2	12.2	913	6	CF265421	CF265421 AGENCOURT	386	32.8	12.0	746	8	BZ478982	BZ478982 BOND91TF
314	33.2	12.2	922	7	CNS021553	CNS021553 AGENCOURT	387	32.8	12.0	759	9	CG965617	CG965617 BOICH96TF
315	33.2	12.2	941	9	CL473821	CL473821 SAIL_207	388	32.8	12.0	774	9	CC947023	CC947023 BOGPE27TF
316	33.2	12.2	961	9	CNS06E0W	CL394518 T7 end of	389	32.8	12.0	779	8	BH531124	BH531124 BOHPQ77TF

390	32.8	12.0	788	8	BH691536	BH691536 BOMPR33TR	C 463	32.2	11.8	456	7	H47818	H47818 YP76a12.r1
391	32.8	12.0	789	8	BZ480692	BZ480692 BOOAP11TF	464	32.2	11.8	486	6	BY787899	BY787899 BY787899
392	32.8	12.0	832	9	CR248652	CR248652 Reverse s	C 465	32.2	11.8	502	4	BG405295	BG405295 sac50f03.
393	32.8	12.0	839	8	BZ467378	BZ467378 BONQT82TR	466	32.2	11.8	527	9	CE213588	CE213588 tigr-gss-
394	32.8	12.0	846	7	CR567520	CR567520 CRBENJ32TR	C 467	32.2	11.8	587	8	AZ286405	AZ286405 RPCI-23-1
395	32.8	12.0	853	9	CG950485	CG950485 MBENJ13TR	468	32.2	11.8	611	8	BH816757	BH816757 AM_Ba002
396	32.8	12.0	862	8	BH656093	BH656093 BOMCP71TF	469	32.2	11.8	632	9	EX139349	EX139349 Danilo rer
397	32.8	12.0	865	9	CNS03JTC	AL247305 Tetraodon	C 470	32.2	11.8	662	8	AZ497096	AZ497096 IM03331L13
398	32.8	12.0	993	6	BH701936	BH701936 BOMTY40TR	471	32.2	11.8	681	5	BQ406241	BQ406241 UI-H-FL0-
400	32.8	12.0	1116	6	CD386521	CD386521 AGENCOURT	472	32.2	11.8	690	2	BE054270	BE054270 GA_Ea009
401	32.6	11.9	5537	1	BH771020	BH771020 LLMGT874	473	32.2	11.8	704	4	BJ378703	BJ378703 BJ378703
402	32.6	11.9	332	1	AA253529	AA253529 zs13d10.s	474	32.2	11.8	706	8	BH558901	BH558901 BOGDC37TF
403	32.6	11.9	332	9	CG966605	CG966605 ZMMBB038	475	32.2	11.8	754	5	EX870491	EX870491 AGNCOURT
404	32.6	11.9	361	5	BQ125486	BQ125486 rce68h08.Y	C 476	32.2	11.8	769	5	BX764960	BX764960 BX764960
405	32.6	11.9	376	5	BQ473106	BQ473106 rce68h08.Y	C 477	32.2	11.8	771	5	BX764960	BX764960 BX764960
406	32.6	11.9	381	6	AQ868747	AQ868747 nbeab0031C	C 478	32.2	11.8	771	5	BX764960	BX764960 BX764960
407	32.6	11.9	391	6	CA855583	CA855583 Ffstaoas	C 479	32.2	11.8	771	5	BX764960	BX764960 BX764960
408	32.6	11.9	395	6	CD178507	CD178507 MSI-0014P	C 480	32.2	11.8	771	5	BX764960	BX764960 BX764960
409	32.6	11.9	439	4	BH677223	BH677223 RPCI-24-3	C 481	32.2	11.8	796	5	BX764960	BX764960 BX764960
410	32.6	11.9	524	2	BH766927	BH766927 BH766927	C 482	32.2	11.8	806	5	BX877562	BX877562 BX877562
411	32.6	11.9	538	5	BP426416	BP426416 BP426416	483	32.2	11.8	832	8	BZ165561	BZ165561 CH230-258
412	32.6	11.9	548	5	BQ792164	BQ792164 EST 8619	484	32.2	11.8	840	4	BG446861	BG446861 GA_EB003
413	32.6	11.9	549	5	BH767607	BH767607 STEATH11	485	32.2	11.8	840	9	CC578373	CC578373 CH240 457
414	32.6	11.9	573	2	AW330139	AW330139 TENUA485	C 486	32.2	11.8	871	8	BZ076507	BZ076507 lke16f03.
415	32.6	11.9	580	8	CC065459	CC065459 fgm004f0	487	32.2	11.8	898	7	CF578565	CF578565 AGENCOURT
416	32.6	11.9	625	1	AV700567	AV700567 AV700567	C 488	32.2	11.8	900	2	BF277928	BF277928 GA_EB003
417	32.6	11.9	642	2	BB240810	BB240810 Mus muscu	489	32.2	11.8	1004	9	CL070521	CL070521 CH216-119
418	32.6	11.9	707	9	AG330302	AG330302 Mus muscu	C 490	32.2	11.7	190	4	BG142659	BG142659 iab7g09.Y
419	32.6	11.9	750	8	BH199538	BH199538 Sml-61N22	C 491	32.2	11.7	262	9	BX287317	BX287317 Arabidops
420	32.6	11.9	762	7	CR447767	CR447767 CR447767	C 492	32.2	11.7	308	2	BB090056	BB090056 BB090056
421	32.6	11.9	764	9	BH201462	BH201462 Sml-48H24	C 493	32.2	11.7	312	4	BI790885	BI790885 iab02802.X
422	32.6	11.9	774	9	AG484781	AG484781 Mus muscu	494	32.2	11.7	326	2	BF766730	BF766730 RC5-CS002
423	32.6	11.9	828	9	EX160135	EX160135 Danilo rer	C 495	32.2	11.7	360	1	AA798747	AA798747 VWO7605.Y
424	32.6	11.9	839	9	CNS04973	AL280216 Tetraodon	C 496	32.2	11.7	415	2	BB684811	BB684811 BB684811
425	32.6	11.9	877	1	AL547836	AL547836 AL547836	C 497	32.2	11.7	426	5	BY435818	BY435818 BY435818
426	32.6	11.9	906	8	BH57308	BH57308 ENTSR24TF	C 498	32.2	11.7	457	4	BI846359	BI846359 fca4612.X
427	32.6	11.9	941	5	EX691459	EX691459 BX691459	C 499	32.2	11.7	472	5	BY474141	BY474141 BY474141
428	32.6	11.9	983	2	BE306297	BE306297 601103802	500	32.2	11.7	499	6	CB712278	CB712278 AMGNNUC:U
429	32.6	11.9	1056	8	CC286485	CC286485 CH261-188	501	32.2	11.7	500	4	AZ907113	AZ907113 RPCI-24-1
430	32.6	11.9	1502	5	BU219173	BU219173 603109265	502	32.2	11.7	538	9	AG060697	AG060697 LO906G06-
431	32.6	11.9	1960	3	AK042338	AK042338 Mus muscu	503	32.2	11.7	553	1	CR494829	CR494829 Medicago
432	32.4	11.9	226	2	BH384759	BH384759 Mus muscu	C 505	32.2	11.7	562	4	AU024409	AU024409 AU024409
433	32.4	11.9	263	1	AU306703	AU306703 AU306703	506	32.2	11.7	576	4	BI714065	BI714065 iab1n01.X
434	32.4	11.9	289	2	BB099694	BB099694 BB099694	507	32.2	11.7	585	7	CK940410	CK940410 K0239G06-
435	32.4	11.9	338	2	BB099694	BB099694 BB099694	508	32.2	11.7	585	7	CK940410	CK940410 K0239G06-
436	32.4	11.9	383	8	AQ133478	AQ133478 HS 3039.A	509	32.2	11.7	585	7	CK940410	CK940410 K0239G06-
437	32.4	11.9	460	1	AI623214	AI623214 C678f02.X	510	32.2	11.7	592	8	AZ981384	AZ981384 2M0219P08
438	32.4	11.9	488	8	BZ7379	BZ7379 T6C12TR TAM	511	32.2	11.7	605	4	BG072579	BG072579 H3112E07-
439	32.4	11.9	538	5	BP426416	BP426416 BP426416	512	32.2	11.7	621	7	CK981127	CK981127 4112751.B
440	32.4	11.9	570	6	CB100886	CB100886 K163b08.Y	C 513	32.2	11.7	624	5	BX558500	BX558500 BX558500
441	32.4	11.9	575	8	BZ8599	BZ8599 T14A15TF TA	C 514	32.2	11.7	637	7	CK964438	CK964438 4079275.B
442	32.4	11.9	639	1	AL634708	AL634708 AL634708	515	32.2	11.7	648	2	BA466966	BA466966 BA466966
443	32.4	11.9	640	8	CC114530	CC114530 ND.L.72F9.	516	32.2	11.7	652	7	CK975671	CK975671 4106565.B
444	32.4	11.9	705	5	CC108093	CC108093 BX108093	517	32.2	11.7	656	6	CA294649	CA294649 CAGSLV101
445	32.4	11.9	739	9	CS564868	CS564868 CH240 476	C 517	32.2	11.7	656	6	CK964625	CK964625 4079659.B
446	32.4	11.9	770	8	CN317402	CN317402 AGENCOURT	518	32.2	11.7	658	4	BJ577827	BJ577827 BJ577827
447	32.4	11.9	771	8	AG521363	AG521363 Mus muscu	519	32.2	11.7	663	9	CR025513	CR025513 Forward s
448	32.4	11.9	787	9	AG521363	AG521363 Mus muscu	520	32.2	11.7	672	4	BJ568060	BJ568060 BJ568060
449	32.4	11.9	791	8	BQ097844	BQ097844 CH230-144	521	32.2	11.7	672	4	CK949471	CK949471 4074439.B
450	32.4	11.9	840	7	CO394508	CO394508 AGENCOURT	522	32.2	11.7	678	9	DR37K225	DR37K225 AL976006
451	32.4	11.9	858	9	CS087432	CS087432 ZMMBB028	C 523	32.2	11.7	684	7	CK980645	CK980645 4112606.B
452	32.4	11.9	891	8	AZ546150	AZ546150 ENTEW77TF	524	32.2	11.7	689	4	BJ383498	BJ383498 BJ383498
453	32.4	11.9	903	8	AZ547248	AZ547248 ENTEW77TF	525	32.2	11.7	693	4	BJ577971	BJ577971 BJ577971
454	32.4	11.9	917	8	AZ672153	AZ672153 ENTEW75TF	526	32.2	11.7	695	1	AI905474	AI905474 RC-BT091-
455	32.4	11.9	943	8	AZ545940	AZ545940 ENTDM11TF	C 527	32.2	11.7	695	4	BG649183	BG649183 EMI 77.F0
456	32.4	11.9	1185	9	AG288472	AG288472 Mus muscu	528	32.2	11.7	702	7	CK981807	CK981807 CK981807
457	32.4	11.9	1359	5	BQ804046	BQ804046 SCQRZ309	529	32.2	11.7	710	2	AW546128	AW546128 L0004A03-
458	32.4	11.9	1840	1	BQ804046	BQ804046 SCQRZ309	C 530	32.2	11.7	712	8	B01384	B01384 CSRL-130H2-
459	32.2	11.8	150	1	A1252502	A1252502 QV30b11.X	531	32.2	11.7	727	5	BW074541	BW074541 BW074541
460	32.2	11.8	233	1	A1784317	A1784317 ta70c07.X	532	32.2	11.7	739	4	BJ568395	BJ568395 BJ568395
461	32.2	11.8	267	2	BBS96075	BBS96075 Mus muscu	533	32.2	11.7	748	9	AG492436	AG492436 Mus muscu
462	32.2	11.8	430	8	AZ062614	AZ062614 RPCI-23-4	534	32.2	11.7	750	5	BW396517	BW396517 BW396517

C 536	32	11.7	752	9	CR233254	Forward s	CR233254	Forward s	C 609	31.8	11.6	540	4	BM748487	BM748487	K-EST0023
C 537	32	11.7	757	8	BH396370	AG-NB-150	BH396370	AG-NB-150	C 610	31.8	11.6	542	7	CN368824	CN368824	170004241
C 538	32	11.7	760	4	BJ443263	Bu443263	BJ443263	Bu443263	C 611	31.8	11.6	543	7	BM748495	BM748495	K-EST0023
C 539	32	11.7	775	4	BG566273	602585142	BG566273	602585142	C 612	31.8	11.6	550	4	BG898933	BG898933	EST515784
C 540	32	11.7	781	5	BW008381	BW008381	BW008381	BW008381	C 613	31.8	11.6	550	4	BM069744	BM069744	ie88005.Y
C 541	32	11.7	782	8	BZ427410	BONGU49TF	BZ427410	BONGU49TF	C 614	31.8	11.6	551	4	BM748499	BM748499	K-EST0023
C 542	32	11.7	817	7	CC143641	NDL-18B17	CC143641	NDL-18B17	C 615	31.8	11.6	558	6	CB069549	CB069549	1616F09.Y
C 543	32	11.7	839	5	CK866186	AGENCOURT	CK866186	AGENCOURT	C 616	31.8	11.6	559	2	BF109935	BF109935	7172607.X
C 544	32	11.7	859	6	BU279725	603601647	BU279725	603601647	C 617	31.8	11.6	559	7	CK969042	CK969042	4084607.B
C 545	32	11.7	868	9	CNS0205G	SCQSL303	AL2206269	Tetraodon	C 618	31.8	11.6	565	8	AZ496434	AZ496434	1M0332C21
C 546	32	11.7	870	5	BP434831	BP434831	BP434831	BP434831	C 619	31.8	11.6	565	8	AQ467939	AQ467939	HS 5207.B
C 547	32	11.7	871	9	CR057294	Forward s	CR057294	Forward s	C 620	31.8	11.6	567	7	CF652484	CF652484	58-L02052
C 548	32	11.7	879	9	BH131448	ENVTN06TF	BH131448	ENVTN06TF	C 621	31.8	11.6	570	1	AI674690	AI674690	wd19C11.X
C 549	32	11.7	903	8	CR185526	Forward s	CR185526	Forward s	C 622	31.8	11.6	572	2	BF029821	BF029821	601556756
C 550	32	11.7	909	8	AZ544496	ENTDL80TF	AZ544496	ENTDL80TF	C 623	31.8	11.6	579	2	BF965485	BF965485	602276932
C 551	32	11.7	1004	9	CNS016A3	Drosophil	AL106485	Drosophil	C 624	31.8	11.6	585	4	BI792829	BI792829	1e47f07.X
C 552	32	11.7	1101	9	CNS0037Q	AL528663	AL528663	AL528663	C 625	31.8	11.6	600	1	AI084624	AI084624	0x78C04.X
C 553	32	11.7	1117	1	AL528663	AL528663	AL528663	AL528663	C 626	31.8	11.6	603	5	BI081232	BI081232	UI-H-BUO-
C 554	32	11.7	1188	4	BM906039	AGENCOURT	BM906039	AGENCOURT	C 627	31.8	11.6	605	6	CB373629	CB373629	TGESTxyg8
C 555	32	11.7	1198	4	BM920747	AGENCOURT	BM920747	AGENCOURT	C 628	31.8	11.6	610	4	BI844207	BI844207	UI-H-EZO-
C 556	32	11.7	1410	9	AY407448	Homo sapi	AY407448	Homo sapi	C 629	31.8	11.6	619	4	BI707889	BI707889	f39a12.X
C 557	32	11.7	3033	3	AK051858	Mus muscu	AK051858	Mus muscu	C 630	31.8	11.6	625	2	BF520182	BF520182	EST457651
C 558	32	11.7	3885	3	AK078489	Mus muscu	AK078489	Mus muscu	C 631	31.8	11.6	630	6	BE748705	BE748705	1006973.H
C 559	32	11.7	250	4	BJ330109	BJ330109	BJ330109	BJ330109	C 632	31.8	11.6	632	2	BE748705	BE748705	601571749
C 560	31.8	11.6	255	5	BQ353775	RC1-HT088	BQ353775	RC1-HT088	C 633	31.8	11.6	633	5	BU079251	BU079251	C06260406-
C 561	31.8	11.6	265	1	AA745282	nv48h06.r	AA745282	nv48h06.r	C 634	31.8	11.6	636	6	CA441120	CA441120	UI-H-PFO-
C 562	31.8	11.6	330	4	BM164456	EST566968	BM164456	EST566968	C 635	31.8	11.6	638	6	CD677019	CD677019	ho10b09.Y
C 563	31.8	11.6	330	3	BM168236	EST570759	BM168236	EST570759	C 636	31.8	11.6	650	5	BU687196	BU687196	UI-H-PFO-
C 564	31.8	11.6	330	3	BY497972	BY497972	BY497972	BY497972	C 637	31.8	11.6	657	5	BU678196	BU678196	UI-H-PFO-
C 565	31.8	11.6	340	4	BM766372	K-EST0048	BM766372	K-EST0048	C 638	31.8	11.6	659	1	AV701892	AV701892	UI-H-PFO-
C 566	31.8	11.6	372	4	BM758246	K-EST0037	BM758246	K-EST0037	C 639	31.8	11.6	659	5	BQ020825	BQ020825	UI-H-PFO-
C 567	31.8	11.6	391	2	AM899946	CMO-NR100	AM899946	CMO-NR100	C 640	31.8	11.6	665	6	CA414926	CA414926	UI-H-EZO-
C 568	31.8	11.6	408	1	AV735196	AV735196	AV735196	AV735196	C 641	31.8	11.6	667	7	CK232087	CK232087	ILLUMIGEN
C 569	31.8	11.6	431	4	BT318025	fq58a05.X	BT318025	fq58a05.X	C 642	31.8	11.6	668	6	CA418101	CA418101	UI-H-PHO-
C 570	31.8	11.6	440	2	B5919369	EST423222	B5919369	EST423222	C 643	31.8	11.6	686	4	BG260297	BG260297	602371413
C 571	31.8	11.6	443	4	BM748302	K-EST0023	BM748302	K-EST0023	C 644	31.8	11.6	686	6	CA423061	CA423061	UI-H-FLO-
C 572	31.8	11.6	444	4	BM756639	K-EST0035	BM756639	K-EST0035	C 645	31.8	11.6	693	6	CA423061	CA423061	UI-H-FLO-
C 573	31.8	11.6	446	4	BM748439	K-EST0023	BM748439	K-EST0023	C 646	31.8	11.6	696	5	BQ775449	BQ775449	UI-H-PHO-
C 574	31.8	11.6	446	4	BT844079	fs33c05.X	BT844079	fs33c05.X	C 647	31.8	11.6	704	5	BU022266	BU022266	QHS6G07.Y
C 575	31.8	11.6	448	4	BT844081	fs33c05.X	BT844081	fs33c05.X	C 648	31.8	11.6	704	5	BU022266	BU022266	QHS6G07.Y
C 576	31.8	11.6	448	4	BT844081	fs33c05.X	BT844081	fs33c05.X	C 649	31.8	11.6	708	5	BU631680	BU631680	UI-H-FLO-
C 577	31.8	11.6	448	4	BT844081	fs33c05.X	BT844081	fs33c05.X	C 650	31.8	11.6	710	6	CB268065	CB268065	UI-H-FLO-
C 578	31.8	11.6	448	4	BT844081	fs33c05.X	BT844081	fs33c05.X	C 651	31.8	11.6	717	8	BZ402875	BZ402875	OGABI71TM
C 579	31.8	11.6	451	4	BM081951	AE93h04.s	BM081951	AE93h04.s	C 652	31.8	11.6	731	6	CA407340	CA407340	1003489.H
C 580	31.8	11.6	452	7	CF605579	RADIC01.0	CF605579	RADIC01.0	C 653	31.8	11.6	731	6	CA420254	CA420254	UI-H-FGO-
C 581	31.8	11.6	457	7	CF605579	RADIC01.0	CF605579	RADIC01.0	C 654	31.8	11.6	735	4	BG611799	BG611799	602613189
C 582	31.8	11.6	457	7	CF605579	RADIC01.0	CF605579	RADIC01.0	C 655	31.8	11.6	741	7	CA445618	CA445618	CR445618
C 583	31.8	11.6	458	4	BM747238	K-EST0021	BM747238	K-EST0021	C 656	31.8	11.6	742	2	BE619679	BE619679	601472827
C 584	31.8	11.6	471	1	AA602346	no89h06.s	AA602346	no89h06.s	C 657	31.8	11.6	745	6	CA419475	CA419475	UI-H-PHO-
C 585	31.8	11.6	473	4	AA602346	no89h06.s	AA602346	no89h06.s	C 658	31.8	11.6	751	4	BI876265	BI876265	f170b10.Y
C 586	31.8	11.6	474	1	AA602346	no89h06.s	AA602346	no89h06.s	C 659	31.8	11.6	756	8	BH067154	BH067154	RPCT-24-2
C 587	31.8	11.6	474	1	AA602346	no89h06.s	AA602346	no89h06.s	C 660	31.8	11.6	758	9	AGS82002	AGS82002	Mus muscu
C 588	31.8	11.6	481	8	B2136635	CH230-288	B2136635	CH230-288	C 661	31.8	11.6	765	5	BQ000046	BQ000046	UI-H-FLO-
C 589	31.8	11.6	482	1	AI650765	wa19d07.X	AI650765	wa19d07.X	C 662	31.8	11.6	767	5	BQ000046	BQ000046	UI-H-FLO-
C 590	31.8	11.6	486	6	CB117195	K-EST0162	CB117195	K-EST0162	C 663	31.8	11.6	789	5	BU621975	BU621975	UI-H-FHI-
C 591	31.8	11.6	490	4	BM758018	K-EST0037	BM758018	K-EST0037	C 664	31.8	11.6	791	2	BE130361	BE130361	601818042
C 592	31.8	11.6	491	2	AM518950	ha4ra04.X	AM518950	ha4ra04.X	C 665	31.8	11.6	795	2	BE130361	BE130361	601818042
C 593	31.8	11.6	496	4	BM727333	if30b08.X	BM727333	if30b08.X	C 666	31.8	11.6	823	7	CO123357	CO123357	GR_EB05H
C 594	31.8	11.6	496	4	BM749835	K-EST0025	BM749835	K-EST0025	C 667	31.8	11.6	845	7	CK261783	CK261783	EST707861
C 595	31.8	11.6	509	6	CB851476	K-EST0025	CB851476	K-EST0025	C 668	31.8	11.6	845	7	CK261783	CK261783	EST707861
C 596	31.8	11.6	522	4	BF591055	hb8e10.X	BF591055	hb8e10.X	C 669	31.8	11.6	852	7	BF699711	BF699711	602127132
C 597	31.8	11.6	526	2	BF591055	hb8e10.X	BF591055	hb8e10.X	C 670	31.8	11.6	859	8	AZ691760	AZ691760	ENTHGS5TF
C 598	31.8	11.6	527	2	BM748246	K-EST0022	BM748246	K-EST0022	C 671	31.8	11.6	867	7	CF935665	CF935665	TrEST-B06
C 599	31.8	11.6	527	4	BM758950	K-EST0038	BM758950	K-EST0038	C 672	31.8	11.6	871	8	AZ684257	AZ684257	ENTHGS5TF
C 600	31.8	11.6	527	6	CA952634	iq14h06.X	CA952634	iq14h06.X	C 673	31.8	11.6	906	9	CG094421	CG094421	PUJEC47TB
C 601	31.8	11.6	527	6	CA952634	iq14h06.X	CA952634	iq14h06.X	C 674	31.8	11.6	908	9	CG094421	CG094421	PUJEC47TB
C 602	31.8	11.6	528	4	BM354082	if30b08.Y	BM354082	if30b08.Y	C 675	31.8	11.6	916	5	BU114803	BU114803	603128944
C 603	31.8	11.6	531	6	CA774029	in21e07.X	CA774029	in21e07.X	C 676	31.8	11.6	920	8	AZ540979	AZ540979	ENTHGS5TF
C 604	31.8	11.6	533	4	BM749301	K-EST0024	BM749301	K-EST0024	C 677	31.8	11.6	928	1	AL547861	AL547861	full-leng
C 605	31.8	11.6	533	9	CE215831	tigr-gss-	CE215831	tigr-gss-	C 678	31.8	11.6	930	8	CR614279	CR614279	full-leng
C 606	31.8	11.6	536	2	BF435767	nab41e03.	BF435767	nab41e03.	C 679	31.8	11.6	961	9	CNS05559	CNS05559	Tetraodon
C 608	31.8	11.6	538	4	BM748424	K-EST0023	BM748424	K-EST0023	C 680	31.8	11.6	961	9	CNS05559	CNS05559	Tetraodon

C 682	31.8	11.6	975	4	BM907408	BM907408	AGENCYCOURT	755	31.4	11.5	478	1	AI631259	ts64d07.x
C 683	31.8	11.6	982	4	BG249108	602361709		C 756	31.4	11.5	510	7	COS84368	DG2-102i5
C 684	31.8	11.6	984	7	CO725856	ILLUMIGEN		C 757	31.4	11.5	512	2	AM772380	h0772e11.x
C 685	31.8	11.6	1017	9	CNS06JNC	AI401806	T3 end of	C 758	31.4	11.5	527	4	BM313876	ih077h04.x
C 686	31.8	11.6	1035	5	BX343776	BX343776		C 759	31.4	11.5	530	6	CA653163	wre1n.pk1
C 687	31.8	11.6	1073	9	CNS01217A	AI101992	Drosophila	C 760	31.4	11.5	549	8	BZ119880	CH230-422
C 688	31.8	11.6	1078	3	CR723675	CR723675	Tetraodon	C 761	31.4	11.5	552	8	AZ705309	RPCI-23-2
C 689	31.8	11.6	1454	4	BM909611	BM909611	AGENCYCOURT	C 762	31.4	11.5	579	8	AZ954790	2M0220D12
C 690	31.6	11.6	201	1	AJ541584	AJ541584		C 763	31.4	11.5	593	6	CB923973	TCAmad101
C 691	31.6	11.6	236	4	BM858425	fx75009.Y		C 764	31.4	11.5	604	4	BJ246974	BJ246974
C 692	31.6	11.6	309	2	BM858425	fx75009.Y		C 765	31.4	11.5	606	9	CR352181	Medicago
C 693	31.6	11.6	315	9	CG944261	BM858425		C 766	31.4	11.5	616	9	CE610173	tigr-986-
C 694	31.6	11.6	327	7	CF372498	CE610173		C 767	31.4	11.5	620	8	AO932452	RPCI-23-2
C 695	31.6	11.6	331	2	AW232823	CF372498	CE610173	C 768	31.4	11.5	631	9	EX120182	EX120182
C 696	31.6	11.6	341	8	AO262818	AW232823	fj32b08.x	C 769	31.4	11.5	645	4	BZ289249	BZ289249
C 697	31.6	11.6	354	9	CG618105	AO262818	CTBT-E1	C 770	31.4	11.5	648	8	BH306438	BH306438
C 698	31.6	11.6	358	4	BI781040	CG618105	ZMMB5028	C 771	31.4	11.5	650	6	CA269477	CA269477
C 699	31.6	11.6	365	2	AW287914	BI781040	ESma03.SQ	C 772	31.4	11.5	651	8	AZ410018	LA10182104
C 700	31.6	11.6	458	5	BY591352	AW287914	N100758e	C 773	31.4	11.5	658	9	CG089400	PUICX77TB
C 701	31.6	11.6	497	1	AI395722	BY591352	MA004603	C 774	31.4	11.5	664	9	CR310978	Medicago
C 702	31.6	11.6	497	8	BM670431	AI395722	BOMB050TF	C 775	31.4	11.5	667	7	CR373721	CR373721
C 703	31.6	11.6	500	4	BM059415	BM670431	2253-55.h	C 776	31.4	11.5	671	9	AG298199	Mus muscu
C 704	31.6	11.6	503	6	CD472989	BM059415	rad03-30m	C 777	31.4	11.5	674	8	BZ002718	osg89g05
C 705	31.6	11.6	552	9	CR116960	CD472989	forward.s	C 778	31.4	11.5	674	8	BZ002718	osg89g05
C 706	31.6	11.6	561	8	AZ262540	CR116960	forward.s	C 779	31.4	11.5	680	9	CL768663	OR_BBa014
C 707	31.6	11.6	564	1	AI395728	AZ262540	RPCI-23-1	C 780	31.4	11.5	693	9	CG937059	CG937059
C 708	31.6	11.6	567	6	CB616359	AI395728	MA004617	C 781	31.4	11.5	703	6	CA447316	CA447316
C 709	31.6	11.6	587	9	CK983975	CB616359	AMGNNUC.U	C 782	31.4	11.5	711	6	CF236980	CF236980
C 710	31.6	11.6	596	7	CC747990	CK983975	re31f07.Y	C 783	31.4	11.5	717	6	BZ338947	BZ338947
C 711	31.6	11.6	605	4	BI969146	CC747990	ZMMB5012	C 784	31.4	11.5	726	7	CA268781	CA268781
C 712	31.6	11.6	612	4	BZ365480	BI969146	GMB30007B	C 785	31.4	11.5	741	6	CA268781	CA268781
C 713	31.6	11.6	616	5	BQ92549	BZ365480	BQ92549	C 786	31.4	11.5	747	9	EX169228	EX169228
C 714	31.6	11.6	626	4	BM530202	BQ92549	fz43d06.x	C 787	31.4	11.5	772	9	CR485170	CR485170
C 715	31.6	11.6	636	9	CL294642	BM530202	fw73b11.x	C 788	31.4	11.5	795	9	CG960567	CG960567
C 716	31.6	11.6	653	1	AL599989	CL294642	01S0787-0	C 789	31.4	11.5	797	9	AG491703	AG491703
C 717	31.6	11.6	653	8	AZ271764	AL599989	DKF2p313L	C 790	31.4	11.5	799	9	CR104679	CR104679
C 718	31.6	11.6	654	2	BF646404	AZ271764	IM0123018	C 791	31.4	11.5	801	7	CO486286	CO486286
C 719	31.6	11.6	655	6	CB864686	BF646404	NF071F11E	C 792	31.4	11.5	805	7	CO486286	CO486286
C 720	31.6	11.6	660	2	BF633086	CB864686	HD06020w	C 793	31.4	11.5	806	7	CF446335	CF446335
C 721	31.6	11.6	661	9	AG160661	BF633086	NF054F11D	C 794	31.4	11.5	811	8	BH464837	BH464837
C 722	31.6	11.6	677	2	BF633019	AG160661	Pan trogl	C 795	31.4	11.5	836	9	CR066459	CR066459
C 723	31.6	11.6	712	8	AZ090855	BF633019	RF035H04D	C 796	31.4	11.5	864	8	BZ461882	BZ461882
C 724	31.6	11.6	733	8	BH922688	AZ090855	odg85e10	C 797	31.4	11.5	868	8	AZ691312	AZ691312
C 725	31.6	11.6	734	6	CB597117	BH922688	odg85e10	C 798	31.4	11.5	878	8	AZ684491	AZ684491
C 726	31.6	11.6	747	9	CR135401	CB597117	Reverse.s	C 799	31.4	11.5	881	9	CG284443	CG284443
C 727	31.6	11.6	748	1	AJ798288	CR135401	Reverse.s	C 800	31.4	11.5	885	8	BZ390894	BZ390894
C 728	31.6	11.6	758	7	CO475911	AJ798288	Q0065.B3	C 801	31.4	11.5	889	8	CG936628	CG936628
C 729	31.6	11.6	765	8	BH063988	CO475911	Q0065.B3	C 802	31.4	11.5	894	8	CA433270	CA433270
C 730	31.6	11.6	807	9	CNS0128R	BH063988	RPCI-24-3	C 803	31.4	11.5	901	9	CG957513	CG957513
C 731	31.6	11.6	816	7	CK471902	CNS0128R	RPCI-24-3	C 804	31.4	11.5	927	9	CF781995	CF781995
C 732	31.6	11.6	823	8	BZ202402	CK471902	Drosophila	C 805	31.4	11.5	929	4	BG540654	BG540654
C 733	31.6	11.6	827	8	BZ202402	BZ202402	Drosophila	C 806	31.4	11.5	934	8	BZ789470	BZ789470
C 734	31.6	11.6	829	9	CG974451	BZ202402	CH230-342	C 807	31.4	11.5	1053	9	CG807565	CG807565
C 735	31.6	11.6	836	9	AG404896	CG974451	MBE8K07R	C 808	31.4	11.5	1296	9	CG749901	CG749901
C 736	31.6	11.6	838	5	BQ145143	AG404896	Mus muscu	C 809	31.4	11.5	209	4	BJ324312	BJ324312
C 737	31.6	11.6	914	8	BO145143	BQ145143	NF003F08G	C 810	31.4	11.5	311	2	BB828463	BB828463
C 738	31.6	11.6	919	6	CA787541	BO145143	FUHSO95TD	C 811	31.4	11.5	315	1	AA814453	AA814453
C 739	31.6	11.6	923	9	CG926291	CA787541	AGENCYCOURT	C 812	31.4	11.5	317	1	AU284820	AU284820
C 740	31.6	11.6	927	6	CB588874	CG926291	MBEWA58TR	C 813	31.4	11.5	340	7	CF799982	CF799982
C 741	31.6	11.6	959	7	CK262294	CB588874	AGENCYCOURT	C 814	31.4	11.5	345	1	AA953436	AA953436
C 742	31.6	11.6	1101	9	CNS00GJH	CK262294	ESR708372	C 815	31.2	11.4	347	8	BH735680	BH735680
C 743	31.6	11.6	1458	8	CC194846	CNS00GJH	Drosophila	C 816	31.2	11.4	357	5	BP628977	BP628977
C 744	31.4	11.5	350	2	BF485185	CC194846	CH261-183	C 817	31.2	11.4	363	4	PG055183	PG055183
C 745	31.4	11.5	363	1	AI789940	BF485185	WHB1789.D	C 818	31.2	11.4	393	5	BX699991	BX699991
C 746	31.4	11.5	365	4	BI941631	AI789940	ue66a05.I	C 819	31.2	11.4	413	8	CC051903	CC051903
C 747	31.4	11.5	365	4	BM354574	BI941631	sc06f10.Y	C 820	31.2	11.4	422	1	AV710208	AV710208
C 748	31.4	11.5	375	7	CF975259	BM354574	rx66b12.Y	C 821	31.2	11.4	425	1	AV710208	AV710208
C 749	31.4	11.5	397	8	AQ513953	CF975259	HS-5179.B	C 822	31.2	11.4				
C 750	31.4	11.5	427	8	AZ233692	AQ513953	RPCI-23-7	C 823	31.2	11.4				
C 751	31.4	11.5	448	4	BI841385	AZ233692	RPCI-23-7	C 824	31.2	11.4				
C 752	31.4	11.5	457	8	AQ802788	BI841385	fq55c02.x	C 825	31.2	11.4				
C 753	31.4	11.5	462	5	BX624277	AQ802788	HS 3186.A	C 826	31.2	11.4				
C 754	31.4	11.5	464	8	BH090341	BX624277	BX624277	C 827	31.2	11.4				

828	31.2	11.4	431	5	BP626278	BP626278	BP626278	901	31.2	11.4	697	8	BH734085	BOMHY11TR
C 829	31.2	11.4	432	9	BX126618	Danio rer	BX126618	902	31.2	11.4	704	8	BH523506	BOGYB68TF
830	31.2	11.4	441	9	CE361132	tigr-gss-	CE361132	903	31.2	11.4	707	8	BH542065	BOGTJ31TR
831	31.2	11.4	442	7	CF760342	DSAF1_58	CF760342	904	31.2	11.4	707	8	BH662758	BOHCP07TR
C 832	31.2	11.4	445	2	BH831756	BH831756	BH831756	C 905	31.2	11.4	708	8	BH977446	ODH46G07
C 833	31.2	11.4	445	5	BY393558	BY393558	BY393558	C 906	31.2	11.4	711	6	CA240187	SCSBL406
C 834	31.2	11.4	454	6	CB051297	CB051297	CB051297	C 907	31.2	11.4	713	9	AG355011	Mus muscu
C 835	31.2	11.4	457	4	BM081381	BM081381	BM081381	C 908	31.2	11.4	723	8	BH727106	BOMKZ43TR
C 836	31.2	11.4	476	1	AI923335	AI923335	AI923335	909	31.2	11.4	730	8	QA486221	RPCI-11-2
837	31.2	11.4	489	7	AI284016	AI284016	AI284016	910	31.2	11.4	733	8	BH727106	BOMKZ43TR
838	31.2	11.4	495	7	T90549	T90549	T90549	911	31.2	11.4	733	8	QA486221	RPCI-11-2
C 839	31.2	11.4	499	1	AU150063	AU150063	AU150063	912	31.2	11.4	738	8	BH542065	BOGTJ31TR
840	31.2	11.4	507	4	BI097077	BI097077	BI097077	913	31.2	11.4	740	8	BH542065	BOGTJ31TR
841	31.2	11.4	509	9	CC959503	CC959503	CC959503	914	31.2	11.4	744	5	BH727106	BOMKZ43TR
C 842	31.2	11.4	512	8	AZ143095	AZ143095	AZ143095	915	31.2	11.4	745	8	BH681873	BOMJ15TF
C 843	31.2	11.4	513	4	BM027534	BM027534	BM027534	C 916	31.2	11.4	745	8	BH727106	BOMKZ43TR
C 844	31.2	11.4	515	1	AI877961	AI877961	AI877961	917	31.2	11.4	747	8	BH727106	BOMKZ43TR
C 845	31.2	11.4	522	7	CK984000	CK984000	CK984000	918	31.2	11.4	748	8	BH727106	BOMKZ43TR
846	31.2	11.4	523	1	AI251121	AI251121	AI251121	C 919	31.2	11.4	748	8	BH727106	BOMKZ43TR
847	31.2	11.4	525	8	BH429404	BH429404	BH429404	920	31.2	11.4	753	8	BH727106	BOMKZ43TR
848	31.2	11.4	525	5	BX555726	BX555726	BX555726	921	31.2	11.4	753	8	BH727106	BOMKZ43TR
C 849	31.2	11.4	530	5	BQ519555	BQ519555	BQ519555	C 922	31.2	11.4	755	8	BH727106	BOMKZ43TR
C 850	31.2	11.4	542	8	AZ235048	AZ235048	AZ235048	923	31.2	11.4	755	8	BH727106	BOMKZ43TR
C 851	31.2	11.4	542	9	CC945033	CC945033	CC945033	C 924	31.2	11.4	756	8	BH727106	BOMKZ43TR
C 852	31.2	11.4	549	8	AQ239387	AQ239387	AQ239387	925	31.2	11.4	757	8	BH727106	BOMKZ43TR
853	31.2	11.4	556	2	AW192827	AW192827	AW192827	926	31.2	11.4	757	8	BH727106	BOMKZ43TR
C 854	31.2	11.4	561	8	AZ265662	AZ265662	AZ265662	927	31.2	11.4	760	8	BH727106	BOMKZ43TR
C 855	31.2	11.4	566	5	BX758864	BX758864	BX758864	C 928	31.2	11.4	760	8	BH727106	BOMKZ43TR
C 856	31.2	11.4	572	8	BQ501740	BQ501740	BQ501740	C 929	31.2	11.4	761	8	BH727106	BOMKZ43TR
C 857	31.2	11.4	573	8	BH655150	BH655150	BH655150	930	31.2	11.4	765	8	BH727106	BOMKZ43TR
C 858	31.2	11.4	581	8	AZ792758	AZ792758	AZ792758	C 931	31.2	11.4	767	7	CR582642	CR582642
859	31.2	11.4	581	8	CO211249	CO211249	CO211249	C 932	31.2	11.4	767	7	CR582642	CR582642
C 860	31.2	11.4	586	7	BQ307729	BQ307729	BQ307729	C 933	31.2	11.4	771	8	BH727106	BOMKZ43TR
C 861	31.2	11.4	594	5	AI834656	AI834656	AI834656	C 934	31.2	11.4	772	9	CC958085	CC958085
C 862	31.2	11.4	595	1	A1834656	A1834656	A1834656	C 935	31.2	11.4	776	8	BH727106	BOMKZ43TR
C 863	31.2	11.4	602	8	AZ662330	AZ662330	AZ662330	936	31.2	11.4	777	8	BH727106	BOMKZ43TR
864	31.2	11.4	604	8	BH448915	BH448915	BH448915	C 937	31.2	11.4	778	8	BH727106	BOMKZ43TR
865	31.2	11.4	608	8	BH573912	BH573912	BH573912	C 938	31.2	11.4	778	8	BH727106	BOMKZ43TR
866	31.2	11.4	609	8	BH573912	BH573912	BH573912	C 939	31.2	11.4	779	9	CC944354	CC944354
867	31.2	11.4	611	4	BJ392510	BJ392510	BJ392510	940	31.2	11.4	780	8	BH727106	BOMKZ43TR
C 868	31.2	11.4	613	8	BH516855	BH516855	BH516855	941	31.2	11.4	785	8	BH727106	BOMKZ43TR
C 869	31.2	11.4	617	6	CC2455	CC2455	CC2455	942	31.2	11.4	786	8	BH727106	BOMKZ43TR
870	31.2	11.4	619	1	AA595431	AA595431	AA595431	C 943	31.2	11.4	788	9	CC947464	CC947464
871	31.2	11.4	622	5	BU741375	BU741375	BU741375	944	31.2	11.4	791	8	BH727106	BOMKZ43TR
872	31.2	11.4	626	8	BZ484237	BZ484237	BZ484237	945	31.2	11.4	792	8	BH727106	BOMKZ43TR
873	31.2	11.4	632	8	BH581306	BH581306	BH581306	946	31.2	11.4	793	8	BH727106	BOMKZ43TR
874	31.2	11.4	634	9	CC965741	CC965741	CC965741	947	31.2	11.4	793	8	BH727106	BOMKZ43TR
875	31.2	11.4	639	8	BZ426514	BZ426514	BZ426514	948	31.2	11.4	795	8	BH727106	BOMKZ43TR
876	31.2	11.4	643	9	CE817360	CE817360	CE817360	C 949	31.2	11.4	797	8	BH727106	BOMKZ43TR
C 877	31.2	11.4	645	8	BH420850	BH420850	BH420850	C 950	31.2	11.4	799	8	BH727106	BOMKZ43TR
878	31.2	11.4	645	8	BH557542	BH557542	BH557542	C 951	31.2	11.4	800	9	CC638130	CC638130
879	31.2	11.4	647	6	CB498586	CB498586	CB498586	C 952	31.2	11.4	802	8	BH727106	BOMKZ43TR
880	31.2	11.4	647	6	BH176053	BH176053	BH176053	C 953	31.2	11.4	804	8	BH727106	BOMKZ43TR
881	31.2	11.4	647	9	CC95079F	CC95079F	CC95079F	C 954	31.2	11.4	805	8	BH727106	BOMKZ43TR
882	31.2	11.4	647	9	CC95079F	CC95079F	CC95079F	955	31.2	11.4	805	9	CC957080	CC957080
C 883	31.2	11.4	648	7	CR419706	CR419706	CR419706	C 956	31.2	11.4	808	9	CC957080	CC957080
884	31.2	11.4	649	5	BU704542	BU704542	BU704542	C 957	31.2	11.4	813	5	BX110929	BX110929
885	31.2	11.4	654	6	CD320716	CD320716	CD320716	958	31.2	11.4	813	8	BH727106	BOMKZ43TR
886	31.2	11.4	664	8	BH322598	BH322598	BH322598	959	31.2	11.4	814	8	BH727106	BOMKZ43TR
C 887	31.2	11.4	664	8	BH922598	BH922598	BH922598	C 960	31.2	11.4	816	8	BH727106	BOMKZ43TR
C 888	31.2	11.4	668	8	BH962764	BH962764	BH962764	961	31.2	11.4	818	7	CC655536	CC655536
C 889	31.2	11.4	668	8	BZ515138	BZ515138	BZ515138	C 962	31.2	11.4	820	8	BH727106	BOMKZ43TR
890	31.2	11.4	670	6	CB496810	CB496810	CB496810	963	31.2	11.4	820	8	BH727106	BOMKZ43TR
891	31.2	11.4	673	7	CC95079F	CC95079F	CC95079F	964	31.2	11.4	822	8	BH727106	BOMKZ43TR
892	31.2	11.4	673	8	BZ002948	BZ002948	BZ002948	C 965	31.2	11.4	824	8	BH727106	BOMKZ43TR
893	31.2	11.4	677	8	BZ030573	BZ030573	BZ030573	966	31.2	11.4	826	8	BH727106	BOMKZ43TR
C 894	31.2	11.4	679	1	AI723581	AI723581	AI723581	C 967	31.2	11.4	829	8	BH727106	BOMKZ43TR
C 895	31.2	11.4	679	9	AG058330	AG058330	AG058330	968	31.2	11.4	835	8	BH727106	BOMKZ43TR
C 896	31.2	11.4	683	8	BZ474265	BZ474265	BZ474265	C 969	31.2	11.4	838	8	BH727106	BOMKZ43TR
897	31.2	11.4	690	2	CL602167	CL602167	CL602167	C 970	31.2	11.4	847	5	BH727106	BOMKZ43TR
C 898	31.2	11.4	693	2	AW968577	AW968577	AW968577	C 971	31.2	11.4	849	5	BH727106	BOMKZ43TR
C 899	31.2	11.4	694	9	CC943675	CC943675	CC943675	972	31.2	11.4	859	8	BH727106	BOMKZ43TR
900	31.2	11.4	696	9	CC956127	CC956127	CC956127	C 973	31.2	11.4	868	8	BH727106	BOMKZ43TR

C 974	31.2	11.4	875	9	CG140773	CG140773	PUPUK27TD	c1047	31	11.4	582	6	CF295469	CF295469	30DGS--05
975	31.2	11.4	885	9	CNS0340Y	AL227707	Tetraodon	c1048	31	11.4	584	6	CD939371	CD939371	OV.113G08
976	31.2	11.4	889	9	AZ680321	ENT1222TF		c1049	31	11.4	589	5	BP167582	BP167582	BJ098160
977	31.2	11.4	892	9	CG140772	PUPUK27TB		1050	31	11.4	596	4	BJ098160	BJ098160	L30-968T01
978	31.2	11.4	895	8	BZ464176	BONK77TR		c1051	31	11.4	602	1	AI823113	AI823113	SCS-968T01
979	31.2	11.4	899	8	CC073399	CSU-K33r		1052	31	11.4	606	6	CA238402	CA238402	SCS9F0501
C 980	31.2	11.4	922	8	AZ201809	SP 0054 A		c1053	31	11.4	608	8	CC775517	CC775517	CH240_129
C 981	31.2	11.4	934	7	CK019980	AGENCOURT		1054	31	11.4	611	8	AZ290809	AZ290809	RPCI-23-1
982	31.2	11.4	937	8	BZ503116	BONK41TR		1055	31	11.4	616	1	CG532209	CG532209	3530_1_21
983	31.2	11.4	956	5	BU799121	SJF2BKOC09		c1056	31	11.4	617	1	AJ612942	AJ612942	AJ612942
C 984	31.2	11.4	976	5	EX399892	BU799121	SJF2BKOC09	c1057	31	11.4	616	1	BG512599	BG512599	daq29h09
C 985	31.2	11.4	996	4	EG293245	BG293245	602390817	c1058	31	11.4	617	8	BH178581	BH178581	O12_1_16-
C 986	31.2	11.4	1012	9	CNS00M52	AL079146	Drosophila	c1059	31	11.4	617	9	CNS07KVA	CNS07KVA	T3_end of
C 987	31.2	11.4	1048	8	BZ479922	BONBR65TR		c1060	31	11.4	621	9	CL134449	CL134449	104_418_1
988	31.2	11.4	1126	4	BM919403	AGENCOURT		1061	31	11.4	623	8	BF937612	BF937612	fm66910_Y
C 989	31.2	11.4	1346	9	AG320795	AG320795	Mus muscu	1062	31	11.4	628	8	AQ274874	AQ274874	RPCI-5-10
C 990	31.2	11.4	1355	9	CL647488	CL647488	CH213-139	c1063	31	11.4	630	4	BM168382	BM168382	EST570905
C 991	31	11.4	153	1	AI583469	AI583469	tt69a04.x	c1064	31	11.4	632	5	BM692219	BM692219	BX629219
C 992	31	11.4	153	1	AI583757	AI583757	tt71b07.x	c1065	31	11.4	632	5	BX741103	BX741103	BX741103
C 993	31	11.4	154	1	AI251496	AI251496	qv27f08.x	c1066	31	11.4	632	5	BX741103	BX741103	BX741103
C 994	31	11.4	154	1	AI337772	AI337772	qw87c10.x	1067	31	11.4	642	8	AZ612933	AZ612933	IM0441L05
C 995	31	11.4	154	1	AI349147	AI349147	tt73a11.x	1068	31	11.4	647	2	BH155036	BH155036	BH155036
C 996	31	11.4	154	1	AI612105	AI612105	tt58a07.x	1069	31	11.4	647	8	AZ632336	AZ632336	IM0486719
C 997	31	11.4	171	1	AI345478	AI345478	tb82g04.x	c1070	31	11.4	656	8	AZ362907	AZ362907	Danio rer
C 998	31	11.4	181	1	AI366980	AI366980	tb80c06.x	1071	31	11.4	659	6	CD076985	CD076985	MX3-0001U
C 999	31	11.4	194	2	AW302960	AW302960	xt-87b07.x	c1072	31	11.4	666	5	BU339554	BU339554	603515603
1000	31	11.4	244	7	N74539	N74539	za06f05.s1	c1073	31	11.4	676	1	AL720783	AL720783	AL720783
1001	31	11.4	267	1	AL727325	AL727325		1074	31	11.4	682	1	AL795980	AL795980	AL795980
1002	31	11.4	277	1	AA808570	AA808570	OB50d10.s	1075	31	11.4	685	7	CR444643	CR444643	CR444643
1003	31	11.4	299	8	BZ261563	BZ261563	CH230-458	1076	31	11.4	689	8	AZ867402	AZ867402	2M0178B15
1004	31	11.4	307	1	AA037769	AA037769	zk38e02.s	c1077	31	11.4	692	1	BX296671	BX296671	BX296671
1005	31	11.4	356	9	CE449406	CE449406	tigr-gss-	c1078	31	11.4	697	5	AL720784	AL720784	AL720784
1006	31	11.4	382	7	CN106467	CN106467	EC2CAA29C	c1079	31	11.4	698	9	AG280611	AG280611	Mus muscu
C1007	31	11.4	390	9	CE146509	CE146509	tigr-gss-	1080	31	11.4	707	5	BQ446347	BQ446347	UI-H-EU1-
1008	31	11.4	395	4	BG230575	BG230575	na4f0d06.	c1081	31	11.4	721	8	AZ726941	AZ726941	RPCI-24-6
1009	31	11.4	411	7	CK905214	CK905214	lh07h04.x	c1082	31	11.4	723	8	CO578353	CO578353	TYEST092B
1010	31	11.4	415	6	CK368364	CK368364	UI-H-FT1-	c1083	31	11.4	723	8	CO578353	CO578353	TYEST092B
1011	31	11.4	416	7	W04688	W04688	zb94a02.s1	c1084	31	11.4	738	9	AG398293	AG398293	Mus muscu
1012	31	11.4	421	1	AL727334	AL727334		c1085	31	11.4	742	4	BU445132	BU445132	BU445132
1013	31	11.4	440	7	H99912	H99912	yx30a04.s1	1086	31	11.4	742	4	CO578353	CO578353	TYEST092B
1014	31	11.4	445	1	AI012541	AI012541	EST266992	c1087	31	11.4	745	9	AG492672	AG492672	Mus muscu
1015	31	11.4	462	5	BX318848	BX318848		c1088	31	11.4	754	9	AG508545	AG508545	Mus muscu
1016	31	11.4	463	1	AI629034	AI629034	ty79g05.x	1089	31	11.4	758	5	BU295223	BU295223	603740221
C1017	31	11.4	467	2	BF287851	BF287851	EST452442	1090	31	11.4	758	5	AG466450	AG466450	Mus muscu
1018	31	11.4	468	9	BX237531	BX237531	Danio rer	c1091	31	11.4	762	9	CL689284	CL689284	PR10150d-
1019	31	11.4	473	4	BM165144	BM165144	EST567678	c1092	31	11.4	767	5	BX752161	BX752161	BX752161
C1020	31	11.4	474	8	AQ251221	AQ251221	P22118-Sp	c1093	31	11.4	769	5	BH207622	BH207622	Sm1-60D4.
1021	31	11.4	475	2	BF594595	BF594595	th77g07.x	1094	31	11.4	776	8	BX152605	BX152605	Danio rer
1022	31	11.4	478	2	BE675224	BE675224	7f04g12.x	c1095	31	11.4	784	7	CR442330	CR442330	CR442330
C1023	31	11.4	479	8	AQ735330	AQ735330	HS_3024 B	c1096	31	11.4	794	7	CR560857	CR560857	CR560857
1024	31	11.4	480	1	AI498630	AI498630	lm47a05.x	c1097	31	11.4	796	5	BX699668	BX699668	BX699668
C1025	31	11.4	482	7	CNO96565	CNO96565	EC2CAA11C	c1098	31	11.4	801	9	CL666553	CL666553	PR10152d
1026	31	11.4	488	1	AI707886	AI707886		c1099	31	11.4	802	8	BZ147201	BZ147201	CH230-40G
1027	31	11.4	491	8	BH5656848	BH5656848		c1100	31	11.4	816	8	BH435142	BH435142	BOH1565TF
1028	31	11.4	493	1	AJ679240	AJ679240	AV682130	c1101	31	11.4	832	5	BX692695	BX692695	BX692695
C1029	31	11.4	493	1	AJ679240	AJ679240	AV682130	c1102	31	11.4	833	5	BX690307	BX690307	EX690307
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9 BX763826 1583 11.2 30.6

BY764989 BY764989
CR106561 Reverse s
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AQ287425 nbxb0030C
CR038726 Reverse s
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C1266	30.6	11.2	600	2	BF685778	602140460	1339	30.6	11.2	1063	2	BE035382	BE035382	MO03G01 M
C1267	30.6	11.2	601	8	AZ468046	1M0279P16	C1340	30.6	11.2	1101	9	CNS00HGZ	AL073472	Drosophila
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C1269	30.6	11.2	614	7	CF668596	RTCNT1_37	C1342	30.6	11.2	1283	9	CL027106	CL027106	CH216-25B
C1270	30.6	11.2	621	7	CR444002	CR444002	1343	30.6	11.2	2189	3	AK052218	AK052218	Mus muscu
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C1272	30.6	11.2	629	1	AV723953	AV723953	C1345	30.4	11.1	132	9	CG570961	CG570961	OST200282
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C1276	30.6	11.2	641	1	AI731024	AI731024	C1349	30.4	11.1	277	8	AZ584210	AZ584210	1M0388M04
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C1278	30.6	11.2	647	2	AW370646	QV2-BT025	C1351	30.4	11.1	293	8	BZ253986	BZ253986	CH230-354
C1279	30.6	11.2	654	6	CD482621	CD482621	C1352	30.4	11.1	302	2	BB459516	BB459516	BB459516
C1280	30.6	11.2	655	8	BZ414280	atr01-5ms	C1353	30.4	11.1	324	7	CN082848	CN082848	EC2BBA21D
C1281	30.6	11.2	656	9	AG176633	B2414280	C1354	30.4	11.1	325	2	AW130230	AW130230	xf47e02.x
C1282	30.6	11.2	658	9	AG176633	fan trogl	C1355	30.4	11.1	329	8	AZ724135	AZ724135	RPCI-24-6
C1283	30.6	11.2	659	9	CD408449	Gm.cK3468	C1356	30.4	11.1	340	7	H99508	H99508	YK25H02.g1
C1284	30.6	11.2	667	2	AW960750	EST372821	C1357	30.4	11.1	343	8	AQ031373	AQ031373	HS_22222_A
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C1286	30.6	11.2	678	5	BU957945	AGENCOURT	C1359	30.4	11.1	349	5	BM135258	BM135258	BM135258
C1287	30.6	11.2	695	3	CNS0A6F8	BU957945	C1360	30.4	11.1	360	8	AZ923859	AZ923859	4908.qf22
C1288	30.6	11.2	696	5	BQ187611	Arabicdops	C1361	30.4	11.1	376	1	AI529904	AI529904	uig3h01.y
C1289	30.6	11.2	719	8	AZ849815	2M0151I21	C1362	30.4	11.1	393	5	BP667496	BP667496	BP667496
C1290	30.6	11.2	723	9	AG611113	Mus muscu	C1363	30.4	11.1	393	5	BY419018	BY419018	BY419018
C1291	30.6	11.2	726	1	AV698319	AV698319	C1364	30.4	11.1	399	1	AI812105	AI812105	tw77C12.x
C1292	30.6	11.2	732	9	CG091823	PUII232TD	C1365	30.4	11.1	412	6	CB093240	CB093240	te82a06.b
C1293	30.6	11.2	734	5	BA470456	BA470456	C1366	30.4	11.1	419	4	BI506035	BI506035	BB170018B
C1294	30.6	11.2	748	7	AW960749	EST372820	C1367	30.4	11.1	423	1	AAV733287	AAV733287	zj41h06.s
C1295	30.6	11.2	754	2	AW960749	EST372820	C1368	30.4	11.1	430	1	AV733287	AV733287	AV733287
C1296	30.6	11.2	757	9	CE489304	tigr-gss-	C1369	30.4	11.1	430	4	RJ064522	RJ064522	RJ064522
C1297	30.6	11.2	774	8	BZ843723	CH240_205	C1370	30.4	11.1	434	1	AU088901	AU088901	AU088901
C1298	30.6	11.2	776	9	BI156366	Danio rer	C1371	30.4	11.1	437	4	BI945737	BI945737	sc66901.y
C1299	30.6	11.2	784	5	BY706221	BY706221	C1372	30.4	11.1	443	2	BB840436	BB840436	BB840436
C1300	30.6	11.2	785	9	CG360221	CGV053TV	C1373	30.4	11.1	444	6	CB911004	CB911004	VVD125B06
C1301	30.6	11.2	798	5	BA470455	BA470455	C1374	30.4	11.1	447	2	BF086482	BF086482	CM0-GN007
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C1303	30.6	11.2	806	9	AG588721	Mus muscu	C1376	30.4	11.1	471	8	AQ811127	AQ811127	HS_5504.B
C1304	30.6	11.2	820	6	CA468446	AGENCOURT	C1377	30.4	11.1	480	5	BY392496	BY392496	BY392496
C1305	30.6	11.2	829	8	BZ138754	Danio rer	C1378	30.4	11.1	482	1	AJ787923	AJ787923	AJ787923
C1306	30.6	11.2	832	9	AG083626	CH230-256	C1379	30.4	11.1	485	8	AQ844268	AQ844268	an29c06.J
C1307	30.6	11.2	840	8	BZ843744	BZ843744	C1380	30.4	11.1	488	7	CN658404	CN658404	TGSEZym3
C1308	30.6	11.2	849	5	BY702608	BY702608	C1381	30.4	11.1	500	1	AU087633	AU087633	AU087633
C1309	30.6	11.2	849	8	BZ980536	BZ980536	C1382	30.4	11.1	503	1	AI950471	AI950471	wq35g11.x
C1310	30.6	11.2	850	7	CO164459	FUDD1_48.D	C1383	30.4	11.1	505	8	AQ691601	AQ691601	HS_5369.A
C1311	30.6	11.2	851	8	CC427947	PUNY30TB	C1384	30.4	11.1	508	1	AJ787923	AJ787923	AJ787923
C1312	30.6	11.2	858	7	CO079226	GR_Ea410	C1385	30.4	11.1	511	8	AZ579058	AZ579058	179112.T7
C1313	30.6	11.2	870	5	BU604888	AGENCOURT	C1386	30.4	11.1	514	2	BF057253	BF057253	7k18A05.x
C1314	30.6	11.2	876	5	BU906920	BU906920	C1387	30.4	11.1	520	4	BM521871	BM521871	ESSU0408
C1315	30.6	11.2	882	5	BQ707597	AGENCOURT	C1388	30.4	11.1	535	1	AV842434	AV842434	AV842434
C1316	30.6	11.2	884	7	CO164532	FUDD1_48.D	C1389	30.4	11.1	545	2	BE511201	BE511201	946058F03
C1317	30.6	11.2	885	9	CC580436	CC580436	C1390	30.4	11.1	551	5	BE749504	BE749504	200458.MA
C1318	30.6	11.2	890	5	BY769562	BY769562	C1391	30.4	11.1	554	6	CA163126	CA163126	SCRLRZ304
C1319	30.6	11.2	896	5	BQ710085	BQ710085	C1392	30.4	11.1	555	6	AZ951345	AZ951345	2M0215E13
C1320	30.6	11.2	896	5	BA431293	BA431293	C1393	30.4	11.1	561	5	BU576461	BU576461	TGSEZym6
C1321	30.6	11.2	897	5	BR431294	BR431294	C1394	30.4	11.1	562	1	AA521672	AA521672	vi29607.r
C1322	30.6	11.2	911	7	CR432749	CR432749	C1395	30.4	11.1	563	8	AX523859	AX523859	AX523859
C1323	30.6	11.2	917	9	CG666768	CG666768	C1396	30.4	11.1	565	5	BX353341	BX353341	HS_5016.B
C1324	30.6	11.2	921	5	BQ708550	BQ708550	C1397	30.4	11.1	567	8	AZ852883	AZ852883	2M0155D20
C1325	30.6	11.2	923	6	CF265753	CF265753	C1398	30.4	11.1	569	6	AU038969	AU038969	AU038969
C1326	30.6	11.2	944	9	CG341974	CG341974	C1399	30.4	11.1	576	8	AD077288	AD077288	MA3-0001U
C1327	30.6	11.2	961	2	BE036341	BE036341	C1400	30.4	11.1	576	8	AQ566956	AQ566956	AQ566956
C1328	30.6	11.2	963	5	BY72154	BY72154	C1401	30.4	11.1	585	4	BJ614768	BJ614768	BJ614768
C1329	30.6	11.2	970	5	CL088352	CL088352	C1402	30.4	11.1	587	8	AZ877344	AZ877344	2M0192F16
C1330	30.6	11.2	972	2	BE037538	BE037538	C1403	30.4	11.1	602	9	CR491016	CR491016	Medicago
C1331	30.6	11.2	978	8	BA471145	BA471145	C1404	30.4	11.1	604	5	BM001195	BM001195	BM001195
C1332	30.6	11.2	979	6	CA471145	CA471145	C1405	30.4	11.1	606	9	CR327039	CR327039	Medicago
C1333	30.6	11.2	987	8	CC418840	CC418840	C1406	30.4	11.1	607	8	AZ234057	AZ234057	RPCI-23-8
C1334	30.6	11.2	988	2	BE036234	BE036234	C1407	30.4	11.1	615	7	CN555700	CN555700	tae15g10.
C1335	30.6	11.2	997	8	CC260964	CC260964	C1408	30.4	11.1	619	9	CR494021	CR494021	Medicago
C1336	30.6	11.2	1000	8	AZ206622	SP_0105_B	C1409	30.4	11.1	624	9	CE140488	CE140488	tigr-gss-
C1337	30.6	11.2	1041	5	BE365011	BE365011	C1411	30.4	11.1					

1412	30.4	11.1	625	8	BH615481	BMSAC302G
1413	30.4	11.1	627	5	EX088299	EX088299
1414	30.4	11.1	630	5	BW029741	BW029741
1415	30.4	11.1	631	8	AZ857058	2M0161P07
1416	30.4	11.1	634	6	CA144524	SCSFR2016
1417	30.4	11.1	639	8	BH615318	BMSAC301G
1418	30.4	11.1	655	3	CR715783	Tetraodon
1419	30.4	11.1	655	9	AG043742	Pan trogl
1420	30.4	11.1	664	9	BX243682	Danio rer
1421	30.4	11.1	666	4	BJ100073	BJ100073
1422	30.4	11.1	675	4	BJ083439	BJ083439
1423	30.4	11.1	676	6	CD407936	Gm. ck3371
1424	30.4	11.1	680	7	CK552006	rsWla0.00
1425	30.4	11.1	681	8	AZ842325	2M0140D18
1426	30.4	11.1	686	9	BX153661	Danio rer
1427	30.4	11.1	688	8	AZ436643	1M0224A05
1428	30.4	11.1	689	9	BX196439	Danio rer
1429	30.4	11.1	695	8	BZ516365	BOMSFS3TF
1430	30.4	11.1	707	8	BZ082327	11e25d10.
1431	30.4	11.1	709	9	BX158905	Danio rer
1432	30.4	11.1	715	8	B00565	CSRL-116a2-
1433	30.4	11.1	724	9	BX225189	Danio rer
1434	30.4	11.1	727	9	BX153753	Danio rer
1435	30.4	11.1	730	9	BX198146	Danio rer
1436	30.4	11.1	732	8	BH508236	BOHLN52TF
1437	30.4	11.1	734	9	CR341025	Medicago
1438	30.4	11.1	744	4	BG963627	602828426
1439	30.4	11.1	748	4	BJ643874	BJ643874
1440	30.4	11.1	750	7	CN321385	AGENCOCURT
1441	30.4	11.1	752	9	BX204766	Danio rer
1442	30.4	11.1	758	9	AG478910	Mus muscu
1443	30.4	11.1	761	9	BX221122	Danio rer
1444	30.4	11.1	768	9	BX174189	Danio rer
1445	30.4	11.1	779	8	BZ598943	BZ598943
1446	30.4	11.1	782	9	BX247173	WHAAT33TR
1447	30.4	11.1	783	9	CF238527	Forward s
1448	30.4	11.1	789	7	CO228657	WS01030.B
1449	30.4	11.1	789	8	BZ387136	EINDJ24TF
1450	30.4	11.1	799	4	BG617410	602615251
1451	30.4	11.1	799	6	CF284577	AGENCOCURT
1452	30.4	11.1	821	9	BX175149	Danio rer
1453	30.4	11.1	822	9	AG574668	Mus muscu
1454	30.4	11.1	832	9	CG335547	Medicago
1455	30.4	11.1	844	9	CG664123	CGNAC83TH
1456	30.4	11.1	854	9	BX177640	Danio rer
1457	30.4	11.1	854	9	CG664134	CGNAC83TV
1458	30.4	11.1	867	9	CG964933	MBEHW96TR
1459	30.4	11.1	878	9	CNS01878	Drosophil
1460	30.4	11.1	886	4	BX358159	GA_Ea000
1461	30.4	11.1	923	9	CNS0508DN	Drosophil
1462	30.4	11.1	933	9	CR220556	Forward s
1463	30.4	11.1	954	9	CL510313	SAIL B27
1464	30.4	11.1	960	9	CG766530	TcB49.2.D
1465	30.4	11.1	1047	9	CNS03842	AL239948
1466	30.4	11.1	1100	7	CGN643169	ILUUMIGEN
1467	30.4	11.1	1138	9	CNS0165L	CH216-65E
1468	30.4	11.1	1200	9	CL106327	ISB1-4631
1469	30.4	11.1	1222	9	AG279416	Mus muscu
1470	30.4	11.1	1223	9	AG279416	CH216-31G
1471	30.4	11.1	1252	9	CL030691	CH216-31G
1472	30.4	11.1	1357	5	BUI379489	603813001
1473	30.4	11.1	1880	9	AG430399	Mus muscu
1474	30.2	11.1	227	5	BUT770194	SUBCID01
1475	30.2	11.1	259	6	CD530279	05I06 Ara
1476	30.2	11.1	259	6	CD533801	33M2 Arab
1477	30.2	11.1	260	7	CF800175	RpL31-V-B
1478	30.2	11.1	275	2	AW103710	Xe83c01.X
1479	30.2	11.1	286	2	BV078926	BB078926
1480	30.2	11.1	301	1	AV099673	AV099673
1481	30.2	11.1	302	7	CF800383	RpL31-XI-
1482	30.2	11.1	320	7	D61771	HUM208F09B
1483	30.2	11.1	330	7	D22650	RIC00738B R
1484	30.2	11.1	337	8	AQ710629	HS_5339_A

ALIGNMENTS

RESULT 1
AUI85777/c
LOCUS AUI85777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens
DEFINITION cDNA clone B02302-019, mRNA sequence.
ACCESSION AUI85777 GI:14623690
VERSION AUI85777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 663)
AUTHORS Sugita,Y., Oshida,T. and Oya,Y.
TITLE Human cDNA sequencing
JOURNAL Unpublished (2001)
COMMENT Contact: Yuji Sugita
Genox Research, Inc.
907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan
Tel: 81-44-797-2281
Fax: 81-44-797-2622
Email: syuji@genox.co.jp, URL: http://www.genox.co.jp.

FEATURES

source
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B02302-019"
/cell_type="Mast cell"
/clone_lib="Homo sapiens Mast cell library (Sugita Y)"

ORIGIN

Query Match 82.5%; Score 225.2; DB 1; Length 663;
Best Local Similarity 95.6%; Pred. No. 1.8e-54;
Matches 262; Conservative 0; Mismatches 7; Indels 5; Gaps 3;
QY 1 ATGACATTTTCTGTCTATTATTATTGTTGGTATGGAAGCTATTGG-AGATCCAA 59
DB 507 ATGACATTTTCTGTCTATTATTATTGTTGGTATGGAAGCTATTGGNAGATCCA 448
QY 60 TTCAGGAGCAACATTTGGAGATGGCTACTTCTATCAAGAATAAAGAGACCACAG 119
DB 447 TTCAGNAG--CACCATTGAGATGGCTACTTCTATCAAGAATAAAGAGACCACAG 391
QY 120 TCAACCCACACAATCATCTTTAGAGACAGTGTGACTCCTTACCAAGCTGTCAAAACAC 179
DB 390 TCAACCCACACATTCATCTTTAGAGACAGTGTGACTCCTTACCAAGCTGTCAAAACAC 332
QY 180 AGGCAAGGCATAGTTTAAGACCGAACTTGTACTCAAGAGGGTTAAATCTTGGTGTGA 239
DB 331 AGGCAAGGCATAGTTTAAGAGCGGAATCTTGACTCAAGAGGGTTAAATCTTGGTGTGA 272

QY 240 AGCTGGGGCAGGGGTGTAAGAAAAACACTTAG 273
|||||
Db 271 AGCTGGGGCAGGGGTGTAAGAAAAACACTTAG 238
|||||

RESULT 2
CB958894
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB958894 800 bp mRNA linear EST 29-APR-2003
AGENCOURT 13785021 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30352338 5', mRNA sequence.
CB958894
CB958894.1 GI:30215010
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LILNL at:
<http://image.llnl.gov>
Plate: NDCM151 row: e column: 19
High quality sequence stop: 488.
Location/Qualifiers
1..800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352338"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattagggc); Site_2: SfiI (ggcgctgggc);
Library is oligo-dr primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCCGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 64.9%; Score 177.2; DB 6; Length 800;
Best Local Similarity 98.4%; Pred. No. 1.6e-40;
Matches 179; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGACATTTTCTGCTCACTATTATTATGTTGGTATGTAAGCTATTGGAGATCCAAAT 60
|||||
Db 342 ATGACATTTTCTGCTCACTATTATTATGTTGGTATGTAAGCTATTGGAGATCCAAAT 401
|||||

QY 61 TCAGAGACACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAACACACAGT 120
|||||
Db 402 TCAGAGACACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAACACACAGT 461
|||||

QY 121 CAACCCACACATCATCTTTAGAACAGTGTGACTCTCTACCAAGCTGTCAAAACACACA 180
|||||
Db 462 CAACCCACACATCATCTTTAGAACAGTGTGACTCTCTACCAAGCTGTCAAAACACAC 521
|||||

QY 181 GG 182
|||

Db 522 GG 523

RESULT 3
BI018962/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI018962 659 bp mRNA linear EST 14-JUN-2001
IL3-MT0267-050101-437-A02 MT0267 Homo sapiens cDNA, mRNA sequence.
BI018962
BI018962.1 GI:14425592
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 659)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-MT0267-050101-437-A02&t3=2001-01-05&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 639.
Location/Qualifiers
1..659
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0267"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 50.7%; Score 138.4; DB 4; Length 659;
Best Local Similarity 99.3%; Pred. No. 3.1e-29;
Matches 139; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 43 GCTATTTGGAGATCCAAATTCAGGAAGCAACATTCAGGATGGCTACTTTCTATCAAGA 102
|||||
Db 572 GCTATTTGGAGTCCAAATTCAGGAAGCAACATTCAGGATGGCTACTTTCTATCAAGA 513
|||||

QY 103 AATAAGAGAACCAAGTCACACCAATCATCTTTTAGAAGACAGTGTGACTCTTACC 162
|||||
Db 512 AATAAGAGAACCAAGTCACACCAATCATCTTTTAGAAGACAGTGTGACTCTTACC 453
|||||

QY 163 AAAGCTGTCAAAACACAGG 182
|||||
Db 452 AAAGCTGTCAAAACACAGG 433
|||||

```

RESULT 4
AZ121459/c
LOCUS          663 bp      DNA      linear      GSS 12-MAY-2000
DEFINITION    RPCI-23-30A15.TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,
                genomic survey sequence.
ACCESSION     AZ121459
VERSION       AZ121459.1 GI:7798387
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 663)
AUTHORS       Zhao,S., Nieman,M., Feldblyum,T., Malek,J., Shatsman,S., de
                Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
                Jong,P. and Fraser,C.M.
TITLE        Mouse BAC End Sequences from Library RPCI-23
JOURNAL
COMMENT      Unpublished (1999)
                Other_GSSs: RPCI-23-30A15.TJ
                Contact: Shaying Zhao
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel: 301 838 0200
                Fax: 301 838 0208
                Email: szhao@tigr.org
                Clones are derived from the mouse BAC library RPCI-23. For BAC
                library availability, please contact Pieter de Jong
                (pieter@dejong.med.buffalo.edu). Clones may be purchased from
                BACPAC resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
                or from Resea ch Genetics (info@resgen.com). BAC end page:
                http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                Plate: 30 row: A column: 15
                Seq primer: T7
                Class: BAC ends.
FEATURES             source
    Location/Qualifiers
        1..663
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="RPCI-23-30A15"
            /sex="Female"
            /lab_host="DH10B"
            /clone_lib="RPCI-23"
            /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
            EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
            brain genomic DNA was isolated and partially digested
            with a combination of EcoRI and EcoRI Methylase. Size
            selected DNA was cloned into the pBACe3.6 vector at the
            EcoRI sites. The ligation products were transformed into
            DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match          44.2%; Score 120.6; DB 8; Length 663;
Best Local Similarity 73.3%; Pred. No. 4.6e-24;
Matches 184; Conservative 0; Mismatches 59; Indels 8; Gaps 2;

QY      8  TTTTCTGCTACTATTATTATTGTTGGTATGGAAGCTATTGGAGATCCCAATTCAGGAA 67
DB      250 TTTTCTGCTACTATTGCTGTCGTGACGTATGAGCATTTTGGTGACACATTCAGGGA 191
QY      68  GCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAGCTCAACCCA 127
DB      150  GAAATCCAGAGAGAGAAAACAACTTCTATCAAGAAATAAGAGAACCCACA---AGCCCA 134
QY      128  CACATCATCTTTAGAGACAGTGTGATCTCTACCAAGCTGTCAAAACCAGCAGCAAGG 187
DB      133  CAGAATCATCTTTAGATGAGAGGTGGCTCCCTCCCAAGGCATCCCAAACTACAGCAAGG 74
QY      188  GCATAGTTAAAGGA-----CGGAATCTTGACTCAAGAGGTTAAATTTCTGGTGTGAAGC 242
DB      73  GCAGCAGCAAGGAAGCAATGGGATCCCGGATTCAGAGGTTTCATTTCTGGTGTGCTGAGGC 14

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QY      243  CTGGGGCAGGG 253
DB      13  CTGGGGTGGGG 3

RESULT 5
AV721179
LOCUS          673 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION    AV721179 HTB Homo sapiens cDNA clone HTBAKFl1 5', mRNA sequence.
ACCESSION     AV721179
VERSION       AV721179.1 GI:10818331
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 673)
AUTHORS       Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
                Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
                Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
                Chen,J., Chen,Z. and Han,Z.
TITLE        Homo sapiens cDNA HTB clones
JOURNAL
COMMENT      Unpublished (2000)
                Contact: Zeguang Han
                Chinese National Human Genome Center at Shanghai
                351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                201203, P. R. China
                Tel: 86-21-50801919(ex.45)
                Fax: 86-21-50801922
                Email: hanzg@chgc.sh.cn
                This clone is available at CHGC in Shanghai.
FEATURES             source
    Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HTBAKFl1"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /clone_lib="HTB"
            /note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2:
            XhoI"
ORIGIN
Query Match          44.0%; Score 120; DB 1; Length 673;
Best Local Similarity 100.0%; Pred. No. 6.9e-24;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      63  AGGAAGCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAGTCA 122
DB      1  AGGAAGCAACACATTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAGTCA 60
QY      123  ACCCACACAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCACAGG 182
DB      61  ACCCACACAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCACAGG 120

RESULT 6
CB420818
LOCUS          582 bp      mRNA      linear      EST 25-MAR-2003
DEFINITION    593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION     CB420818
VERSION       CB420818.1 GI:29187264
KEYWORDS      EST.
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
REFERENCE     1 (bases 1 to 582)
AUTHORS       Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,

```

Wray, J.E. and Keele, J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: FQY8014 row: B column: 7
 Seq primer: GTATACGACTCACTATAGG.
 Location/Qualifiers
 1. .582

FEATURES

source

/organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 6BOV"
 /notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with RNA pooled from multiple tissues
 including liver, lung, hypothalamus, pituitary, and
 placenta/endometrium."

ORIGIN

Query Match 38.4%; Score 104.8; DB 6; Length 582;
 Best Local Similarity 84.3%; Pred. No. 1.9e-19;
 Matches 118; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 43 GCTATTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTACTTTCTATCAAGA 102
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 Db 244 GGTATTGGAGATCCAGTTCCAGGGAACAACCTCTTGAAGAGTGACAGCTTTCATCAAGA 303
 |||||
 QY 103 AATAAGAGAACACACAGTCAACCCACACATATCATCTTTAGAACAGTGTGATCTCTACC 162
 |||||
 Db 304 AATAAGAGAACACAGTCAACCCACACATATCATCTTTAGAACAGTGTGATCTCTACC 363
 |||||
 QY 163 AAGCTGTCAAAACACACAGG 182
 |||||
 Db 364 AGGCTCTCAGACCAAGG 383
 |||||

RESULT 7
 BI107684
 LOCUS
 DEFINITION
 602891529F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036647 5',
 mRNA sequence.
 BI107684
 VERSION
 KEYWORDS
 SOURCE
 Mus musculus
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 855)
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11101 row: j column: 08
 High quality sequence start: 27
 High quality sequence stop: 825.

FEATURES

source

Location/Qualifiers
 1. .855
 /organism="Mus musculus"
 /mol_type="mRNA"
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 /tissue_type="spontaneous tumor, metastatic to mammary.
 Stem cell origin."
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu29"
 /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 27.0%; Score 73.8; DB 4; Length 855;
 Best Local Similarity 75.2%; Pred. No. 1.9e-10;
 Matches 106; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
 QY 42 AGCTATTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTACTTTCTATCAAG 101
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 Db 310 AGCATTTATGGAGACACATTTTCAGGAGAAATCCAGGAAGAGAAACACATTTCCCATCAAG 369
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 QY 102 AATAAGAGAACACACAGTCAACCCACACATCTTTAGAGACAGTGTGATCTCTAC 161
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 Db 370 AATAAGAGAACACACA--AGCCACAGATCATCTTTAGATGAGAAGTGCTGCTCCTC 426
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 QY 162 CAAAGCTGTCAAAACACACAGG 182
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 Db 427 CAAGGCATCCCAAACTACAGG 447
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RESULT 8

BI547544

LOCUS

DEFINITION

BI547544

VERSION

KEYWORDS

SOURCE

Mus musculus

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 363)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Khanpin, A., Matsuda, H.,

Batalow, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Sempole, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wieming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arkawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 PUBMED
 12466851
 COMMENT
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 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imamura, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1. 363
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 /db_xref="taxon:10090"
 /clone="F730119008"
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 +ve dendritic cells"
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 Best Local Similarity 72.7%; Pred. No. 0.0018;
 Matches 64; Conservative 0; Mismatches 24; Indels 0; Gaps 0
 QY 8 TTTTTCGTCACTATATATTGTTGGTATGTGAGCTATTGGAGATCCAAATTCAGAA 67
 Db 276 TTTTTCGTCACTATTGCTGTGTCGACGATGAAGCATTTTGGCGACAAATTCAGGA 335
 QY 68 GCAACACATTGGGAATGCTACTTCT 95
 Db 336 GAAATCCAGAGGAAAGACAACTTCT 363
 RESULT 9
 BY536666 419 bp mRNA linear EST 14-DEC-2000
 LOCUS
 BY536666 RIKEN full-length enriched, NOD-derived CD11c +ve
 dendritic cells Mus musculus cDNA clone F630311P20 3', mRNA
 sequence.

assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
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Best Local Similarity 72.7%; Pred. No. 0.0019;
Matches 64; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 8 TTTTCTGTCACATATTATTGTTGGTATGTGAAGCTATTGGAGATCAATTCAGGAA 67
Db TTTTCTGTCACATATTATTGTTGGTATGTGAAGCTATTGGAGATCAATTCAGGAA 67
Qy 68 GCAACATGCGAGATGGCTACTTTCT 95
Db GAAATCCAGAGAGAGAAAGACAACTTCT 419

RESULT 10
BW159356/c
LOCUS
DEFINITION
822 bp mRNA linear EST 03-NOV-2002
BW159356 Nori Satoh unpublished cdna library, gonad Ciona
intestinalis cdna clone rcigd037h12 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE
1 (bases 1 to 822)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
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Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source
1..822
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcigd037h12"
/tissue_type="gonad"
/clone_lib="Nori Satoh unpublished cdna library, gonad"
ORIGIN

Query Match 14.9%; Score 40.8; DB 5; Length 822;
Best Local Similarity 50.5%; Pred. No. 0.76;
Matches 99; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
Qy 4 ACATTTTCTGTCACATATTATTGTTGGTATGTGAAGCTATTGGAGATCAATTC 63
Db ATATTAAATTTAACTCTTTTATATTAATTTGGTATGTTGATCTTTTCGTTTACAA 366
Qy 64 GGAAGCAACATGCGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACACACAGTCAA 123
Db TCTAGAAAAGAAACAATATCTCTGCACGCTTTACAAAACATATCATAGAAGAACCACTTTA 306

Qy 124 CCCACACAATCATCTTTTAGAAGACAGGTGTGACTCTCTACCAAGCTGTCAAAACACACAGGC 183
Db TCCAAACTTTTCTATCATATAAATCTCATATCACTGTTAAACTGAITTAATTTAATTC 246
Qy 184 AAGGCATAGTTAAAG 199
Db AAGTGCAGATACAAAG 230

RESULT 11
BP117361
LOCUS
DEFINITION
450 bp mRNA linear EST 03-APR-2003
BP117361 ce-- Bombyx mori cdna clone ce--0217, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bombyx mori (domestic silkworm)
Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.

REFERENCE
1 (bases 1 to 450)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cdna (Mita, K. 2003)
Unpublished (2003)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmita@nias.affrc.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3').

FEATURES
source

Location/Qualifiers
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/note="mixed stages from 5th instar larva to pupa"

ORIGIN

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Best Local Similarity 52.0%; Pred. No. 0.79;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 97 TCAAGAAATPAAAGAGAACACAGTCAACCCACACATCATCTTTAGAACAGTGTGACT 156
Db TCAATTTTTCAGCAGCAGAGACTTCGAATTCACCTCACCAGCTTTAGAAAGAGATATCA 235
Qy 157 CCTACCAAGCTGTCAAAACACAGCAGGCGCATAGTTAAAGGACGGAACTTGTACTCA 216
Db GTGAAGAAATCTTTAAATTCACAGAACTACAGCAAAATAATCCACTGAACATGAGATA 295
Qy 217 AGAGGGTTAAATCTTGGTGTCTGAAGCTGGGCGAGGGGTGTAAAGAAACAACTT 271
Db ACGGATTTAGTGTAGTACTAACCGCTCTCCCACTAACTAAGGCTATACAT 350

RESULT 12
AV882594/c

LOCUS
DEFINITION
516 bp mRNA linear EST 08-NOV-2001
AV882594 Nori Satoh unpublished cdna library, larva Ciona
intestinalis cdna clone rcilv29904 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE
1 (bases 1 to 516)

AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
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Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
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Location/Qualifiers
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ORIGIN

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Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 ACATTTTTCGTGCACATTAATTATTTGGTATGTGAAGCTATTTGGAGATCCCAATTCA 63
Db 326 ATATTAATTTTAACTCCTTTTATATAATTAGTAGTGTGATCGTTTCGTTTACAATAGA 267
QY 64 GGAGCACACATTGGGAATGGCTACTTCTATCAAGAAATAAGAGAACACACAGTCAA 123
Db 266 TCTAGAAAGAAACAATATCTCTGCACGCTTTACAAAACCTATCATAGAACCACAACTTTA 207
QY 124 CCCACAAATCATCTTTAGAGACAGTGTGACTCTCAACAAAGCTGTCAAAACACACAGGC 183
Db 206 TCCAAACTTTTCTATCAATAATCTCATATCACTGTGTTAAACTGATGTTAAATTTAATTC 147
QY 184 AAGGCATAGTTAAAG 199
Db 146 AAGTCAGATACAAAG 131

RESULT 13
AV996730 602 bp mRNA linear EST 15-MAR-2002
LOCUS AV996730 Nori Satoh unpublished cDNA library, larva Ciona
DEFINITION intestinalis cDNA clone cilv29g04 5', mRNA sequence.

ACCESSION AV996730
VERSION AV996730.1 GI:19488064
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 602)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..602
Location/Qualifiers
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ORIGIN

Query Match 14.4%; Score 39.2; DB 1; Length 602;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 ACATTTTTCGTGCACATTAATTATTTGGTATGTGAAGCTATTTGGAGATCCCAATTCA 63
Db 184 ATATTAATTTTAACTCCTTTTATATAATTAGTAGTGTGATCGTTTCGTTTACAATAGA 243
QY 64 GGAGCACACATTGGGAATGGCTACTTCTATCAAGAAATAAGAGAACACACAGTCAA 123
Db 244 TCTAGAAAGAAACAATATCTCTGCACGCTTTACAAAACCTATCATAGAACCACAACTTTA 303
QY 124 CCCACAAATCATCTTTAGAGACAGTGTGACTCTCAACAAAGCTGTCAAAACACACAGGC 183
Db 304 TCCAAACTTTTCTATCAATAATCTCATATCACTGTGTTAAACTGATGTTAAATTTAATTC 363
QY 184 AAGGCATAGTTAAAG 199
Db 364 AAGTCAGATACAAAG 379

RESULT 14

LOCUS BW404792 703 bp mRNA linear EST 28-MAY-2004
DEFINITION BW404792 Yutaka Satou unpublished cDNA library, embryo whole animal
Ciona intestinalis cDNA clone ciem846h18 3', mRNA sequence.

ACCESSION BW404792
VERSION BW404792.1 GI:47820620
KEYWORDS EST.
SOURCE Ciona intestinalis

ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 703)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
AUTHORS Expressed genes in Ciona intestinalis (2004)
TITLE Unpublished (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Yutaka Satou
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Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
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FEATURES
source
1..703
Location/Qualifiers

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/clone="ciem846h18"
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ORIGIN

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Best Local Similarity 50.0%; Pred. No. 2.2;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 ACATTTTTCGTGCACATTAATTATTTGGTATGTGAAGCTATTTGGAGATCCCAATTCA 63
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QY 64 GGAGCACACATTGGGAATGGCTACTTCTATCAAGAAATAAGAGAACACACAGTCAA 123
Db 332 TCTAGAAAGAAACAATATCTCTGCACGCTTTACAAAACCTATCATAGAACCACAACTTTA 273
QY 124 CCCACAAATCATCTTTAGAGACAGTGTGACTCTCAACAAAGCTGTCAAAACACACAGGC 183

Search completed: December 2, 2004, 02:36:59
Job time : 1554.11 secs

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OM nucleic - nucleic search, using sw model

Run on: December 1, 2004, 23:10:21 ; Search time 3773.98 Seconds
(without alignments)
8934.210 Million cell updates/sec

Title: US-09-989-293A-376
Perfect score: 713
Sequence: 1 aatatatcatctattatca.....tgggtcccaaggaaaaaaa 713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : GenEmbl.*

1: gb.ba.*

2: gb.btg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	713	100.0	713	6	AR252626 Sequence
2	713	100.0	713	6	AX055452 Sequence
3	713	100.0	713	6	AX403489 Sequence
4	713	100.0	713	6	AX464340 Sequence
5	713	100.0	713	6	AX358685 Sequence
6	705.6	99.0	165414	9	AC024224 Homo sapi
7	590.2	82.8	240864	2	AC006510 Homo sapi
8	186	26.1	221471	2	AC138620 Mus muscu
9	147.6	20.7	273867	2	AC112033 Rattus no
10	142	19.9	881	9	AF400602 Homo sapi
11	140	19.6	625	9	AF400597 Homo sapi
12	140	19.6	741	6	E21012 Novel membr
13	140	19.6	744	9	AF400595 Homo sapi
14	140	19.6	744	9	AF026769 Homo sapi
15	140	19.6	787	9	AF400601 Homo sapi
16	140	19.6	1018	6	BD136999 Isolated
17	140	19.6	1153	6	AX664609 Sequence
18	140	19.6	1153	9	HS4312373 Homo sapi
19	140	19.6	1606	6	CQ779237 Sequence

20	140	19.6	1606	9	AF313468 Homo sapi
21	134	18.8	534	6	E21014 Novel membr
22	130.4	18.3	744	9	AF508729 Macaca mu
23	83	11.6	85	6	AX312349 Sequence
24	83	11.6	85	6	BD047882 Sequence
25	77.6	10.9	2298	6	CQ779241 Sequence
26	77.6	10.9	2298	6	BD056525 Unique de
27	77.6	10.9	2298	10	AF262985 Mus muscu
28	76	10.7	735	10	AY534909 Mus muscu
29	75.4	10.6	1329	10	BC027742 Mus muscu
30	75.2	10.5	528	6	BD056528 Unique de
31	56.2	7.9	170627	2	AC125567 Rattus no
32	54.2	7.6	9098	3	AF465306 Dictyoste
33	54.2	7.5	33321	3	AC116986 Dictyoste
34	53.6	7.5	220114	10	AC115804 Mus muscu
35	53.6	7.5	343010	2	AC120175 Mus muscu
36	53	7.4	37360	3	U41019 Caenorhabdi
37	53	7.4	132749	3	AC006778 Caenorhab
38	52.2	7.3	159347	2	BX470105 Danio rer
39	51.4	7.2	209873	2	AC024966 Mus muscu
40	50.8	7.1	218979	2	AC102424 Mus muscu
41	50.6	7.1	4601	3	DMU11584 Drosophila
42	50.6	7.1	19517	3	DMU37541 Drosophila
43	50.4	7.1	205429	2	AC005506 Plasmodiu
44	50.4	7.1	253132	3	AE014846 Plasmodiu
45	50.2	7.0	205919	2	BX470184 Danio rer
46	50	7.0	199551	2	AC006281 Plasmodiu
47	50	7.0	250331	3	AE014845 Plasmodiu
48	49.8	7.0	203030	10	AL603792 Mouse DNA
49	49.8	7.0	213872	2	AC023441 Mus muscu
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52	49.4	6.9	155350	9	CNS06C7U_ Human DNA
53	49.2	6.9	74012	9	AL336159 Human chr
54	49.2	6.9	165252	2	AC016241 Homo sapi
55	49.2	6.9	173814	9	AC093840 Homo sapi
56	49.2	6.9	249943	3	AE014823 Plasmodiu
57	49	6.9	90018	10	AC092509 Mus muscu
58	49	6.9	302156	3	AC116977 Dictyoste
59	48.8	6.8	209843	2	CR382300 Danio rer
60	48.6	6.8	110000	2	PFMAL8P1_10 Continuation (11 o
61	48.6	6.8	190665	5	BX470086 Zebrafish
62	48.4	6.8	110000	2	AC099306_5 Continuation (6 of
63	48.4	6.8	110000	2	AL954295_0 Danio rer
64	48.4	6.8	117189	2	AC147547 Rattus no
65	48.4	6.8	166715	9	AC011294 Homo sapi
66	48.4	6.8	220737	2	AC128459 Rattus no
67	48.4	6.8	266766	2	AC094770 Rattus no
68	48.2	6.8	192865	5	AL845282 Zebrafish
69	48.2	6.8	250029	3	AE014838 Plasmodiu
70	48	6.7	110000	3	PFMAL1P2_0 Homo sapi
71	48	6.7	164708	2	BX927247 Danio rer
72	48	6.7	196294	5	BX088581 Zebrafish
73	48	6.7	273275	3	AE014828 Plasmodiu
74	47.8	6.7	13594	3	AE001367 Plasmodiu
75	47.8	6.7	146112	2	AC150300 Atelerix
76	47.8	6.7	153588	9	AC010533 Homo sapi
77	47.8	6.7	183151	5	CR381646 Zebrafish
78	47.6	6.7	12590	6	AX346822 Sequence
79	47.6	6.7	197054	2	CR450840 Danio rer
80	47.6	6.7	250054	2	BX901955 Danio rer
81	47.6	6.7	253924	3	AE014822 Plasmodiu
82	47.4	6.6	143903	2	CR391976 Danio rer
83	47.2	6.6	110000	2	PFMAL13_05 Continuation (6 of
84	47.2	6.6	129989	2	AC145806 Xenopus t
85	47.2	6.6	146285	9	AC005083 Homo sapi
86	47	6.6	166617	2	CR450847 Danio rer
87	47	6.6	172254	2	BX005170 Mus muscu
88	47	6.6	221029	2	AC140292 Mus muscu
89	46.8	6.6	91074	10	AL669888 Mouse DNA
90	46.8	6.6	169546	2	AC004157 Plasmodiu
91	46.8	6.6	180525	10	AC107834 Mus muscu
92	46.8	6.6	212304	2	AC099975 Mus muscu

93	46.8	6.6	250707	3	AE014848	AE014848 Plasmidii	C 166	45.2	6.3	10048	8	MSNOD25	X13287 Medicago sa
94	46.8	6.6	250884	10	AC122879	Mus muscu	C 167	45.2	6.3	96924	5	EX890635	EX890635 Zebrafish
95	46.8	6.6	259299	10	AC116383	Mus muscu	C 168	45.2	6.3	113421	5	EX284637	EX284637 Zebrafish
C 96	46.6	6.5	7218	6	I66494	Sequence 14	169	45.2	6.3	134768	5	EX537293	EX537293 Zebrafish
C 97	46.6	6.5	169142	2	EX119972	Danio rer	170	45.2	6.3	175603	10	AC115301	AC115301 Homo sapi
C 98	46.6	6.5	228633	5	EX649600	Zebrafish	171	45.2	6.3	213056	9	AC103590	AC103590 Homo sapi
C 99	46.4	6.5	176837	2	CR392355	Danio rer	C 172	45.2	6.3	252394	3	AE014833	AE014833 Plasmidii
C 100	46.4	6.5	184851	2	AC144748	Pan trogl	C 173	45	6.3	5762	3	PFASBP86A	L34027 Plasmidii
C 101	46.4	6.5	250195	3	AE014831	Plasmidii	C 174	45	6.3	47573	3	AF030694	AF030694 Plasmidii
C 102	46.4	6.5	335913	6	AX196295	Sequence	C 175	45	6.3	76568	3	MBREV	AF380533 Monobiga
C 103	46.4	6.5	335913	6	AX196296	Sequence	C 176	45	6.3	145253	9	AC006329	AC006329 Homo sapi
C 104	46.2	6.5	66303	9	AX70173	Human DNA	C 177	45	6.3	146775	10	AC145552	AC145552 Mus muscu
C 105	46.2	6.5	152580	5	EX005400	Zebrafish	C 178	45	6.3	166431	10	AC144624	AC144624 Mus muscu
C 106	46.2	6.5	158162	2	AC139232	Mus muscu	C 179	45	6.3	184903	2	AC117846	AC117846 Rattus no
C 107	46.2	6.5	250713	3	AE014850	Plasmidii	C 180	45	6.3	189158	2	CR385084	CR385084 Danio rer
C 108	46.2	6.5	259995	2	AC113601	Mus muscu	C 181	45	6.3	202382	2	AC009618	AC009618 Homo sapi
C 109	46.2	6.5	349418	3	CR382398	Plasmidii	C 182	45	6.3	206470	2	AC135811	AC135811 Rattus no
C 110	46	6.5	7041	6	AX344659	Sequence	C 183	45	6.3	208387	9	CNS01DX8	AL139165 Human chr
C 111	46	6.5	113713	2	AF212833	Homo sapi	C 184	45	6.3	208391	9	CNS01DWI	AL137226 Human chr
C 112	46	6.5	114875	9	AC090281	Homo sapi	C 185	45	6.3	251551	3	AE014844	AE014844 Plasmidii
C 113	46	6.5	138653	9	AL445431	Human DNA	C 186	45	6.3	253924	3	AE014822	AE014822 Plasmidii
C 114	46	6.5	158065	10	AC138768	Mus muscu	C 187	45	6.3	272677	2	AC097289	AC097289 Rattus no
C 115	46	6.5	164399	3	PFMAL3P6	Sequence	C 188	45	6.3	334593	2	AC113743	AC113743 Rattus no
C 116	46	6.5	171868	9	AX359697	Human DNA	C 189	44.8	6.3	100994	9	HSJ154G14	AL121964 Human DNA
C 117	46	6.5	174347	9	AC008066	Homo sapi	C 190	44.8	6.3	100994	9	HSJ154G14	AL121964 Human DNA
C 118	46	6.5	189616	2	AC121093	Mus muscu	C 191	44.8	6.3	157511	9	AC074348	AC074348 Homo sapi
C 119	46	6.5	196124	2	AC135684	Rattus no	C 192	44.8	6.3	157591	2	EX232068	EX232068 Homo sapi
C 120	46	6.5	222714	2	AC125779	Rattus no	C 193	44.8	6.3	161161	2	CR354544	CR354544 Danio rer
C 121	46	6.5	223122	2	AC111532	Rattus no	C 194	44.8	6.3	180558	10	AC121840	AC121840 Mus muscu
C 122	46	6.5	231092	2	AC148019	Mus muscu	C 195	44.8	6.3	186780	2	AC132226	AC132226 Mus muscu
C 123	46	6.5	231965	2	AC098665	Rattus no	C 196	44.8	6.3	193192	5	EX004842	EX004842 Zebrafish
C 124	46	6.5	238060	10	AC148336	Mus muscu	C 197	44.8	6.3	200469	2	AL161435	AL161435 Homo sapi
C 125	46	6.5	242465	2	AC128332	Rattus no	C 198	44.8	6.3	202551	2	EX936451	EX936451 Danio rer
C 126	46	6.5	243377	2	AC110661	Rattus no	C 199	44.8	6.3	212864	3	AE017682	AE017682 Mus muscu
C 127	46	6.5	245450	2	AC095889	Rattus no	C 200	44.8	6.3	250663	3	AE014826	AE014826 Plasmidii
C 128	46	6.5	289989	2	AC099595	Mus muscu	C 201	44.8	6.3	331039	3	AC116979	AC116979 Dictyoste
C 129	46	6.5	293431	2	PFMAL13P4	Plasmidii	C 202	44.6	6.3	71184	8	AP001298	AP001298 Arabidops
C 130	45.8	6.4	155553	2	AC102214	Mus muscu	C 203	44.6	6.3	113157	10	AL840640	AL840640 Mouse DNA
C 131	45.8	6.4	168526	10	AC125185	Mus muscu	C 204	44.6	6.3	125122	2	AC115903	AC115903 Mus muscu
C 132	45.8	6.4	168587	2	CR382372	Danio rer	C 205	44.6	6.3	156114	2	AL929495	AL929495 Danio rer
C 133	45.8	6.4	180395	5	AL844152	Zebrafish	C 206	44.6	6.3	160534	2	CR450837	CR450837 Danio rer
C 134	45.8	6.4	182524	10	AC120153	Mus muscu	C 207	44.6	6.3	163447	2	AC102741	AC102741 Mus muscu
C 135	45.8	6.4	195422	2	CR450745	Danio rer	C 208	44.6	6.3	166353	5	EX323090	EX323090 Zebrafish
C 136	45.6	6.4	84550	3	PFMAL1P2	Continuation (4 of	C 209	44.6	6.3	167862	9	AC011966	AC011966 Homo sapi
C 137	45.6	6.4	110000	2	EX890561	Danio rer	C 210	44.6	6.3	169067	5	AL929396	AL929396 Zebrafish
C 138	45.6	6.4	110000	2	PFMAL13P0	Plasmidii	C 211	44.6	6.3	172376	2	EX640588	EX640588 Danio rer
C 139	45.6	6.4	125787	9	AL645820	Human DNA	C 212	44.6	6.3	181967	2	CR677513	CR677513 Danio rer
C 140	45.6	6.4	125787	9	HSJ13817A	Human DNA	C 213	44.6	6.3	190708	2	CR381533	CR381533 Danio rer
C 141	45.6	6.4	153876	2	EX571709	Danio rer	C 214	44.6	6.3	191272	2	CR376745	CR376745 Danio rer
C 142	45.6	6.4	162258	9	AC105748	Homo sapi	C 215	44.6	6.3	192707	2	AC130824	AC130824 Mus muscu
C 143	45.6	6.4	162515	2	AC132239	Mus muscu	C 216	44.6	6.3	192929	2	AC005505	AC005505 Plasmidii
C 144	45.6	6.4	170534	2	CR391918	Danio rer	C 217	44.6	6.3	200179	5	EX950183	EX950183 Zebrafish
C 145	45.6	6.4	187685	2	AC126269	Mus muscu	C 218	44.6	6.3	216381	10	AC120138	AC120138 Mus muscu
C 146	45.6	6.4	197620	9	AF003905	Sequence	C 219	44.6	6.3	217817	5	EX511298	EX511298 Zebrafish
C 147	45.6	6.4	234718	2	AC139323	Mus muscu	C 220	44.6	6.3	218369	2	AC122351	AC122351 Mus muscu
C 148	45.6	6.4	249943	3	AE014823	Plasmidii	C 221	44.6	6.3	230756	2	AC109986	AC109986 Rattus no
C 149	45.6	6.4	337203	3	CR382401	Plasmidii	C 222	44.6	6.3	234431	2	AC130025	AC130025 Rattus no
C 150	45.4	6.4	110807	10	AP003184	Mus muscu	C 223	44.6	6.3	264321	10	AL807762	AL807762 Mouse DNA
C 151	45.4	6.4	119996	9	AC006155	Homo sapi	C 224	44.4	6.2	640	5	AY130978	AY130978 Cygnus dna
C 152	45.4	6.4	11166	10	AC122423	Mus muscu	C 225	44.4	6.2	1675	6	CO414205	CO414205 Sequence
C 153	45.4	6.4	169838	10	AL713861	Mouse DNA	C 226	44.4	6.2	6268	9	HSM803505	HSM803505 Homo sapi
C 154	45.4	6.4	249671	2	AC130977	Rattus no	C 227	44.4	6.2	6448	9	HSM804585	HSM804585 Homo sapi
C 155	45.4	6.4	250022	3	AE014824	Plasmidii	C 228	44.4	6.2	6497	6	Q0798103	Q0798103 Sequence
C 156	45.4	6.4	254208	2	AC132689	Rattus no	C 229	44.4	6.2	27031	1	AY220730	AY220730 Staphyloc
C 157	45.4	6.4	272636	2	AC108647	Rattus no	C 230	44.4	6.2	76121	9	AC008463	AC008463 Homo sapi
C 158	45.4	6.4	276523	10	AC012382	Mus muscu	C 231	44.4	6.2	110000	3	PFMAL13_03	PFMAL13_03 Continuation (4 of
C 159	45.4	6.4	300054	2	AC125268	Rattus no	C 232	44.4	6.2	110000	3	AC116984	AC116984 Continuation (5 of
C 160	45.4	6.4	337732	2	AC105843	Rattus no	C 233	44.4	6.2	115863	9	HS268D13	HS268D13 Human DNA
C 161	45.2	6.3	832	6	AR415176	Sequence	C 234	44.4	6.2	158443	10	MMHC214C16	MMHC214C16 Mouse maj
C 162	45.2	6.3	832	6	AX972010	Sequence	C 235	44.4	6.2	159179	10	MMHC322F16	MMHC322F16 Mouse maj
C 163	45.2	6.3	832	6	BD110729	EST and e	C 236	44.4	6.2	179818	9	AC012339	AC012339 Homo sapi
C 164	45.2	6.3	1141	6	AX083744	Sequence	C 237	44.4	6.2	181102	9	AC090058	AC090058 Homo sapi
C 165	45.2	6.3	1141	6	AX083744	Sequence	C 238	44.4	6.2	185651	2	AP001090	AP001090 Homo sapi

C 239	44.4	6.2	189963	2	AC023376	AC023376 Homo sapi	C 312	43.6	6.1	127945	9	AC074033	AC074033 Homo sapi
C 240	44.4	6.2	195400	2	AC119022	AC119022 Rattus no	C 313	43.6	6.1	139409	9	AC069181	AC069181 Homo sapi
C 241	44.4	6.2	201659	2	AC146419	AC146419 Pan trogl	C 314	43.6	6.1	143786	3	AC024859	AC024859 Caenorhab
C 242	44.4	6.2	217741	2	AC131587	AC131587 Mus muscu	C 315	43.6	6.1	147681	3	AC027532	AC027532 Homo sapi
C 243	44.4	6.2	226594	10	AC087216	AC087216 Mus muscu	C 316	43.6	6.1	149795	10	AC125173	AC125173 Mus muscu
C 244	44.4	6.2	269040	2	AC099002	AC099002 Rattus no	C 317	43.6	6.1	153244	5	EX784022	EX784022 Zebrafish
C 245	44.2	6.2	33473	9	AL603751	AL603751 Human DNA	C 318	43.6	6.1	158621	9	AC092951	AC092951 Homo sapi
C 246	44.2	6.2	65581	9	HS037381	AL109740 Human DNA	C 319	43.6	6.1	158699	9	AP006183	AP006183 Homo sapi
C 247	44.2	6.2	149288	2	CR376830	CR376830 Danio rer	C 320	43.6	6.1	159619	2	AC012440	AC012440 Homo sapi
C 248	44.2	6.2	149450	2	AC067880	AC067880 Homo sapi	C 321	43.6	6.1	160133	2	AC025140	AC025140 Homo sapi
C 249	44.2	6.2	151238	10	AC124477	AC124477 Mus muscu	C 322	43.6	6.1	163283	2	AC112980	AC112980 Mus muscu
C 250	44.2	6.2	158548	3	PFMA13P2	AL034558 Plasmodiu	C 323	43.6	6.1	167940	10	AL773517	AL773517 Mouse DNA
C 251	44.2	6.2	172778	5	AL935329	AL935329 Zebrafish	C 324	43.6	6.1	168766	2	EX936450	EX936450 Danio rer
C 252	44.2	6.2	179498	5	AL845314	AL845314 Zebrafish	C 325	43.6	6.1	169003	2	AC026071	AC026071 Homo sapi
C 253	44.2	6.2	179607	2	CR388084	CR388084 Danio rer	C 326	43.6	6.1	169546	2	AC004157	AC004157 Plasmodiu
C 254	44.2	6.2	185769	10	AC129178	AC129178 Mus muscu	C 327	43.6	6.1	171941	2	AC114305	AC114305 Homo sapi
C 255	44.2	6.2	187601	2	CR388137	CR388137 Danio rer	C 328	43.6	6.1	172811	9	AC066608	AC066608 Homo sapi
C 256	44.2	6.2	205064	10	AC125045	AC125045 Mus muscu	C 329	43.6	6.1	178126	2	AC113411	AC113411 Homo sapi
C 257	44.2	6.2	205186	5	EX000362	EX000362 Zebrafish	C 330	43.6	6.1	180121	2	EX927193	EX927193 Danio rer
C 258	44.2	6.2	209085	2	CR387996	CR387996 Danio rer	C 331	43.6	6.1	184092	9	AC073363	AC073363 Homo sapi
C 259	44.2	6.2	235793	2	AC126218	AC126218 Rattus no	C 332	43.6	6.1	189418	2	AC107844	AC107844 Mus muscu
C 260	44.2	6.2	245015	2	EX005225	EX005225 Danio rer	C 333	43.6	6.1	189554	5	EX004812	EX004812 Zebrafish
C 261	44.2	6.2	332324	2	AC108311	AC108311 Rattus no	C 334	43.6	6.1	191275	2	AC133067	AC133067 Danio rer
C 262	44.2	6.2	340552	3	PFAS29354	AL929354 Plasmodiu	C 335	43.6	6.1	192712	2	EX537285	EX537285 Danio rer
C 263	44	6.2	68450	8	CNS08CCC	AL928782 Oryza sat	C 336	43.6	6.1	197320	2	AC112979	AC112979 Mus muscu
C 264	44	6.2	92495	8	ATT5L19	AL049481 Arabidops	C 337	43.6	6.1	205766	2	CR318620	CR318620 Danio rer
C 265	44	6.2	110000	3	AC116957	Continuation (3 of	C 338	43.6	6.1	214440	2	AC091422	AC091422 Mus muscu
C 266	44	6.2	110000	6	AR409405	Continuation (2 of	C 339	43.6	6.1	226883	10	AC112680	AC112680 Mus muscu
C 267	44	6.2	110000	5	BD061520	Continuation (2 of	C 340	43.6	6.1	250707	3	AE014848	AE014848 Plasmodiu
C 268	44	6.2	136176	8	AL929119	AL929119 Zebrafish	C 341	43.6	6.1	254449	3	AE014817	AE014817 Plasmodiu
C 269	44	6.2	147611	8	CNS08C98	AL732533 Oryza sat	C 342	43.6	6.1	265575	2	AC111050	AC111050 Mus muscu
C 270	44	6.2	188844	2	AC127475	AL721475 Canis fam	C 343	43.6	6.1	298960	2	AC006896	AC006896 Caenorhab
C 271	44	6.2	198005	8	ATC8RIV28	AL615156 Arabidops	C 344	43.6	6.1	5632	3	AF310892	AF310892 Dictyoste
C 272	44	6.2	204398	10	AC107367	AL107367 Mus muscu	C 345	43.4	6.1	122440	3	AE001424	AE001424 Plasmodiu
C 273	44	6.2	212499	2	CR626887	CR626887 Danio rer	C 346	43.4	6.1	58953	9	AL670318	AL670318 Human DNA
C 274	44	6.2	217176	2	EX005436	EX005436 Danio rer	C 347	43.4	6.1	94460	9	AP000474	AP000474 Homo sapi
C 275	44	6.2	218922	5	AL929292	AL929292 Zebrafish	C 348	43.4	6.1	110000	2	AC147967	AC147967 Continuation (4 of
C 276	44	6.2	229213	10	AL772138	AL772138 Mouse DNA	C 349	43.4	6.1	110000	2	PFMA17P1_08	Continuation (9 of
C 277	44	6.2	281042	2	AC119900	AC119900 Mus muscu	C 350	43.4	6.1	132943	9	AC011287	AC011287 Homo sapi
C 278	44	6.2	281723	3	PFAS29359	AL929359 Plasmodiu	C 351	43.4	6.1	142324	5	EX005420	EX005420 Zebrafish
C 279	44	6.2	347550	1	AP001118	AP001118 Buchnera	C 352	43.4	6.1	145876	3	AC025773	AC025773 Homo sapi
C 280	43.8	6.1	3994	9	AC131096	AC131096 Homo sapi	C 353	43.4	6.1	148322	5	EX072568	EX072568 Zebrafish
C 281	43.8	6.1	36612	9	AC098486	AC098486 Homo sapi	C 354	43.4	6.1	154305	9	EX005249	EX005249 Zebrafish
C 282	43.8	6.1	96630	9	AC120055	AC120055 Homo sapi	C 355	43.4	6.1	155948	9	BS000092	BS000092 Pan trogl
C 283	43.8	6.1	110000	2	PFMA13_13	Continuation (14 o	C 356	43.4	6.1	156060	2	AC004153	AC004153 Plasmodiu
C 284	43.8	6.1	110000	2	PFMA13_15	Continuation (16 o	C 357	43.4	6.1	159699	2	AC026833	AC026833 Homo sapi
C 285	43.8	6.1	128919	2	AC146711	AC146711 Medicago	C 358	43.4	6.1	160149	2	AC118692	AC118692 Mus muscu
C 286	43.8	6.1	133817	10	EX001045	EX001045 Mouse DNA	C 359	43.4	6.1	166988	10	AC144552	AC144552 Mus muscu
C 287	43.8	6.1	136087	2	AC068350	AC068350 Homo sapi	C 360	43.4	6.1	171538	2	AC024436	AC024436 Homo sapi
C 288	43.8	6.1	159758	5	AL772250	AL772250 Zebrafish	C 361	43.4	6.1	172921	2	AP002454	AP002454 Homo sapi
C 289	43.8	6.1	162237	9	AL133549	AL133549 Human DNA	C 362	43.4	6.1	179639	2	AC117743	AC117743 Mus muscu
C 290	43.8	6.1	162954	2	EX548252	EX548252 Danio rer	C 363	43.4	6.1	180124	2	CR450699	CR450699 Danio rer
C 291	43.8	6.1	169277	2	EX322642	EX322642 Mus muscu	C 364	43.4	6.1	188295	9	AC098869	AC098869 Homo sapi
C 292	43.8	6.1	174565	10	AC125166	AC125166 Mus muscu	C 365	43.4	6.1	190332	2	AC116756	AC116756 Mus muscu
C 293	43.8	6.1	174596	2	AC022812	AC022812 Homo sapi	C 366	43.4	6.1	194209	2	AC119581	AC119581 Rattus no
C 294	43.8	6.1	179026	2	CR352332	CR352332 Danio rer	C 367	43.4	6.1	195446	10	AC133967	AC133967 Mus muscu
C 295	43.8	6.1	181275	2	EX511308	EX511308 Danio rer	C 368	43.4	6.1	199317	10	AL928611	AL928611 Mouse DNA
C 296	43.8	6.1	182870	3	AC116960	AC116960 Dictyoste	C 369	43.4	6.1	201663	10	AL596386	AL596386 Mouse DNA
C 297	43.8	6.1	183551	10	AC134570	AC134570 Mus muscu	C 370	43.4	6.1	221622	10	AC125183	AC125183 Mus muscu
C 298	43.8	6.1	191524	9	AC084016	AC084016 Homo sapi	C 371	43.4	6.1	228327	2	CR536612	CR536612 Danio rer
C 299	43.8	6.1	202001	10	AL772303	AL772303 Mouse DNA	C 372	43.4	6.1	229416	2	AC126129	AC126129 Rattus no
C 300	43.8	6.1	213347	10	AL831741	AL831741 Mouse DNA	C 373	43.4	6.1	233095	2	AC094266	AC094266 Rattus no
C 301	43.8	6.1	234676	2	AC127042	AC127042 Rattus no	C 374	43.4	6.1	237187	10	AC116463	AC116463 Mus muscu
C 302	43.8	6.1	246007	2	EX914205	EX914205 Danio rer	C 375	43.4	6.1	237525	2	AC105856	AC105856 Rattus no
C 303	43.8	6.1	254436	3	AE014827	AE014827 Plasmodiu	C 376	43.4	6.1	281723	3	PFAS29359	AL929359 Plasmodiu
C 304	43.8	6.1	333321	3	AC116986	AC116986 Dictyoste	C 377	43.4	6.1	318930	2	AC073495	AC073495 Mus muscu
C 305	43.6	6.1	434	5	CGZ83791	EX93791 G. gallus mi	C 378	43.4	6.1	340000	9	AP001689	AP001689 Homo sapi
C 306	43.6	6.1	1933	9	HS0806724	EX40667 Homo sapi	C 379	43.4	6.1	348174	3	CR382399	CR382399 Plasmodiu
C 307	43.6	6.1	47577	3	AF396436	AF396436 Tetrahyme	C 380	43.2	6.1	325	4	MME309057	AJ309057 Meles mel
C 308	43.6	6.1	54441	9	AC115584	AC115584 Dictyoste	C 381	43.2	6.1	6509	6	AX345129	Z68134 Caenorhabdi
C 309	43.6	6.1	56479	9	AC006034	AC006034 Homo sapi	C 382	43.2	6.1	28039	3	CET27A8	268134 Caenorhabdi
C 310	43.6	6.1	93633	9	AL627317	AL627317 Human DNA	C 383	43.2	6.1	67840	2	AC103375	AC103375 Mus muscu
C 311	43.6	6.1	110000	2	PFMA18P1_05	Continuation (6 of	C 384	43.2	6.1	67840	2	AC103375	AC103375 Mus muscu

C 385	43.2	6.1	139786	10	AC1234343	AC1234343 Mus muscu	C 458	43	6.0	252420	3	AE014841	AE014841 Plasmodiu
C 386	43.2	6.1	152323	5	AL954183	AL954183 Zebrafish	C 459	43	6.0	253151	3	AE014842	AE014842 Plasmodiu
C 387	43.2	6.1	156422	10	AC016102	AC016102 Homo sapi	C 460	43	6.0	253698	2	AC095997	AC095997 Rattus no
C 388	43.2	6.1	157021	9	AL357519	AL357519 Human DNA	C 461	43	6.0	253938	2	AC120488	AC120488 Rattus no
C 389	43.2	6.1	160269	9	AC024230	AC024230 Homo sapi	C 462	43	6.0	255812	2	AC114117	AC114117 Plasmodiu
C 390	43.2	6.1	169215	2	CR318593	CR318593 Homo sapi	C 463	43	6.0	257757	3	AE014837	AE014837 Rattus no
C 391	43.2	6.1	170327	2	CR318593	CR318593 Homo sapi	C 464	43	6.0	257942	2	AC121448	AC121448 Rattus no
C 392	43.2	6.1	170327	2	CR318593	CR318593 Homo sapi	C 465	43	6.0	257942	2	AC121448	AC121448 Rattus no
C 393	43.2	6.1	170996	2	AL592432	AL592432 Homo sapi	C 466	43	6.0	257942	2	AC121448	AC121448 Rattus no
C 394	43.2	6.1	171410	2	AC107689	AC107689 Mus muscu	C 467	43	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 395	43.2	6.1	175199	2	AC133940	AC133940 Mus muscu	C 468	43	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 396	43.2	6.1	177062	10	AC121924	AC121924 Mus muscu	C 469	43	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 397	43.2	6.1	180692	10	AC134559	AC134559 Mus muscu	C 470	43	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 398	43.2	6.1	192187	3	AC117072	AC117072 Dictyoste	C 471	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 399	43.2	6.1	193713	2	AC093658	AC093658 Homo sapi	C 472	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 400	43.2	6.1	194209	10	AL929249	AL929249 Mouse DNA	C 473	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 401	43.2	6.1	195381	2	AC132334	AC132334 Mus muscu	C 474	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 402	43.2	6.1	206080	2	EX272727	EX272727 Danio rer	C 475	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 403	43.2	6.1	209383	2	AC133953	AC133953 Mus muscu	C 476	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 404	43.2	6.1	209697	10	AL672286	AL672286 Mouse DNA	C 477	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 405	43.2	6.1	212940	10	AL591143	AL591143 Mouse DNA	C 478	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 406	43.2	6.1	223306	10	AC125181	AC125181 Mus muscu	C 479	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 407	43.2	6.1	223589	2	AC128861	AC128861 Rattus no	C 480	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 408	43.2	6.1	233041	2	AC113842	AC113842 Rattus no	C 481	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 409	43.2	6.1	233489	2	AC097798	AC097798 Rattus no	C 482	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 410	43.2	6.1	235236	5	AL954130	AL954130 Zebrafish	C 483	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 411	43.2	6.1	242705	2	AC027766	AC027766 Mus muscu	C 484	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 412	43.2	6.1	247341	2	AC099178	AC099178 Rattus no	C 485	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 413	43.2	6.1	250029	3	AE014816	AE014816 Plasmodiu	C 486	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 414	43.2	6.1	253441	2	AC135668	AC135668 Mus muscu	C 487	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 415	43.2	6.1	254650	2	AC128790	AC128790 Rattus no	C 488	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 416	43.2	6.1	257396	2	AC095524	AC095524 Rattus no	C 489	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 417	43	6.1	302156	3	AC116977	AC116977 Dictyoste	C 490	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 418	43	6.0	785	5	AV289550	AV289550 Petroica	C 491	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 419	43	6.0	4434	3	AV392441	AV392441 Dictyoste	C 492	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 420	43	6.0	110000	2	AC141302	Continuation (3 of	C 493	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 421	43	6.0	110000	2	PFMAL3_14	Continuation (15 o	C 494	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 422	43	6.0	118504	9	AC094080	AC094080 Homo sapi	C 495	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 423	43	6.0	125837	2	CR381597	CR381597 Danio rer	C 496	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 424	43	6.0	133877	2	AC120883	AC120883 Homo sapi	C 497	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 425	43	6.0	134448	2	AC148373	AC148373 Cryptotlag	C 500	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 426	43	6.0	140359	10	AC123220	AC123220 Mus muscu	C 501	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 427	43	6.0	147460	5	EX222595	EX222595 Zebrafish	C 502	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 428	43	6.0	151151	5	EX005294	EX005294 Zebrafish	C 503	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 429	43	6.0	152838	2	AC011589	AC011589 Homo sapi	C 504	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 430	43	6.0	157666	9	AC034151	AC034151 Homo sapi	C 505	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 431	43	6.0	158087	9	AC128677	AC128677 Homo sapi	C 506	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 432	43	6.0	158548	3	PFMAL3P2	PFMAL3P2 Plasmodiu	C 507	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 433	43	6.0	159167	5	EX649445	EX649445 Zebrafish	C 508	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 434	43	6.0	160460	2	AC140516	AC140516 Homo sapi	C 509	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 435	43	6.0	161808	2	AC139268	AC139268 Homo sapi	C 510	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 436	43	6.0	163642	9	AC022748	AC022748 Homo sapi	C 511	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 437	43	6.0	168878	10	AC109166	AC109166 Mus muscu	C 512	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 438	43	6.0	170797	9	AC011379	AC011379 Homo sapi	C 513	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 439	43	6.0	170916	9	AL136300	AL136300 Human DNA	C 514	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 440	43	6.0	176518	5	AL929307	AL929307 Zebrafish	C 515	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 441	43	6.0	188453	10	AC123741	AC123741 Mus muscu	C 516	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 442	43	6.0	189963	2	CR559944	CR559944 Danio rer	C 517	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 443	43	6.0	193047	9	CNS0000Q	AL049874 Human chr	C 518	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 444	43	6.0	196488	2	AC084410	AC084410 Mus muscu	C 519	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 445	43	6.0	197959	5	AC147972	AC147972 Gallus ga	C 520	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 446	43	6.0	202882	10	AC144006	AC144006 Mus muscu	C 521	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 447	43	6.0	204915	10	AC079134	AC079134 Homo sapi	C 522	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 448	43	6.0	207840	2	AC142383	AC142383 Homo sapi	C 523	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 449	43	6.0	210346	2	AC132917	AC132917 Mus muscu	C 524	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 450	43	6.0	210491	10	AC136018	AC136018 Mus muscu	C 525	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 451	43	6.0	210675	2	AC026272	AC026272 Homo sapi	C 526	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 452	43	6.0	213037	2	AC093986	AC093986 Rattus no	C 527	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 453	43	6.0	213676	9	AC103975	AC103975 Homo sapi	C 528	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 454	43	6.0	217036	5	EX470198	EX470198 Zebrafish	C 529	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 455	43	6.0	219080	2	AC120087	AC120087 Rattus no	C 530	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 456	43	6.0	219394	2	EX901878	EX901878 Danio rer	C 531	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 457	43	6.0	226724	2	AC116221	AC116221 Rattus no	C 532	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 458	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 533	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 459	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 534	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 460	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 535	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 461	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 536	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 462	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 537	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 463	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 538	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 464	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 539	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 465	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 540	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 466	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 541	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 467	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 542	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 468	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 543	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 469	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 544	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 470	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 545	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 471	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 546	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 472	43	6.0	234248	2	AC119385	AC119385 Rattus no	C 547	42.8	6.0	272698	3	PFMAL4P4	PFMAL4P4 Plasmodiu
C 473													

C 531	42.6	6.0	167455	10	AC129211	AC129211 Mus muscu	C 604	42.4	5.9	262416	2	AC126181	AC126181 Rattus no
C 532	42.6	6.0	175899	2	AC115205	AC115205 Rattus no	605	42.4	5.9	318221	3	PFMAL13P3	AL049184 Plasmodiu
533	42.6	6.0	176310	2	EX997686	EX997686 Danio rer	606	42.2	5.9	925	3	AY653023	AY653023 Tetrahyme
534	42.6	6.0	178157	2	AC101748	AC101748 Mus muscu	C 607	42.2	5.9	32799	9	AC137591	AC137591 Homo sapi
C 535	42.6	6.0	181714	2	AC128189	AC128189 Rattus no	C 608	42.2	5.9	36188	3	AC116922	AC116922 Dictyoste
C 536	42.6	6.0	181933	10	AL672033	AL672033 Mouse DNA	609	42.2	5.9	68626	3	PFMAL3P5	AL034556 Plasmodiu
C 537	42.6	6.0	182118	9	AL356287	AL356287 Human DNA	610	42.2	5.9	94147	9	AC016604	AC016604 Homo sapi
538	42.6	6.0	182810	10	BX284626	BX284626 Mouse DNA	611	42.2	5.9	96799	9	AC104647	AC104647 Homo sapi
539	42.6	6.0	186299	5	AL954166	AL954166 Zebrafish	C 612	42.2	5.9	102733	9	AC108865	AC108865 Homo sapi
540	42.6	6.0	186642	5	EX004979	EX004979 Zebrafish	C 613	42.2	5.9	119048	2	AC005504	AC005504 Plasmodiu
541	42.6	6.0	191047	2	AC102653	AC102653 Mus muscu	614	42.2	5.9	119555	9	AC004827	AC004827 Human DNA
542	42.6	6.0	193256	10	AL935124	AL935124 Mouse DNA	C 615	42.2	5.9	122458	2	AC010391	AC010391 Homo sapi
543	42.6	6.0	194220	5	BX571880	BX571880 Zebrafish	C 616	42.2	5.9	124037	8	AC136974	AC136974 Medicago
C 544	42.6	6.0	196175	10	AC069019	AC069019 Mus muscu	617	42.2	5.9	127345	5	BX248503	BX248503 Zebrafish
C 545	42.6	6.0	199533	2	AC118384	AC118384 Rattus no	C 618	42.2	5.9	132135	10	AL928890	AL928890 Mouse DNA
C 546	42.6	6.0	199993	10	AC102783	AC102783 Mus muscu	C 619	42.2	5.9	133952	2	CR450765	CR450765 Danio rer
547	42.6	6.0	201145	10	AC132442	AC132442 Mus muscu	C 620	42.2	5.9	136116	8	AC148762	AC148762 Medicago
C 548	42.6	6.0	232609	10	AL670472	AL670472 Mouse DNA	C 621	42.2	5.9	136116	8	EX470114	EX470114 Zebrafish
549	42.6	6.0	240807	2	AC107634	AC107634 Mus muscu	622	42.2	5.9	138545	5	EX470114	EX470114 Zebrafish
550	42.6	6.0	248308	2	AC123259	AC123259 Rattus no	C 623	42.2	5.9	144071	2	CR405688	CR405688 Danio rer
551	42.6	6.0	250053	3	AE014825	AE014825 Plasmodiu	C 624	42.2	5.9	151802	3	AC114263	AC114263 Dictyoste
552	42.6	6.0	251448	3	AE014819	AE014819 Plasmodiu	C 625	42.2	5.9	154770	5	BX005102	BX005102 Zebrafish
C 553	42.6	6.0	269576	2	AC073684	AC073684 Mus muscu	626	42.2	5.9	156699	2	CR318633	CR318633 Danio rer
C 554	42.6	6.0	274148	1	AC132554	AC132554 Rattus no	C 627	42.2	5.9	159317	2	AC147520	AC147520 Ocolemur
C 555	42.6	6.0	291205	1	AE017040	AE017040 Bacillus	628	42.2	5.9	161350	10	AC121983	AC121983 Mus muscu
C 556	42.6	6.0	345730	1	EX957219	EX957219 Methanoco	C 629	42.2	5.9	163536	9	AC016635	AC016635 Homo sapi
557	42.6	6.0	348174	3	CR382399	CR382399 Plasmodiu	C 630	42.2	5.9	163728	9	AP003715	AP003715 Homo sapi
558	42.4	5.9	1818	1	AF267209	AF267209 Candidatu	C 631	42.2	5.9	167782	2	AC010943	AC010943 Homo sapi
559	42.4	5.9	5304	6	AX346291	AX346291 Sequence	C 632	42.2	5.9	170235	9	AC027118	AC027118 Homo sapi
C 560	42.4	5.9	5858	6	AX346214	AX346214 Sequence	C 633	42.2	5.9	171297	2	AC137743	AC137743 Mus muscu
C 561	42.4	5.9	6543	10	AF516878	AF516878 Mus muscu	634	42.2	5.9	172164	2	CR387936	CR387936 Danio rer
562	42.4	5.9	14211	3	AE001368	AE001368 Plasmodiu	C 635	42.2	5.9	172871	10	AL607131	AL607131 Mouse DNA
C 563	42.4	5.9	31129	10	AF441733	AF441733 Mus muscu	C 636	42.2	5.9	173316	2	AC141726	AC141726 Apis mell
564	42.4	5.9	34777	9	AL596282	AL596282 Human DNA	C 637	42.2	5.9	174963	2	AC134419	AC134419 Mus muscu
C 565	42.4	5.9	76837	2	AC108581	Continuation (4 of	C 638	42.2	5.9	176142	2	CR388010	CR388010 Danio rer
C 566	42.4	5.9	103768	10	AL954716	AL954716 Mouse DNA	639	42.2	5.9	177058	2	AL954846	AL954846 Zebrafish
C 567	42.4	5.9	109868	5	BX322798	BX322798 Zebrafish	C 640	42.2	5.9	177176	2	AC139877	AC139877 Didelphis
568	42.4	5.9	110000	2	AC114021	AC114021 Rattus no	641	42.2	5.9	177876	10	AC133093	AC133093 Mus muscu
C 569	42.4	5.9	110000	2	PFMAL13_10	Continuation (11 o	642	42.2	5.9	177929	2	CR3842813	CR3842813 Danio rer
570	42.4	5.9	119361	2	AC092771	AC092771 Homo sapi	643	42.2	5.9	178093	2	AC137849	AC137849 Mus muscu
C 571	42.4	5.9	139760	2	CR388023	CR388023 Danio rer	644	42.2	5.9	180062	2	AC140792	AC140792 Rattus no
C 572	42.4	5.9	152506	10	AC145589	AC145589 Mus muscu	645	42.2	5.9	181165	2	EX908767	EX908767 Danio rer
C 573	42.4	5.9	152857	2	CR450744	CR450744 Danio rer	646	42.2	5.9	183155	10	AC140194	AC140194 Mus muscu
574	42.4	5.9	157865	2	CR450836	CR450836 Danio rer	647	42.2	5.9	184434	2	AC105976	AC105976 Mus muscu
C 575	42.4	5.9	158341	9	AC021733	AC021733 Homo sapi	648	42.2	5.9	185395	2	AC118699	AC118699 Rattus no
C 576	42.4	5.9	163053	2	AC103920	AC103920 Canis fam	C 649	42.2	5.9	186699	2	AC098336	AC098336 Rattus no
577	42.4	5.9	163888	10	AC133185	AC133185 Mus muscu	650	42.2	5.9	197146	5	EX470199	EX470199 Zebrafish
578	42.4	5.9	165548	2	BX511015	BX511015 Danio rer	651	42.2	5.9	198595	5	AL953887	AL953887 Zebrafish
C 579	42.4	5.9	165529	10	AC147621	AC147621 Mus muscu	652	42.2	5.9	198895	10	AC118025	AC118025 Mus muscu
C 580	42.4	5.9	189006	2	AC142178	AC142178 Rattus no	653	42.2	5.9	200689	2	AC067865	AC067865 Homo sapi
581	42.4	5.9	189874	5	AL929378	AL929378 Zebrafish	654	42.2	5.9	202324	2	AC147112	AC147112 Danio rer
582	42.4	5.9	177066	9	AC091001	AC091001 Papio anu	655	42.2	5.9	203197	2	AC139843	AC139843 Mus muscu
C 583	42.4	5.9	179099	10	AC090046	AC090046 Mus muscu	C 656	42.2	5.9	204729	5	EX890575	EX890575 Zebrafish
C 584	42.4	5.9	182172	8	CNS07YPC	AL713943 Oryza sat	C 657	42.2	5.9	207957	2	AC119096	AC119096 Rattus no
C 585	42.4	5.9	185486	2	AC128857	AC128857 Rattus no	C 658	42.2	5.9	214591	2	AC114131	AC114131 Rattus no
586	42.4	5.9	186133	2	AC120092	AC120092 Rattus no	C 659	42.2	5.9	217352	10	AL645784	AL645784 Mouse DNA
587	42.4	5.9	186279	10	AC121977	AC121977 Mus muscu	660	42.2	5.9	221645	2	AC103253	AC103253 Rattus no
588	42.4	5.9	187362	5	BX511178	BX511178 Zebrafish	C 661	42.2	5.9	222658	10	AC055766	AC055766 Mus muscu
589	42.4	5.9	188522	2	AC102406	AC102406 Mus muscu	C 662	42.2	5.9	226080	2	AC116292	AC116292 Rattus no
C 590	42.4	5.9	189924	2	AC119933	AC119933 Mus muscu	C 663	42.2	5.9	231534	2	AC098001	AC098001 Rattus no
591	42.4	5.9	193996	2	AC129222	AC129222 Mus muscu	C 664	42.2	5.9	239050	2	AC127603	AC127603 Rattus no
592	42.4	5.9	198047	2	CR376763	CR376763 Danio rer	665	42.2	5.9	245217	2	AC110848	AC110848 Rattus no
593	42.4	5.9	210077	2	AC113348	AC113348 Rattus no	666	42.2	5.9	246996	2	CR392340	CR392340 Danio rer
C 594	42.4	5.9	215604	2	CR376804	CR376804 Danio rer	667	42.2	5.9	250421	3	AE014849	AE014849 Plasmodiu
595	42.4	5.9	219799	10	AC133835	AC133835 Mus muscu	668	42.2	5.9	251571	2	AC114093	AC114093 Rattus no
C 596	42.4	5.9	223992	2	AC134196	AC134196 Rattus no	669	42.2	5.9	252512	2	AC097326	AC097326 Pan trogl
597	42.4	5.9	229171	2	AC126947	AC126947 Rattus no	C 670	42.2	5.9	257391	2	AC097400	AC097400 Rattus no
598	42.4	5.9	230576	2	AC095934	AC095934 Rattus no	C 671	42.2	5.9	265040	2	AC111525	AC111525 Rattus no
599	42.4	5.9	235062	2	AC132976	AC132976 Rattus no	672	42.2	5.9	270296	2	AC132541	AC132541 Rattus no
C 600	42.4	5.9	235514	2	AC094224	AC094224 Rattus no	673	42.2	5.9	296575	2	AC095901	AC095901 Rattus no
601	42.4	5.9	240439	2	AC117289	AC117289 Rattus no	674	42.2	5.9	299112	2	AC123342	AC123342 Rattus no
602	42.4	5.9	244428	2	AC130959	AC130959 Rattus no	C 675	42.2	5.9	330373	2	AC119565	AC119565 Rattus no
603	42.4	5.9	245496	10	AC109204	AC109204 Mus muscu	C 676	42.2	5.9	349895	2	AC129168	AC129168 Rattus no

677	42	5.9	969	3	DNA132902	AJ132902 Drosophila	750	41.8	5.9	110000	9	AF438327_0	AF438327 Homo sapi
678	42	5.9	1162	8	BT009308	Triticum	c 751	41.8	5.9	122035	2	CR382371	CR382371 Danio rer
679	42	5.9	1383	5	BC074687	Xenopus t	c 752	41.8	5.9	125958	3	AC115592	AC115592 Dictyost
680	42	5.9	57203	3	AC115581	Dictyost	c 753	41.8	5.9	128891	5	BX548007	BX548007 Zebrafish
681	42	5.9	60209	3	AC078875	Homo sapi	754	41.8	5.9	141264	2	AC129628	AC129628 Rattus no
682	42	5.9	74328	8	F13K23	Sequence	755	41.8	5.9	146761	2	CR394532	CR394532 Danio rer
683	42	5.9	81332	8	AP004959	Lotus cor	756	41.8	5.9	148116	2	AC078838	AC078838 Homo sapi
684	42	5.9	97771	9	BX088563	Human DNA	c 757	41.8	5.9	150875	2	AC121705	AC121705 Rattus no
685	42	5.9	106806	5	AL935319	Zebrafish	c 758	41.8	5.9	151503	10	AL732319	AL732319 Mouse DNA
686	42	5.9	109530	8	AC122172	Medicago	c 759	41.8	5.9	151853	5	BX936417	BX936417 Zebrafish
687	42	5.9	110000	2	AC116090_3	Continuation (4 of	c 760	41.8	5.9	153960	2	BX950200	BX950200 Danio rer
688	42	5.9	110000	2	PFMAL13_18	Continuation (19 o	c 761	41.8	5.9	156736	9	AC006502	AC006502 Homo sapi
689	42	5.9	118865	8	AF267176	Pyricular	762	41.8	5.9	157152	9	AC073427	AC073427 Homo sapi
690	42	5.9	125623	3	AC115599	Dictyost	763	41.8	5.9	157605	2	BX957232	BX957232 Danio rer
691	42	5.9	142938	4	AC150709	Bos tauru	764	41.8	5.9	157871	2	AC025074	AC025074 Homo sapi
692	42	5.9	144022	5	BX088594	Zebrafish	c 765	41.8	5.9	158573	2	AC078823	AC078823 Homo sapi
693	42	5.9	144279	2	AP001570	Homo sapi	c 766	41.8	5.9	158766	2	AC122775	AC122775 Mus muscu
694	42	5.9	146850	2	CR3944559	Danio rer	c 767	41.8	5.9	159830	10	AC145267	AC145267 Mus muscu
695	42	5.9	148465	5	AL772396	Zebrafish	768	41.8	5.9	160207	10	AC121889	AC121889 Mus muscu
696	42	5.9	150847	10	AL807390	Mouse DNA	769	41.8	5.9	160472	2	AC080140	AC080140 Mus muscu
697	42	5.9	152883	9	AC106716	Homo sapi	c 770	41.8	5.9	160892	10	AC122294	AC122294 Mus muscu
698	42	5.9	153666	2	AC021742	Homo sapi	c 771	41.8	5.9	163216	2	AC122557	AC122557 Mus muscu
699	42	5.9	155359	9	AL358777	Human DNA	c 772	41.8	5.9	164064	2	AC044809	AC044809 Homo sapi
700	42	5.9	160737	2	AC139612	Rattus no	c 773	41.8	5.9	164271	2	AC009571	AC009571 Homo sapi
701	42	5.9	161790	2	AC022371	Homo sapi	c 774	41.8	5.9	164940	2	AC112978	AC112978 Homo sapi
702	42	5.9	161863	9	AL606970	Human DNA	c 775	41.8	5.9	167082	2	AP001903	AP001903 Homo sapi
703	42	5.9	165424	10	AC141636	Homo sapi	c 776	41.8	5.9	168139	2	AC118638	AC118638 Mus muscu
704	42	5.9	168064	2	BX914202	Danio rer	777	41.8	5.9	170607	2	AC102151	AC102151 Mus muscu
705	42	5.9	180545	10	AC115736	Homo sapi	778	41.8	5.9	182525	10	AC147222	AC147222 Mus muscu
706	42	5.9	182038	9	AC073042	Homo sapi	c 779	41.8	5.9	184144	2	AC079734	AC079734 Mus muscu
707	42	5.9	182330	2	BX927279	Danio rer	c 780	41.8	5.9	188417	9	AC025205	AC025205 Homo sapi
708	42	5.9	182416	10	AC099724	Homo sapi	c 781	41.8	5.9	189355	5	BX649503	BX649503 Zebrafish
709	42	5.9	186898	2	CR388057	Danio rer	c 782	41.8	5.9	191470	2	AC128948	AC128948 Rattus no
710	42	5.9	192528	10	AC124512	Mus muscu	c 783	41.8	5.9	191721	10	AC101883	AC101883 Mus muscu
711	42	5.9	192849	5	BX572079	Zebrafish	c 784	41.8	5.9	194104	10	AC124510	AC124510 Mus muscu
712	42	5.9	193741	9	AC079363	Homo sapi	c 785	41.8	5.9	195057	2	BX897664	BX897664 Danio rer
713	42	5.9	200814	5	BX571825	Zebrafish	c 786	41.8	5.9	195275	10	AC102255	AC102255 Mus muscu
714	42	5.9	204318	5	BX005374	Zebrafish	c 787	41.8	5.9	197927	10	AC101735	AC101735 Mus muscu
715	42	5.9	212597	2	AC105463	Rattus no	c 788	41.8	5.9	200300	2	AC111531	AC111531 Rattus no
716	42	5.9	213630	10	AC124250	Mus muscu	c 789	41.8	5.9	201012	2	AC021189	AC021189 Homo sapi
717	42	5.9	215174	2	AC150765	Bos tauru	c 790	41.8	5.9	202374	10	AC122868	AC122868 Mus muscu
718	42	5.9	215347	2	CR626883	Danio rer	c 791	41.8	5.9	207051	2	AC110030	AC110030 Mus muscu
719	42	5.9	216972	9	AC067819	Homo sapi	c 792	41.8	5.9	207362	2	AC118163	AC118163 Rattus no
720	42	5.9	221794	10	AC118005	Mus muscu	c 793	41.8	5.9	209484	2	AC024116	AC024116 Mus muscu
721	42	5.9	222533	10	AC115760	Mus muscu	c 794	41.8	5.9	209952	2	AC105980	AC105980 Mus muscu
722	42	5.9	223646	5	BX511306	Zebrafish	c 795	41.8	5.9	209952	2	AC147480	AC147480 Mus muscu
723	42	5.9	224003	2	BX324134	Danio rer	c 796	41.8	5.9	211721	2	AC138297	AC138297 Mus muscu
724	42	5.9	231919	2	AC111770	Rattus no	c 797	41.8	5.9	211744	2	AC133645	AC133645 Mus muscu
725	42	5.9	232415	2	AC095640	Rattus no	c 798	41.8	5.9	211776	10	AC115744	AC115744 Mus muscu
726	42	5.9	238358	2	AC102876	Mus muscu	c 799	41.8	5.9	223162	2	AC137176	AC137176 Rattus no
727	42	5.9	240507	2	AC103202	Rattus no	c 800	41.8	5.9	227420	2	AC099202	AC099202 Rattus no
728	42	5.9	250022	3	AE014824	Plasmid	c 801	41.8	5.9	227441	2	CR589875	CR589875 Danio rer
729	42	5.9	250078	3	AE014829	Plasmid	c 802	41.8	5.9	227605	2	AC121445	AC121445 Rattus no
730	42	5.9	250663	3	AE014826	Plasmid	c 803	41.8	5.9	228289	2	BX247888	BX247888 Danio rer
731	42	5.9	250880	10	AC102040	Mus muscu	c 804	41.8	5.9	234051	2	CR354541	CR354541 Danio rer
732	42	5.9	258658	3	AE014832	Plasmid	c 805	41.8	5.9	235198	10	AL645571	AL645571 Mouse DNA
733	42	5.9	271546	3	AE014843	Plasmid	c 806	41.8	5.9	238019	2	AC127744	AC127744 Rattus no
734	42	5.9	294107	3	AC129247	Rattus no	c 807	41.8	5.9	239146	2	AC103327	AC103327 Rattus no
735	42	5.9	300050	1	AP004171	Myoplasma	c 808	41.8	5.9	240186	2	AC106619	AC106619 Rattus no
736	42	5.9	348034	3	CR382400	Plasmid	c 809	41.8	5.9	241534	2	AC141426	AC141426 Rattus no
737	41.8	5.9	29964	9	AC025246	Homo sapi	c 810	41.8	5.9	247770	2	AC120813	AC120813 Rattus no
738	41.8	5.9	46557	2	AC139178	Ciona sav	c 811	41.8	5.9	250207	2	AC095443	AC095443 Rattus no
739	41.8	5.9	47930	2	AC136253	Rattus no	c 812	41.8	5.9	252027	2	AC096136	AC096136 Rattus no
740	41.8	5.9	48306	9	AL590675	Human DNA	c 813	41.8	5.9	253001	3	AE014834	AE014834 Plasmid
741	41.8	5.9	67572	8	NCB1383	Neurospor	c 814	41.8	5.9	261265	2	AC118885	AC118885 Rattus no
742	41.8	5.9	82584	3	AC113624	Dictyost	c 815	41.8	5.9	262091	2	AC098335	AC098335 Rattus no
743	41.8	5.9	88549	8	AC004669	Arabidops	c 816	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
744	41.8	5.9	89779	8	AC004669	Arabidops	c 817	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
745	41.8	5.9	95546	9	AC022816	Homo sapi	c 818	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
746	41.8	5.9	110000	1	AE017308_5	Continuation (6 of	c 819	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
747	41.8	5.9	110000	2	PFMAL13_16	Continuation (3 of	c 820	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
748	41.8	5.9	110000	2	PFMAL13_16	Continuation (17 o	c 821	41.8	5.9	263394	2	AC098384	AC098384 Rattus no
749	41.8	5.9	110000	3	AC116957_1	Continuation (2 of	c 822	41.8	5.9	263394	2	AC098384	AC098384 Rattus no

823	41.8	5.8	271546	3	AE014843	AE014843 Plasmid	C 896	41.4	5.8	420	6	CQ476954	CQ476954 Sequence
824	41.8	5.9	330050	3	FFA929355	AL929355 Plasmid	897	41.4	5.8	592	3	CQ524169	CQ524169 Sequence
825	41.8	5.9	337193	2	AC109771	AC109771 Rattus no	898	41.4	5.8	1853	6	DROGBRN	M14651 D. yakuba gl
826	41.8	5.9	343050	3	FFA929353	AL929353 Plasmid	C 899	41.4	5.8	2851	3	AF247970	AF247970 Caenorhab
827	41.6	5.8	840	6	CNS0180K	AL110675 Botrytis	900	41.4	5.8	8323	6	AX344960	AX344960 Sequence
828	41.6	5.8	5265	6	AX323805	AX323805 Sequence	C 901	41.4	5.8	11394	6	AX323608	AX323608 Sequence
829	41.6	5.8	7058	6	AX348439	AX348439 Sequence	902	41.4	5.8	73666	9	HSJ333B15	AL109954 Human DNA
830	41.6	5.8	69131	2	AC101356	AC101356 Mus muscu	903	41.4	5.8	73778	6	AX344575	AX344575 Sequence
831	41.6	5.8	70508	10	AL772245	AL772245 Mouse DNA	904	41.4	5.8	97603	5	BS511193	BS511193 Zebrafish
832	41.6	5.8	73295	5	AC110207	AC110207 Mus muscu	C 905	41.4	5.8	105320	3	AC116920	AC116920 Dictyoste
833	41.6	5.8	80521	5	BS914215	BS914215 Zebrafish	C 906	41.4	5.8	110000	2	AC103317	Continuation (3 of
834	41.6	5.8	83083	2	AC115213	AC115213 Rattus no	907	41.4	5.8	110000	2	AC108249	Continuation (4 of
835	41.6	5.8	84222	8	AC149427	AC149427 Populus b	C 908	41.4	5.8	110000	2	AC121632	Continuation (3 of
836	41.6	5.8	104904	2	CR388190	CR388190 Danio rer	909	41.4	5.8	110000	2	AC121632	Continuation (4 of
837	41.6	5.8	104992	2	AC005504	AC005504 Plasmid	C 910	41.4	5.8	110000	2	AC127958	Continuation (2 of
838	41.6	5.8	110000	3	AC116984	Continuation (2 of	911	41.4	5.8	110000	2	AC129389	Continuation (3 of
839	41.6	5.8	117543	9	AC019164	AC019164 Homo sapi	C 912	41.4	5.8	110000	2	AC129389	Continuation (3 of
840	41.6	5.8	138044	2	CR318645	CR318645 Danio rer	C 913	41.4	5.8	110000	2	AC149068	Continuation (5 of
841	41.6	5.8	138242	10	AC126026	AC126026 Mus muscu	914	41.4	5.8	110000	2	AL390202_04	Continuation (16 o
842	41.6	5.8	141199	2	AC119870	AC119870 Mus muscu	C 915	41.4	5.8	110000	2	PFMAL13_15	Continuation (10 o
843	41.6	5.8	147933	5	BS571765	BS571765 Zebrafish	C 916	41.4	5.8	110000	2	PFMAL7B1_09	Continuation (10 o
844	41.6	5.8	153168	2	AC025387	AC025387 Homo sapi	C 917	41.4	5.8	110960	3	CEV39A1A	AL031633 Caenorhab
845	41.6	5.8	158836	10	AC125114	AC125114 Mus muscu	918	41.4	5.8	120405	2	AC046147	AC046147 Mus muscu
846	41.6	5.8	163443	5	AL773542	AL773542 Zebrafish	C 919	41.4	5.8	121609	2	AC137653	AC137653 Bos tauru
847	41.6	5.8	164272	10	AC115714	AC115714 Mus muscu	C 920	41.4	5.8	133095	2	AC133500	AC133500 Mus muscu
848	41.6	5.8	167348	2	AC104201	AC104201 Mus muscu	C 921	41.4	5.8	135628	5	BS547937	BS547937 Zebrafish
849	41.6	5.8	168210	2	AC100743	AC100743 Mus muscu	C 922	41.4	5.8	142457	10	AC123045	AC123045 Mus muscu
850	41.6	5.8	169978	9	AC017013	AC017013 Homo sapi	C 923	41.4	5.8	147788	2	AC015840	AC015840 Homo sapi
851	41.6	5.8	170000	2	AC004579	AC004579 Homo sapi	C 924	41.4	5.8	149078	2	BS927399	BS927399 Danio rer
852	41.6	5.8	171317	9	AC020941	AC020941 Homo sapi	C 925	41.4	5.8	155448	5	BS111180	BS111180 Zebrafish
853	41.6	5.8	173935	10	AL670285	AL670285 Mouse DNA	C 926	41.4	5.8	157067	2	AC137265	AC137265 Rattus no
854	41.6	5.8	177424	2	BS927380	BS927380 Danio rer	C 927	41.4	5.8	161238	9	AP003127	AP003127 Homo sapi
855	41.6	5.8	177899	10	AC123042	AC123042 Mus muscu	928	41.4	5.8	162073	4	CFA012166	AJ012166 Canis fam
856	41.6	5.8	179046	10	AC124542	AC124542 Mus muscu	929	41.4	5.8	162180	10	AC120176	AC120176 Mus muscu
857	41.6	5.8	182125	2	AC099587	AC099587 Mus muscu	930	41.4	5.8	165127	2	AC148043	AC148043 Cercopith
858	41.6	5.8	182870	3	AC116960	AC116960 Dictyoste	931	41.4	5.8	165244	2	AC145039	AC145039 Bos tauru
859	41.6	5.8	183078	2	AC134939	AC134939 Rattus no	932	41.4	5.8	166793	2	AC090401	AC090401 Homo sapi
860	41.6	5.8	187360	2	AC129938	AC129938 Mus muscu	C 933	41.4	5.8	167934	9	AP001034	AP001034 Homo sapi
861	41.6	5.8	188011	10	AC124508	AC124508 Mus muscu	C 934	41.4	5.8	168208	2	AL646100	AL646100 Homo sapi
862	41.6	5.8	190000	2	AC004580	AC004580 Homo sapi	935	41.4	5.8	171125	10	AC130546	AC130546 Mus muscu
863	41.6	5.8	195616	2	AL138777	AL138777 Homo sapi	C 936	41.4	5.8	172884	2	AC140084	AC140084 Cercopith
864	41.6	5.8	196099	2	AC139037	AC139037 Mus muscu	C 937	41.4	5.8	174067	10	AC119950	AC119950 Mus muscu
865	41.6	5.8	196910	2	BS322542	BS322542 Danio rer	C 938	41.4	5.8	174637	2	AC027490	AC027490 Homo sapi
866	41.6	5.8	199545	2	AC118817	AC118817 Rattus no	939	41.4	5.8	175366	10	AC101718	AC101718 Mus muscu
867	41.6	5.8	201621	9	AC027273	AC027273 Homo sapi	940	41.4	5.8	176032	2	BS10656	BS10656 Danio rer
868	41.6	5.8	204312	10	AL669943	AL669943 Mouse DNA	941	41.4	5.8	176395	2	AC149675	AC149675 Bos tauru
869	41.6	5.8	205374	10	AC147160	AC147160 Mus muscu	942	41.4	5.8	176613	2	BS901931	BS901931 Danio rer
870	41.6	5.8	205604	2	CR376742	CR376742 Danio rer	943	41.4	5.8	179529	2	BS10946	BS10946 Danio rer
871	41.6	5.8	209896	10	AC138585	AC138585 Mus muscu	C 944	41.4	5.8	179801	2	AC121443	AC121443 Rattus no
872	41.6	5.8	210269	2	BS927280	BS927280 Danio rer	C 945	41.4	5.8	181040	10	AC125534	AC125534 Mus muscu
873	41.6	5.8	211164	5	BS470072	BS470072 Zebrafish	C 946	41.4	5.8	185084	4	AC147708	AC147708 Canis fam
874	41.6	5.8	211349	10	AL627102	AL627102 Mouse DNA	C 947	41.4	5.8	187430	2	CR392353	CR392353 Danio rer
875	41.6	5.8	211802	2	AC138249	AC138249 Mus muscu	C 948	41.4	5.8	191174	10	AC116586	AC116586 Mus muscu
876	41.6	5.8	216199	10	AL669941	AL669941 Mouse DNA	C 949	41.4	5.8	194720	10	AL592214	AL592214 Mouse DNA
877	41.6	5.8	217076	2	AC101868	AC101868 Mus muscu	C 950	41.4	5.8	195108	9	AC021106	AC021106 Homo sapi
878	41.6	5.8	218508	10	AC113497	AC113497 Mus muscu	C 951	41.4	5.8	199421	9	AL691515	AL691515 Human DNA
879	41.6	5.8	219553	2	AC125967	AC125967 Rattus no	C 952	41.4	5.8	204498	2	BS950853	BS950853 Danio rer
880	41.6	5.8	232742	2	AC111679	AC111679 Rattus no	C 953	41.4	5.8	209764	10	AL645468	AL645468 Mouse DNA
881	41.6	5.8	235930	10	AC131743	AC131743 Mus muscu	C 954	41.4	5.8	211348	2	BS927237	BS927237 Danio rer
882	41.6	5.8	235975	2	AC131353	AC131353 Rattus no	C 955	41.4	5.8	211555	2	AC150451	AC150451 Callithri
883	41.6	5.8	238386	2	AC109763	AC109763 Rattus no	956	41.4	5.8	215548	2	AC123618	AC123618 Mus muscu
884	41.6	5.8	245539	2	AC121656	AC121656 Rattus no	C 957	41.4	5.8	222961	2	AC111933	AC111933 Rattus no
885	41.6	5.8	247722	2	AC099080	AC099080 Rattus no	C 958	41.4	5.8	225438	2	AC106676	AC106676 Rattus no
886	41.6	5.8	248364	2	AC111235	AC111235 Rattus no	959	41.4	5.8	226106	2	AC106228	AC106228 Rattus no
887	41.6	5.8	250421	3	AE014836	AE014836 Plasmid	C 960	41.4	5.8	229903	2	AC097290	AC097290 Rattus no
888	41.6	5.8	250743	3	AE014849	AE014849 Plasmid	961	41.4	5.8	230884	2	AC079523	AC079523 Mus muscu
889	41.6	5.8	251882	2	AC098075	AC098075 Rattus no	C 962	41.4	5.8	232395	2	AC098120	AC098120 Rattus no
890	41.6	5.8	257109	3	AC116963	AC116963 Dictyoste	963	41.4	5.8	232830	2	AC132433	AC132433 Mus muscu
891	41.6	5.8	257570	2	CR354431	CR354431 Danio rer	964	41.4	5.8	232994	2	AC110467	AC110467 Rattus no
892	41.6	5.8	261934	5	BS664745	BS664745 Zebrafish	965	41.4	5.8	233795	2	AC094161	AC094161 Rattus no
893	41.6	5.8	262093	2	AC095577	AC095577 Rattus no	C 966	41.4	5.8	238476	2	AC117978	AC117978 Rattus no
894	41.6	5.8	267396	2	CR352293	CR352293 Danio rer	967	41.4	5.8	241803	2	AC096458	AC096458 Rattus no
895	41.6	5.8	321973	2	AC133971	AC133971 Rattus no	C 968	41.4	5.8	243556	2	AC114066	AC114066 Rattus no

969	41.4	5.8	245472	2	AC097189	AC097189 Rattus no	CI042	41.2	5.8	171356	2	CR318673	CR318673 Danio rer
c 970	41.4	5.8	246986	2	AC149091	AC149091 Mus muscu	CI043	41.2	5.8	174383	5	AL292916	AL292916 Zebrafish
971	41.4	5.8	249684	2	AC132983	AC132983 Rattus no	CI044	41.2	5.8	175223	9	AC004617	AC004617 Homo sapi
c 972	41.4	5.8	254436	3	AE014827	AE014827 Plasmodiu	1045	41.2	5.8	175916	2	CR678384	CR678384 Danio rer
c 973	41.4	5.8	260036	10	AC111125	AC111125 Mus muscu	1046	41.2	5.8	176569	5	EX008540	EX008540 Zebrafish
c 974	41.4	5.8	263848	2	AC094175	AC094175 Rattus no	CI047	41.2	5.8	177581	10	AC110380	AC110380 Mus muscu
c 975	41.4	5.8	265292	2	AC128622	AC128622 Rattus no	CI048	41.2	5.8	177690	10	AC131109	AC131109 Mus muscu
c 976	41.4	5.8	269242	2	CR388212	CR388212 Danio rer	1049	41.2	5.8	179094	2	EX330093	EX330093 Danio rer
c 977	41.4	5.8	275076	10	AC093360	AC093360 Mus muscu	1050	41.2	5.8	179943	10	AC123822	AC123822 Mus muscu
c 978	41.4	5.8	293623	2	AC129800	AC129800 Rattus no	CI051	41.2	5.8	179976	2	CR539318	CR539318 Mus muscu
c 979	41.4	5.8	300486	2	AC129699	AC129699 Rattus no	1052	41.2	5.8	180842	2	CR536619	CR536619 Danio rer
980	41.4	5.8	312430	1	RPXX02	AJ235271 Rickettsi	CI053	41.2	5.8	181948	5	AC146504	AC146504 Danio rer
981	41.4	5.8	314959	2	AC106099	AC106099 Rattus no	1054	41.2	5.8	182109	10	AC108824	AC108824 Mus muscu
c 982	41.4	5.8	344530	6	AC133390	AC133390 Rattus no	CI055	41.2	5.8	182455	2	CR627498	CR627498 Danio rer
c 983	41.2	5.8	348	6	CQ398541	CQ398541 Sequence	CI056	41.2	5.8	184535	2	CNS051CJ	AL355100 Homo sapi
c 984	41.2	5.8	348	6	CQ404828	CQ404828 Sequence	1057	41.2	5.8	186990	10	AC102509	AC102509 Mus muscu
c 985	41.2	5.8	1207	3	AF467679	AF467679 Acidiella	1058	41.2	5.8	189054	2	AC135272	AC135272 Rattus no
986	41.2	5.8	2015	10	BC048407	BC048407 Mus muscu	CI059	41.2	5.8	191642	5	CR524481	CR524481 Zebrafish
987	41.2	5.8	5286	6	CQ806574	CQ806574 Sequence	CI060	41.2	5.8	192470	10	AC098839	AC098839 Genomic s
988	41.2	5.8	5286	6	CQ806843	CQ806843 Sequence	CI061	41.2	5.8	192819	10	AC108423	AC108423 Mus muscu
989	41.2	5.8	5286	6	CQ807117	CQ807117 Sequence	CI062	41.2	5.8	193996	2	AC129222	AC129222 Mus muscu
990	41.2	5.8	5286	6	AX795682	AX795682 Sequence	CI063	41.2	5.8	194103	2	AC060818	AC060818 Homo sapi
991	41.2	5.8	5286	6	AX795781	AX795781 Sequence	1064	41.2	5.8	194673	9	AC009891	AC009891 Genomic S
992	41.2	5.8	5286	6	AX795897	AX795897 Sequence	CI065	41.2	5.8	195130	2	AL359832	AL359832 Human DNA
993	41.2	5.8	5302	3	AC116961	AC116961 Dictyoste	CI066	41.2	5.8	195369	5	EX663499	EX663499 Zebrafish
c 994	41.2	5.8	6294	6	AX345956	AX345956 Sequence	CI067	41.2	5.8	196850	10	AC104872	AC104872 Mus muscu
995	41.2	5.8	72265	6	AC006516	AC006516 Homo sapi	CI068	41.2	5.8	197113	2	CR352331	CR352331 Danio rer
996	41.2	5.8	79926	9	AC125470	AC125470 Homo sapi	CI069	41.2	5.8	198494	10	AC068459	AC068459 Mus muscu
c 997	41.2	5.8	82140	10	EX539309	EX539309 Mouse DNA	1070	41.2	5.8	198742	2	AL355360	AL355360 Homo sapi
c 998	41.2	5.8	96071	10	EX936349	EX936349 Mouse DNA	1071	41.2	5.8	199323	2	AC099943	AC099943 Mus muscu
999	41.2	5.8	98398	2	AC149207	AC149207 Medicago	1072	41.2	5.8	199468	5	EX005256	EX005256 Zebrafish
1000	41.2	5.8	102507	9	HSJ324N14	AL109938 Human DNA	1073	41.2	5.8	200246	10	AC122224	AC122224 Mus muscu
1001	41.2	5.8	119735	5	BS330723	BS330723 Zebrafish	1074	41.2	5.8	202625	2	CR392365	CR392365 Danio rer
1002	41.2	5.8	125893	8	AC124960	AC124960 Medicago	1075	41.2	5.8	205582	2	AC120951	AC120951 Rattus no
1003	41.2	5.8	126091	5	EX119821	EX119821 Zebrafish	CI076	41.2	5.8	207810	2	AC132949	AC132949 Mus muscu
CI004	41.2	5.8	141645	2	AC125004	AC125004 Mus muscu	1077	41.2	5.8	212897	2	AC109898	AC109898 Rattus no
1005	41.2	5.8	146478	10	AC102722	AC102722 Mus muscu	1078	41.2	5.8	214158	5	EX669787	EX669787 Zebrafish
1006	41.2	5.8	142245	2	AC120266	AC120266 Rattus no	1079	41.2	5.8	214715	2	CR457461	CR457461 Danio rer
CI007	41.2	5.8	143516	2	CR388033	CR388033 Danio rer	1080	41.2	5.8	221608	2	AC135934	AC135934 Rattus no
CI008	41.2	5.8	144563	9	AC006204	AC006204 Homo sapi	CI081	41.2	5.8	222775	10	AC084069	AC084069 Mus muscu
CI010	41.2	5.8	147349	2	EX469904	EX469904 Zebrafish	CI082	41.2	5.8	223954	2	AC119904	AC119904 Mus muscu
1011	41.2	5.8	150199	9	AC087568	AC087568 Danio rer	CI083	41.2	5.8	225558	2	AC103066	AC103066 Rattus no
1012	41.2	5.8	151170	2	EX950171	EX950171 Pan trogl	1084	41.2	5.8	225636	2	AC102923	AC102923 Mus muscu
CI013	41.2	5.8	151364	2	EX927233	EX927233 Danio rer	1085	41.2	5.8	226820	2	AC118872	AC118872 Rattus no
1014	41.2	5.8	151616	2	AC121662	AC121662 Rattus no	1086	41.2	5.8	228930	10	AC110919	AC110919 Mus muscu
CI015	41.2	5.8	152780	2	AC139961	AC139961 Rattus no	1087	41.2	5.8	236223	2	AC130047	AC130047 Rattus no
CI016	41.2	5.8	152780	2	EX324140	EX324140 Danio rer	1088	41.2	5.8	230281	2	AC094503	AC094503 Rattus no
1017	41.2	5.8	153089	2	AC068619	AC068619 Homo sapi	CI089	41.2	5.8	230307	2	AC098345	AC098345 Rattus no
CI018	41.2	5.8	154867	4	SSC131112	AJ131112 Sus scrof	1090	41.2	5.8	236427	2	AC132468	AC132468 Mus muscu
CI020	41.2	5.8	154941	10	AC125096	AC125096 Mus muscu	CI091	41.2	5.8	249616	10	AE014183	AE014183 Mus muscu
CI021	41.2	5.8	156056	10	AC125265	AC125265 Mus muscu	1092	41.2	5.8	250050	1	BX248584	BX248584 Blochmann
1022	41.2	5.8	156300	2	AC135079	AC135079 Mus muscu	CI093	41.2	5.8	252504	2	AC073815	AC073815 Mus muscu
1023	41.2	5.8	157007	2	CR627496	CR627496 Danio rer	CI094	41.2	5.8	252504	2	AC073815	AC073815 Mus muscu
1024	41.2	5.8	157564	2	AC025996	AC025996 Homo sapi	CI095	41.2	5.8	245713	2	AC096111	AC096111 Rattus no
1025	41.2	5.8	158242	2	AC109188	AC109188 Mus muscu	CI096	41.2	5.8	248027	2	AC130502	AC130502 Rattus no
1026	41.2	5.8	159475	2	AC023059	AC023059 Mus muscu	1097	41.2	5.8	249616	10	AE014183	AE014183 Mus muscu
CI027	41.2	5.8	160521	2	AC127728	AC127728 Rattus no	1098	41.2	5.8	252504	2	AC073815	AC073815 Mus muscu
CI028	41.2	5.8	161097	2	AC113870	AC113870 Rattus no	1099	41.2	5.8	252504	2	AC073815	AC073815 Mus muscu
1029	41.2	5.8	161812	5	EX005045	EX005045 Zebrafish	CI100	41.2	5.8	259798	2	AC094723	AC094723 Rattus no
1030	41.2	5.8	162737	2	AC007733	AC007733 Homo sapi	1101	41.2	5.8	264488	2	AC121330	AC121330 Rattus no
CI031	41.2	5.8	163179	9	AC022541	AC022541 Homo sapi	1102	41.2	5.8	273532	2	AC115408	AC115408 Homo sapi
1031	41.2	5.8	163795	9	AP000356	AP000356 Homo sapi	CI103	41.2	5.8	280920	2	AC096836	AC096836 Rattus no
CI032	41.2	5.8	164102	2	AC149061	AC149061 Mus muscu	1104	41.2	5.8	290248	2	AC094662	AC094662 Rattus no
1033	41.2	5.8	164899	2	CR318597	CR318597 Danio rer	CI105	41.2	5.8	294430	2	AC116737	AC116737 Mus muscu
1034	41.2	5.8	165396	9	AC105221	AC105221 Homo sapi	1106	41.2	5.8	304407	2	AC073813	AC073813 Mus muscu
CI035	41.2	5.8	166418	2	AC119971	AC119971 Mus muscu	1107	41.2	5.8	325935	2	AC106598	AC106598 Rattus no
CI037	41.2	5.8	167791	2	AC120913	AC120913 Rattus no	1108	41.2	5.8	325935	2	AC106598	AC106598 Rattus no
1038	41.2	5.8	168511	2	EX950221	EX950221 Danio rer	CI109	41.2	5.8	349980	6	AX344573	AX344573 Sequence
1039	41.2	5.8	169591	2	AC026379	AC026379 Mus muscu	1110	41	5.8	353	5	GZ94843	GZ94843 G.gallus mi
1040	41.2	5.8	170453	8	AP005095	AP005095 Oryza sat	1111	41	5.8	515	5	LLA16827	Y16827 Lagopus lag
CI038	41.2	5.8	170750	2	AC103898	AC103898 Bos tauru	CI112	41	5.8	1896	3	AK025084	AK025084 Homo sapi
1041	41.2	5.8	171142	9	AC069026	AC069026 Homo sapi	CI113	41	5.8	2256	3	SPFWTTGRG	M76713 Spodoptera
							CI114	41	5.8	4725	6	BC040525	BC040525 Homo sapi
									5.8	6467	6	AX344761	AX344761 Sequence

1115	41	5.8	7000	10	AF458960	AF458960 Mus muscu	c1188	41	5.8	200604	9	AC087373	AC087373 Homo sapi
1116	41	5.8	7276	10	AL732549	AL732549 Mouse DNA	1189	41	5.8	200970	2	AC110728	AC110728 Mus muscu
c1117	41	5.8	34347	3	U38377	U38377 Caenorhabdi	1190	41	5.8	201681	2	AC115794	AC115794 Mus muscu
1118	41	5.8	34408	10	AF463769	AF463769 Mus muscu	1191	41	5.8	202249	2	BX950214	BX950214 Danio rer
c1119	41	5.8	41321	2	AC149348	AC149348 Phakopsor	1192	41	5.8	202615	2	CR450766	CR450766 Danio rer
c1120	41	5.8	44059	9	AL669815	AL669815 Human DNA	1193	41	5.8	202884	2	AC111083	AC111083 Mus muscu
c1121	41	5.8	84892	5	AL627164	AL627164 Zebrafish	c1194	41	5.8	207454	2	AC129934	AC129934 Mus muscu
c1122	41	5.8	85397	3	AC026301	AC026301 Caenorhab	1195	41	5.8	208519	2	AC131718	AC131718 Mus muscu
c1123	41	5.8	90479	2	AC121463_3	Continuation (4 of	c1196	41	5.8	208594	10	AC131185	AC131185 Mus muscu
c1124	41	5.8	98020	10	AL935152	AL935152 Mouse DNA	c1197	41	5.8	211748	2	CR392346	CR392346 Danio rer
c1125	41	5.8	100141	2	AC091426	AC091426 Mus muscu	c1198	41	5.8	213552	9	AC010928	AC010928 Homo sapi
c1126	41	5.8	103338	8	AC002294	AC002294 Arabidops	1199	41	5.8	214192	2	AC140497	AC140497 Mus muscu
c1127	41	5.8	106951	8	AC147963	AC147963 Medicago	c1200	41	5.8	216410	2	AC140457	AC140457 Mus muscu
1128	41	5.8	110000	1	AE017225_15	Continuation (16 o	1201	41	5.8	216472	2	AC149588	AC149588 Mus muscu
1129	41	5.8	110000	1	AE017355_15	Continuation (16 o	c1202	41	5.8	219626	10	AC098719	AC098719 Mus muscu
1130	41	5.8	110000	1	AE017355_15	Continuation (16 o	c1203	41	5.8	220804	10	AC091283	AC091283 Mus muscu
1131	41	5.8	110000	2	AC101662_0	AC101662 Mus muscu	c1204	41	5.8	223070	10	AC118546	AC118546 Mus muscu
1132	41	5.8	110000	2	AC021632_3	Continuation (4 of	1205	41	5.8	223901	2	AC116674	AC116674 Mus muscu
c1133	41	5.8	110000	2	BX465864_2	Continuation (3 of	1206	41	5.8	232972	2	AC093991	AC093991 Rattus no
c1134	41	5.8	110000	2	PFMAL13_02	Continuation (5 of	1207	41	5.8	234996	2	AC130764	AC130764 Rattus no
c1135	41	5.8	110000	2	PFMAL8PT_04	Continuation (7 of	1208	41	5.8	239719	2	AC116054	AC116054 Rattus no
1136	41	5.8	110000	3	PFMAL8PT_06	Continuation (7 of	c1209	41	5.8	242893	10	AC102550	AC102550 Mus muscu
1137	41	5.8	111882	3	AC115612	AC115612 Dictyoste	c1210	41	5.8	245656	2	AC135590	AC135590 Rattus no
1138	41	5.8	118301	9	AC121342	AC121342 Homo sapi	1211	41	5.8	245802	2	AC006279	AC006279 Plasmodiu
1139	41	5.8	126495	9	AL450310	AL450310 Human DNA	c1212	41	5.8	248883	2	CR626924	CR626924 Danio rer
c1140	41	5.8	129142	10	AC121980	AC121980 Mus muscu	c1213	41	5.8	250823	3	AE014821	AE014821 Plasmodiu
1141	41	5.8	131711	2	AP003954	AP003954 Oryza sat	c1214	41	5.8	251762	3	AE014851	AE014851 Plasmodiu
1142	41	5.8	132710	9	AC093535	AC093535 Homo sapi	1215	41	5.8	253305	3	PFMAL3P7	PFMAL3P7 Plasmodiu
c1143	41	5.8	142732	10	AC084332	AC084332 Mus muscu	1216	41	5.8	254333	2	AC106503	AC106503 Rattus no
c1144	41	5.8	145772	8	AP004269	AP004269 Oryza sat	c1217	41	5.8	254572	2	AC093940	AC093940 Rattus no
c1145	41	5.8	146127	9	AL391838	AL391838 Human DNA	c1218	41	5.8	256172	2	AC005139	AC005139 Plasmodiu
1146	41	5.8	150638	2	AC129994	AC129994 Rattus no	c1219	41	5.8	257351	2	AC134160	AC134160 Rattus no
1147	41	5.8	153191	10	AC125527	AC125527 Mus muscu	c1220	41	5.8	260929	3	AE014852	AE014852 Plasmodiu
c1148	41	5.8	154338	10	AL669826	AL669826 Mouse DNA	1221	41	5.8	260967	2	AC091771	AC091771 Mus muscu
1149	41	5.8	155411	10	AC133602	AC133602 Mus muscu	c1222	41	5.8	262297	2	AC101808	AC101808 Mus muscu
1150	41	5.8	155602	10	AL929147	AL929147 Mouse DNA	1223	41	5.8	262916	2	AC022779	AC022779 Mus muscu
c1151	41	5.8	159500	10	AC005742	AC005742 Mus muscu	c1224	41	5.8	270733	2	AC129455	AC129455 Rattus no
1152	41	5.8	163566	4	AC139340	AC139340 Atelerix	c1225	41	5.8	274011	2	AC096142	AC096142 Rattus no
1153	41	5.8	164217	9	AC093264	AC093264 Homo sapi	1226	41	5.8	282515	4	AC118094	AC118094 Rattus no
1154	41	5.8	165777	10	BX004852	BX004852 Mouse DNA	c1227	41	5.8	286014	2	AC112125	AC112125 Rattus no
c1155	41	5.8	166986	2	AC129579	AC129579 Mus muscu	1228	41	5.8	290525	1	AE017029	AE017029 Bacillus
1156	41	5.8	168008	2	AC027488	AC027488 Homo sapi	c1229	41	5.8	293431	2	PFMAL13P4	PFMAL13P4 Plasmodiu
1157	41	5.8	169102	9	AC078905	AC078905 Homo sapi	c1230	41	5.8	298216	2	AC006875	AC006875 Caenorhab
c1158	41	5.8	169889	2	AC119919	AC119919 Mus muscu	c1231	41	5.8	310779	2	AC005140	AC005140 Plasmodiu
c1159	41	5.8	170053	2	AC133069	AC133069 Macaca mu	1232	41	5.8	336002	2	AC098355	AC098355 Rattus no
c1160	41	5.8	170249	2	AC114548	AC114548 Mus muscu	1233	41	5.8	343937	2	AC124419	AC124419 Rattus no
1161	41	5.8	170534	2	CR391918	CR391918 Danio rer	c1234	41	5.8	344428	2	AC141879	AC141879 Mus muscu
1162	41	5.8	171237	2	CR376858	CR376858 Danio rer	c1235	40.8	5.7	465	11	BV031385	BV031385 S208P6641
c1163	41	5.8	173782	2	AC147797	AC147797 Mus muscu	1236	40.8	5.7	828	11	BV035012	BV035012 S212P6052
c1164	41	5.8	175639	10	AL6262931	AL6262931 Mouse DNA	1237	40.8	5.7	1452	3	AF194170	AF194170 Dictyoste
1165	41	5.8	177056	9	AC091843	AC091843 Homo sapi	c1238	40.8	5.7	1517	3	DDU66911	DDU66911 Dictyoste
c1166	41	5.8	177962	10	AC147251	AC147251 Mus muscu	1239	40.8	5.7	3038	9	BSM806221	BSM806221 Homo sapi
1167	41	5.8	180851	2	AC090210	AC090210 Homo sapi	c1240	40.8	5.7	11105	1	AE010742	AE010742 Methanosa
1168	41	5.8	181211	2	AP001904	AP001904 Homo sapi	1241	40.8	5.7	56568	10	AC096621	AC096621 Mus muscu
c1169	41	5.8	181805	2	AC114445	AC114445 Rattus no	1242	40.8	5.7	70067	2	BX546458_3	BX546458_3 Continuation (4 of
1170	41	5.8	182484	2	AC137445	AC137445 Rattus no	1243	40.8	5.7	85413	8	AC009324	AC009324 Arabidops
c1171	41	5.8	182582	10	AC125532	AC125532 Mus muscu	1244	40.8	5.7	99046	2	BX537307	BX537307 Danio rer
c1172	41	5.8	182758	2	BX511146	BX511146 Danio rer	1245	40.8	5.7	107121	9	AC013461	AC013461 Homo sapi
1173	41	5.8	182760	2	AC120395	AC120395 Mus muscu	c1246	40.8	5.7	110000	3	AC116984	AC116984 Continuation (4 of
c1174	41	5.8	183285	10	AC128665	AC128665 Mus muscu	1247	40.8	5.7	119481	9	AL136234	AL136234 Human DNA
1175	41	5.8	184142	5	BX005122	BX005122 Zebrafish	1248	40.8	5.7	127176	10	CR536609	CR536609 Mouse DNA
c1176	41	5.8	186165	9	AC112187	AC112187 Homo sapi	1249	40.8	5.7	130260	2	AC102747	AC102747 Mus muscu
c1177	41	5.8	186729	2	AC113271	AC113271 Mus muscu	1250	40.8	5.7	131329	9	AC004873	AC004873 Homo sapi
c1178	41	5.8	188515	2	AC102531	AC102531 Mus muscu	c1251	40.8	5.7	135208	2	AC136096	AC136096 Rattus no
1179	41	5.8	189006	2	AC148142	AC148142 Bos tauru	1252	40.8	5.7	139287	10	AC104869	AC104869 Mus muscu
c1180	41	5.8	189158	2	CR385084	CR385084 Danio rer	c1253	40.8	5.7	139636	10	AC124376	AC124376 Mus muscu
c1181	41	5.8	191270	9	AP000776	AP000776 Homo sapi	c1254	40.8	5.7	145084	10	BX000479	BX000479 Mouse DNA
c1182	41	5.8	193622	2	CR392360	CR392360 Danio rer	c1255	40.8	5.7	147560	10	AC112800	AC112800 Rattus no
1183	41	5.8	196739	2	AC150685	AC150685 Mus muscu	1256	40.8	5.7	151341	5	AL929536	AL929536 Zebrafish
1184	41	5.8	197131	10	AC121829	AC121829 Mus muscu	1257	40.8	5.7	151639	2	AP001193	AP001193 Homo sapi
c1185	41	5.8	199320	2	AC016677	AC016677 Homo sapi	1258	40.8	5.7	154632	10	AC131702	AC131702 Mus muscu
1186	41	5.8	199593	10	AL671871	AL671871 Mouse DNA	1259	40.8	5.7	154675	2	CR354440	CR354440 Danio rer
1187	41	5.8	200147	2	AC022774	AC022774 Mus muscu	1260	40.8	5.7	156070	2	AC110726	AC110726 Mus muscu

c1261	40.8	5.7	157435	9	HS50024	AL034380 Human DNA	1334	40.8	5.7	233270	2	AC129038	AC129038 Rattus no
c1262	40.8	5.7	158398	10	AL929020	Mouse DNA	1335	40.8	5.7	237682	2	BX469902	BX469902 Danio rer
c1263	40.8	5.7	160048	10	AC002109	Genomic s	c1336	40.8	5.7	241789	10	AC102545	AC102545 Mus muscu
c1264	40.8	5.7	161244	10	AL773536	Mouse DNA	1337	40.8	5.7	242318	10	AC097354	AC097354 Mus muscu
c1265	40.8	5.7	161277	8	AP002972	Oryza sat	1338	40.8	5.7	243789	10	AL672082	AL672082 Mouse DNA
c1266	40.8	5.7	162240	2	AC145756	Pan trogl	1339	40.8	5.7	246611	2	AC111404	AC111404 Rattus no
c1267	40.8	5.7	163118	2	AC090973	Oryza sat	1340	40.8	5.7	246863	2	AC126809	AC126809 Rattus no
c1268	40.8	5.7	163136	2	CR352212	Danio rer	1341	40.8	5.7	252420	3	AE014841	AE014841 Plasmodiu
c1269	40.8	5.7	163149	9	CNS01DS2	Human chr	1342	40.8	5.7	254007	2	AC094413	AC094413 Rattus no
c1270	40.8	5.7	163161	5	AL928928	Human chr	1343	40.8	5.7	254050	3	PF9A29358	PF9A29358 Plasmodiu
c1271	40.8	5.7	163547	10	AL928788	Mouse DNA	1344	40.8	5.7	256880	3	AC112000	AC112000 Rattus no
c1272	40.8	5.7	164171	2	CR388067	Danio rer	1345	40.8	5.7	257868	2	AC130923	AC130923 Rattus no
c1273	40.8	5.7	165765	2	AC117979	Rattus no	1346	40.8	5.7	258506	2	AC096605	AC096605 Rattus no
c1274	40.8	5.7	166132	2	BX511266	Danio rer	1347	40.8	5.7	261143	2	AC097135	AC097135 Rattus no
c1275	40.8	5.7	166353	5	BX323090	Zebrafish	1348	40.8	5.7	266115	2	AC122201	AC122201 Mus muscu
c1276	40.8	5.7	168050	9	AC090526	Homo sapi	1349	40.8	5.7	268230	2	AC105808	AC105808 Rattus no
c1277	40.8	5.7	168372	8	AP002746	Oryza sat	1350	40.8	5.7	269375	2	AC107165	AC107165 Rattus no
c1278	40.8	5.7	170125	9	CNS01DRJ	Human chr	1351	40.8	5.7	322079	2	AC093481	AC093481 Mus muscu
c1279	40.8	5.7	170141	2	AL611928	Homo sapi	1352	40.8	5.7	335050	3	PF9A29356	PF9A29356 Plasmodiu
c1280	40.8	5.7	171078	5	AL845301	Zebrafish	1353	40.8	5.7	337582	3	PFMAL4P1	PFMAL4P1 Rattus no
c1281	40.8	5.7	173055	2	CR628344	Danio rer	1354	40.6	5.7	298	6	AX192989	AX192989 Sequence
c1282	40.8	5.7	174268	2	CR382293	Danio rer	1355	40.6	5.7	301	6	AX340894	AX340894 Sequence
c1283	40.8	5.7	174608	2	BX980570	Danio rer	1356	40.6	5.7	301	6	AX341827	AX341827 Sequence
c1284	40.8	5.7	176152	2	AC135573	Rattus no	1357	40.6	5.7	548	5	APL272579	APL272579 Anas plat
c1285	40.8	5.7	177242	2	AC147237	Mus muscu	1358	40.6	5.7	581	11	BV030603	BV030603 S208P6642
c1286	40.8	5.7	178746	10	AC125092	Mus muscu	1359	40.6	5.7	588	6	AX387722	AX387722 Sequence
c1287	40.8	5.7	179591	9	AC093902	Homo sapi	1360	40.6	5.7	625	11	HUMU2341	HUMU2341 Human chrom
c1288	40.8	5.7	179714	8	AP002743	Oryza sat	1361	40.6	5.7	1124	9	BC025950	BC025950 Homo sapi
c1289	40.8	5.7	180732	2	AC108393	Mus muscu	1362	40.6	5.7	1130	6	BD222734	BD222734 Human sig
c1290	40.8	5.7	181381	2	CR450818	Danio rer	1363	40.6	5.7	2938	3	TTU12971	TTU12971 Tetrahymena
c1291	40.8	5.7	183291	10	AL808017	Mouse DNA	1364	40.6	5.7	9754	10	MMY14422	MMY14422 M.musculus
c1292	40.8	5.7	185132	10	AC122255	Mus muscu	1365	40.6	5.7	14429	6	AX347144	AX347144 Sequence
c1293	40.8	5.7	187792	2	CR407545	Danio rer	1366	40.6	5.7	14429	6	AX458581	AX458581 Sequence
c1294	40.8	5.7	188776	5	BX537130	Zebrafish	1367	40.6	5.7	15421	3	PFCOMP1RA	PFCOMP1RA Sequence
c1295	40.8	5.7	189115	10	AL772346	Mouse DNA	1368	40.6	5.7	17517	2	AC017365	AC017365 Drosophil
c1296	40.8	5.7	190089	10	AC133092	Mus muscu	1369	40.6	5.7	34750	3	AY217738	AY217738 Eimeria t
c1297	40.8	5.7	190347	10	AC124193	Mus muscu	1370	40.6	5.7	42010	10	AC002298	AC002298 Genomic s
c1298	40.8	5.7	192026	10	AC125072	Mus muscu	1371	40.6	5.7	46530	2	BX293554	BX293554 Sequence
c1299	40.8	5.7	193097	2	CR391913	Danio rer	1372	40.6	5.7	50000	6	AX392736	AX392736 Sequence
c1300	40.8	5.7	194018	10	AC124686	Mus muscu	1373	40.6	5.7	53932	2	AC023371	AC023371 Homo sapi
c1301	40.8	5.7	195428	2	AC115897	Mus muscu	1374	40.6	5.7	64135	9	AL158080	AL158080 Human DNA
c1302	40.8	5.7	196445	10	AC117949	Mus muscu	1375	40.6	5.7	65691	3	PFMAL3P1	PFMAL3P1 Plasmodium
c1303	40.8	5.7	197113	2	CR352231	Danio rer	1376	40.6	5.7	67159	2	AC103698	AC103698 Homo sapi
c1304	40.8	5.7	197616	9	AC069113	Homo sapi	1377	40.6	5.7	71537	2	AC136750	AC136750 Mus muscu
c1305	40.8	5.7	197784	2	CR388005	Danio rer	1378	40.6	5.7	73345	8	ALQ0294725	ALQ0294725 Astasia 1
c1306	40.8	5.7	199014	2	AC108293	Rattus no	1379	40.6	5.7	74998	9	AC009423	AC009423 Homo sapi
c1307	40.8	5.7	199264	10	AC122853	Mus muscu	1380	40.6	5.7	77397	2	AL365175	AL365175 Homo sapi
c1308	40.8	5.7	202260	2	AC118790	Mus muscu	1381	40.6	5.7	78843	2	AC120740	AC120740 Continuation (4 of
c1309	40.8	5.7	202276	2	AC149608	Mus muscu	1382	40.6	5.7	82182	2	BX571840	BX571840 Danio rer
c1310	40.8	5.7	202835	10	AC113307	Mus muscu	1383	40.6	5.7	86097	9	AL662896	AL662896 Human DNA
c1311	40.8	5.7	203128	10	AL732565	Mouse DNA	1384	40.6	5.7	88549	3	AC116924	AC116924 Dictyoste
c1312	40.8	5.7	207472	2	AC108840	Mus muscu	1385	40.6	5.7	97494	5	BX511127	BX511127 Zebrafish
c1313	40.8	5.7	207598	10	AC122901	Mus muscu	1386	40.6	5.7	109761	9	AF271405	AF271405 Homo sapi
c1314	40.8	5.7	208028	10	AC125260	Mus muscu	1387	40.6	5.7	110000	2	AC101867	AC101867 Continuation (2 of
c1315	40.8	5.7	209066	10	AC125260	Mus muscu	1388	40.6	5.7	110000	2	AC113216	AC113216 Rattus no
c1316	40.8	5.7	210193	10	AC127337	Mus muscu	1389	40.6	5.7	110000	2	AC129940	AC129940 Continuation (3 of
c1317	40.8	5.7	210638	10	AC125210	Mus muscu	1390	40.6	5.7	110000	2	AC130739	AC130739 Continuation (2 of
c1318	40.8	5.7	215638	10	AC124200	Mus muscu	1391	40.6	5.7	110000	2	AL928948	AL928948 Mus muscu
c1319	40.8	5.7	215731	2	AC136554	Rattus no	1392	40.6	5.7	110000	2	AL928948	AL928948 Continuation (3 of
c1320	40.8	5.7	215845	2	AC149718	Bos tauru	1393	40.6	5.7	110000	2	PFMAL8P1_02	PFMAL8P1_02 Continuation (3 of
c1321	40.8	5.7	216970	2	AL603630	Mus muscu	1394	40.6	5.7	110000	2	PFMAL8P1_03	PFMAL8P1_03 Continuation (4 of
c1322	40.8	5.7	218701	2	CR626507	Danio rer	1395	40.6	5.7	110000	8	CR382132	CR382132 Continuation (18 of
c1323	40.8	5.7	219469	2	AC095907	Rattus no	1396	40.6	5.7	114285	10	AL844576	AL844576 Mouse DNA
c1324	40.8	5.7	219565	2	AC111520	Rattus no	1397	40.6	5.7	114878	10	AL591131	AL591131 Mouse DNA
c1325	40.8	5.7	220242	10	AC099594	Mus muscu	1398	40.6	5.7	116341	9	AL135936	AL135936 Human DNA
c1326	40.8	5.7	220475	2	AC098107	Rattus no	1399	40.6	5.7	119077	9	AL354982	AL354982 Human DNA
c1327	40.8	5.7	221324	2	AC119606	Rattus no	1400	40.6	5.7	119859	9	AL359075	AL359075 Human DNA
c1328	40.8	5.7	221548	10	AC115689	Mus muscu	1401	40.6	5.7	120458	2	AC146589	AC146589 Medicago
c1329	40.8	5.7	221928	5	BX120008	Zebrafish	1402	40.6	5.7	123556	9	HS507115	HS507115 Zebrafish
c1330	40.8	5.7	222469	2	AC096427	Rattus no	1403	40.6	5.7	124118	8	AP003309	AP003309 Oryza sat
c1331	40.8	5.7	223608	5	AL954308	Zebrafish	1404	40.6	5.7	125020	9	AF429315	AF429315 Homo sapi
c1332	40.8	5.7	224949	2	AC115413	Rattus no	1405	40.6	5.7	127820	9	HSJ612B15	HSJ612B15 Human DNA
c1333	40.8	5.7	226280	2	AC099657	Rattus no	1406	40.6	5.7	128916	2	AC145362	AC145362 Felis cat
c1334	40.8	5.7	229563	10	AC024957	Mus muscu							

1407	40.6	5.7	129355	9	AC004853	1480	40.6	5.7	198197	2	BX322641	BX322641 Mus muscu
1408	40.6	5.7	132013	2	CR354556	1481	40.6	5.7	198197	10	AC125035	AC125035 Mus muscu
1409	40.6	5.7	132896	2	AC122785	1482	40.6	5.7	198551	10	AC068605	AC068605 Mus muscu
1410	40.6	5.7	133381	10	AC109308	1483	40.6	5.7	199283	2	AC146662	AC146662 Callithri
1411	40.6	5.7	137338	2	AC132234	1484	40.6	5.7	199704	10	AC020968	AC020968 Mus muscu
1412	40.6	5.7	138022	2	AC150214	1485	40.6	5.7	200583	2	AC147694	AC147694 Ocolemur
1413	40.6	5.7	139097	2	AC004591	1486	40.6	5.7	201659	5	AL953881	AL953881 Zebrafish
1414	40.6	5.7	139122	8	AC127021	1487	40.6	5.7	202086	10	AC080015	AC080015 Mus muscu
1415	40.6	5.7	140864	10	AC126803	1488	40.6	5.7	202371	2	AC119709	AC119709 Rattus no
1416	40.6	5.7	141121	10	AC099636	1489	40.6	5.7	202561	10	AC118684	AC118684 Mus muscu
1417	40.6	5.7	146397	5	AL772391	1490	40.6	5.7	203273	10	AC112998	AC112998 Mus muscu
1418	40.6	5.7	146835	10	AC100740	1491	40.6	5.7	204385	5	AC118837	AC118837 Zebrafish
1419	40.6	5.7	146868	2	AC016802	1492	40.6	5.7	204666	2	AC118837	AC118837 Zebrafish
1420	40.6	5.7	150276	5	AL627305	1493	40.6	5.7	204804	2	CR354372	CR354372 Danio rer
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1424	40.6	5.7	154448	5	BX511105	1497	40.6	5.7	208979	2	AC023610	AC023610 Mus muscu
1425	40.6	5.7	157894	2	AC104927	1498	40.6	5.7	210632	10	AC120797	AC120797 Mus muscu
1426	40.6	5.7	157894	2	AC104927	1499	40.6	5.7	212280	9	HSB362E11	AL121873 Human DNA
1427	40.6	5.7	158562	9	AL603888	1500	40.6	5.7	212288	2	CR293522	CR293522 Danio rer
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1483	40.6	5.7	199283	2	AC146662	1483	40.6	5.7	199283	2	AC146662	AC146662 Callithri
1484	40.6	5.7	199704	10	AC020968	1484	40.6	5.7	199704	10	AC020968	AC020968 Mus muscu
1485	40.6	5.7	200583	2	AC147694	1485	40.6	5.7	200583	2	AC147694	AC147694 Ocolemur
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1487	40.6	5.7	202086	10	AC080015	1487	40.6	5.7	202086	10	AC080015	AC080015 Mus muscu
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1496	40.6	5.7	208979	2	AC023610	1496	40.6	5.7	208979	2	AC023610	AC023610 Mus muscu
1497	40.6	5.7	210632	10	AC120797	1497	40.6	5.7	210632	10	AC120797	AC120797 Mus muscu
1498	40.6	5.7	212280	9	HSB362E11	1498	40.6	5.7	212280	9	HSB362E11	AL121873 Human DNA
1499	40.6	5.7	212288	2	CR293522	1499	40.6	5.7	212288	2	CR293522	CR293522 Danio rer
1500	40.6	5.7	213387	2	AC109275	1500	40.6	5.7	213387	2	AC109275	AC109275 Mus muscu

ALIGNMENTS

RESULT 1

AR252626

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ORIGIN

Sequence 376 from patent US 6478825.

AR252626

AR252626.1

GI:27300534

Unknown.

Unclassified.

1. (bases 1 to 713)

Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.

Implant, method of making same and use of the implant for the treatment of bone defects

Patent: US 6478825-A 376 12-NOV-2002;

Location/Qualifiers

1..713

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity

Matches 713; Conservative

100.0%;

Score 713;

DB 6;

Length 713;

0;

Indels

Gaps

QY

1

AATATATCATCTATTATTAATCAATAATATGATTTCTTTTATTTCCAAATCAACATTTGGG

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Db

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Db

61

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360

ALIGNMENTS

RESULT 1	AR252626	713 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	Sequence 376 from patent US 6478825.				
DEFINITION	AR252626				
ACCESSION	AR252626				
VERSION	AR252626.1	GI:27300534			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 713)				
AUTHORS	Winterbottom J.M., Shimp, L., Boyce, T.M. and Kaes, D.				
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects				
JOURNAL	Patent: US 6478825-A 376 12-NOV-2002;				
FEATURES	Location/Qualifiers				
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Best Local Similarity	100.0%; Pred. No. 1.5e-135;				
Matches 713; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1	AAATATATCATCTATTTATTCATTAATCAATTAATGATTCATTTTATTCATTAATCAATTCATTTGGG	60		
Qy	61	TTTTGGGATTTTAAATTTTCAACACACAGCAATGACATTTTCTGTCACATTTATTTATT	120		
Db	61	TTTTGGGATTTTAAATTTTCAACACACAGCAATGACATTTTCTGTCACATTTATTTATT	120		
Qy	121	GTTCGGTATGTGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTCGAGATGGCTA	180		
Db	121	GTTCGGTATGTGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTCGAGATGGCTA	180		
Qy	181	CTTTCTATCAAGAAATAAGAGAACACACAGTCAACCCACACATTCATTTAGAGACAG	240		
Db	181	CTTTCTATCAAGAAATAAGAGAACACACAGTCAACCCACACATTCATTTAGAGACAG	240		
Qy	241	TGTGACTCTTACCAAGCTGCTCAAAACACAGGCGGATAGTTAAAGACGGAATCT	300		
Db	241	TGTGACTCTTACCAAGCTGCTCAAAACACAGGCGGATAGTTAAAGACGGAATCT	300		
Qy	301	TGACTCAAGAGGGTTAATTTCTTGGTCTGAAGCCTGGGGCGGGGTGTAAGAAAAACAC	360		

Db 301 TGACTCAAGAGGGTTAAATCTTTGGTCTGAAGCCTGGGCGAGGGGTGTAAGAAAAACAC 360
QY 361 TTAGATTCAATGATTGTTAAATTTAAGGCAATACACATATTAGTATTACCTTAGTGTAT 420
Db 361 TTAGATTCAATGATTGTTAAATTTAAGGCAATACACATATTAGTATTACCTTAGTGTAT 420
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Db 421 GTATCCCTGTCATATATACATTAAGGTGAAATTTATAAGTACCTATGTCAGTTGGCTGGAC 480
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Db 541 GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAGGAAAGAGTGTCTCTCCCC 600
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Db 661 AAGATGACAGGAGAAAGGAAAGGAAATGTTGCCAAGGAAAAAAA 713

RESULT 2
AX055452
LOCUS AX055452 713 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 82 from Patent WO0073452.
ACCESSION AX055452
VERSION AX055452.1 GI:12228719

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,
Tomas, D., Watanabe, C.K., and Wood, W.I.

TITLE Compositions and methods for the treatment of immune related
diseases

JOURNAL Patent: WO 0073452-A 82 07-DEC-2000;

Genentech, Inc. (US)

Location/Qualifiers

1..713

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 713; DB 6; Length 713;
Best Local Similarity 100.0%; Pred. No. 1.5e-135;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATATCATCTATTATCATTAATCAATAATGATTTCTTTTATCCAAATAACATTGGG 60

Db 1 AATATATCATCTATTATCATTAATCAATAATGATTTCTTTTATCCAAATAACATTGGG 60

QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTATT 120

Db 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTATT 120

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Db 121 GTTGGTATGCAAGCTATTTGGAGATCCAAATTCAGGAGCAACATTTGGAGATGGCTA 180

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Db 181 CTTTCTATCAAGAAATAAGAGAACCCACAGTCAACCCACAAATCATCTTTAGAGACAG 240

QY 241 TGTGACTCTCTACCAAGCTGTCAAACACACAGGCAAGGCATAGTTAAAGAGCGGAATCT 300
Db 241 TGTGACTCTCTACCAAGCTGTCAAACACACAGGCAAGGCATAGTTAAAGAGCGGAATCT 300
QY 301 TGACTCAAGAGGGTTAAATCTTTGGTCTGAAGCCTGGGCGAGGGGTGTAAGAAAAACAC 360
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Db 661 AAGATGACAGGAGAAAGGAAAGGAAATGTTGCCAAGGAAAAAAA 713

RESULT 3

AX03489

LOCUS AX03489 713 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 376 from Patent WO0073454.

ACCESSION AX03489

VERSION AX03489.1 GI:21436980

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,

Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,

Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,

Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,

Williams, P., Wood, W.I. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

JOURNAL Patent: WO 0073454-A 376 07-DEC-2000;

Genentech Inc. (US)

Location/Qualifiers

1..713

/organism="Homo sapiens"

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/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 713; DB 6; Length 713;

Best Local Similarity 100.0%; Pred. No. 1.5e-135;

Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AATATATCATCTATTATCATTAATCAATAATGATTTCTTTTATCCAAATAACATTGGG 60

QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTATT 120

Db 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTATT 120

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QY 121 GTTGGTATGTGAGCTATTGAGATCCCAATTCAGGAAGCAACACATTCGAGAAATGGCTA 180
DB |||||
DB 121 GTTGGTATGTGAGCTATTGAGATCCCAATTCAGGAAGCAACACATTCGAGAAATGGCTA 180
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DB |||||
DB 181 CTTTCTATCAAGAAATAAAGAGAACACACAGTCAACCCACACATTCATCTTTGAAGACAG 240
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RESULT 4
AX464340 713 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 473 from Patent WO0140466.
ACCESSION AX464340
VERSION AX464340.1 GI:21899186
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tamas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
same
JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;
Genentech Inc. (US)
FEATURES
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1 . 713
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 100.0%; Score 713; DB 6; Length 713;
Best Local Similarity 100.0%; Pred. No. 1.5e-435;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB |||||
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LOCUS
DEFINITION Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.
ACCESSION AY358685
VERSION AY358685.1 GI:37182491
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 713)
AUTHORS
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E.,
Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiedand, D., Woods, K.,
Xie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W. L. and Godowski, P.
THE SECRETED PROTEIN DISCOVERY INITIATIVE (SPDI), A LARGE-SCALE
EFFORT TO IDENTIFY NOVEL HUMAN SECRETED AND TRANSMEMBRANE PROTEINS:
A BIOINFORMATICS ASSESSMENT
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
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PUBMED 12975309
REFERENCE 2 (bases 1 to 713)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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RESULT 6
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DEFINITION Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
AC024224
VERSION AC024224.33
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 165414)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alabrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burich,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
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Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Haviak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
Holloway,C., Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S.,
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King,L., Koryah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Loulsegue,H., Lozado,R.J., Lu,X.,
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Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
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Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
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Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shim,C., Shoostari,N., Sisson,I.,
Sodergren,E., Sonake,E., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 165414)
Worley,K.C.
Direct Submission
Submitted (28-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 165414)
Worley,K.C.
Direct Submission
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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ACCESSION AC006510
VERSION AC006510.8 GI:10122018
KEYWORDS HTG; HTGS PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 240864)
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Burch,P., Burket,C., Burrell,K.L., Byrd,N.C., Carron,I.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
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Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
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Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,
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Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogub,M., Okwunonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Peters,L., Pickens,E., Primus,E., Pu,L.L.,
Quiles,M., Remy,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N.,
Thomas,S., Umani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 240864)
Worley,K.C.
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2000 this sequence version replaced gi:10086352.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: J-33
Center clone name: RP11-13CL13, RP11-656E20
----- Summary Statistics
Sequencing vector: Plasmid: M7789
Sequencing vector: M13, L08821
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Chemistry: Dye-terminator Big Dye: 23% of reads
Assembly program: Phrap; version 0.990329
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Consensus quality: 93014 bases at least Q30
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Estimated insert size: 331000; agarose-fp estimation
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Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 111086 111185: gap of unknown length
* 111186 134782: contig of 23597 bp in length
* 134783 134882: gap of unknown length
* 134883 163654: contig of 28772 bp in length
* 163655 163754: gap of unknown length
* 163755 185050: contig of 21296 bp in length
* 185051 185150: gap of unknown length
* 185151 194802: contig of 9652 bp in length
* 194803 194902: gap of unknown length
* 194903 202527: contig of 7625 bp in length
* 202528 202627: gap of unknown length

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TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT


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* 14091 20220: contig of 6130 bp in length
* 20221 20220: gap of unknown length
* 33395 33395: contig of 13075 bp in length
* 33496 33496: gap of unknown length
* 46731 46731: contig of 13236 bp in length
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* 80892 80892: contig of 22320 bp in length
* 80933 80933: gap of unknown length
* 103313 103313: gap of unknown length
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Db 86494 GGGAAAGGAAATATAAAGGGAGAAATGAGGAGGAGCACTGAAGACTGTAAATGCTTAATAA 86435
QY 712 AA 713
Db 86434 TA 86433

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RESULT 9

AC112033

LOCUS

DEFINITION

Rattus norvegicus clone CH230-94G2, *** SEQUENCING IN PROGRESS ***

2 unordered pieces.

AC112033

AC112033.3 GI:23667218

VERSION

HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (bases 1 to 273867)

AUTHORS

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bissolo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. W., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gaze, W., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovat, C., Kowis, C., Kraft, C. L., Lebow, H., Levian, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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 Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G., and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 273867)
 Worley, K.C.
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 273867)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GPBG
 Center clone name: CH230-94G2
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 24419 bases at least Q40
 Consensus quality: 247244 bases at least Q30
 Consensus quality: 249002 bases at least Q20
 Estimated insert size: 254595; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 271836: contig of 271836 bp in length
 * 271837 271936: gap of unknown length
 * 271937 273867: contig of 1931 bp in length.
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 QY 61 TTTTGGGATTTTAAATTTCAACACAGCAGATGACATT-TTTTCGTCACTATTATTAT 119
 Db 46029 TGTGTTCATTTTCAGTTTCAAGCAGACAGCAATGACTTTCTTTCTGCACTTTGCTGT 46088
 QY 120 TGTGTGTATGTGAAGCTATTTTGGAGATCCAATTCAGGAAGCAACACATTGGGAATGGCT 179
 Db 46089 TCGTGACATATGAGCATTTCCGAGATTCAATTCAGGAGATATCCAGAGGAGAAAGACA 46148
 QY 180 ACTTTCTATCAAGAAATAAGAGAACACAGTCACCCACACATCATCTTTTGAAGACA 239
 Db 46149 ACTTCCCATCAGAAATAAGGAGAACACCA---AACCCAGAACCATCTTTTAGATGAGA 46205
 QY 240 GTGTGACTCTACCAAGCTGTCAAAACCACAGGCAAGGCGCATAGTTAAAGGA----CG 294
 Db 46206 AGGTGGTCCCTCCAAAGGCATCCCAAACACTACAGCAAGGCGCAGAACTAAGGAGCAATGG 46265
 QY 295 GAATCTTGACTCAAGAGGGTTTAACTTCTGTGCTGAAGCCTGGGGCAGGG 344
 Db 46266 GATCCTGGATTCAGAGGTTTCATTTCTGTACTGAGGCTTGGGGTGGG 46315
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 LOCUS
 DEFINITION Homo sapiens beta-glucan receptor isoform H (BGR) mRNA, complete
 cds, alternatively spliced.
 ACCESSION AF400602
 VERSION AF400602.1 GI:15986713
 KEYWORDS

PC A61K37/02,A61K37/02,C12N15/00,(C12N15/00,C12R1:91) CC
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 CC Topology: Linear;
 FH Key Location/Qualifiers
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 FT /organism='Unidentified'.

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 DB 202 GCTATTGGAGATCCAAATTCAGGAAGCAACACATTCGAGATGGCTACTTCTATCAAGA 261
 QY 194 AATAAGAGAACCACACAGTCACACCAATCATCTTTAGAGACAGTGTGACTCCTACC 253
 DB 262 AATAAGAGAACCACACAGTCACACCAATCATCTTTAGAGACAGTGTGACTCCTACC 321
 QY 254 AAAGCTGTCAAAACACACAGG 273
 DB 322 AAAGCTGTCAAAACACACAGG 341

RESULT 13

AF400595 744 bp mRNA linear PRI 19-NOV-2001
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 DEFINITION cds, alternatively spliced.
 ACCESSION AF400595
 VERSION AF400595.1 GI:15986699
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 744)
 AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
 TITLE Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
 J. Biol. Chem. 276 (47), 43818-43823 (2001)
 JOURNAL 21570237
 MEDLINE 11567029
 PUBMED 2 (bases 1 to 744)
 REFERENCE Willment,J.A., Gordon,S. and Brown,G.D.
 AUTHORS Direct Submission
 TITLE Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
 JOURNAL Oxford University, South Parks Road, Oxford OX1 3RE, UK

FEATURES

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RESULT 14

AY026769 744 bp mRNA linear PRI 05-OCT-2001
 LOCUS Homo sapiens lectin-like receptor 1 (DECTIN1) mRNA, complete cds.
 DEFINITION
 ACCESSION AY026769
 VERSION AY026769.2 GI:15967096
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 744)
 AUTHORS Herranz-Falcon,P., Arce,I., Roda-Navarro,P. and Fernandez-Ruiz,E.
 TITLE Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene expressed on dendritic cells
 Immunogenetics 53 (4), 288-295 (2001)
 JOURNAL 21383615
 MEDLINE 11491532
 PUBMED 2 (bases 1 to 744)
 REFERENCE Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.
 AUTHORS Direct Submission
 TITLE Submitted (01-FEB-2001) Biologia Molecular, Hospital de la
 JOURNAL Princesa, Diego de Leon 62, Madrid 28006, Spain
 REFERENCE 3 (bases 1 to 744)
 AUTHORS Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-2001) Biologia Molecular, Hospital de la
 Princesa, Diego de Leon 62, Madrid 28006, Spain
 REMARK Sequence update by submitter
 COMMENT On Oct 5, 2001 this sequence version replaced gi:14278818.
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gene

CDS

ORIGIN

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QY 134 GCTATTTCGAGATCCAAATTCAGGAGCAACCAACATCATCTTTAGAGACAGTGTGACTCCTACC 193
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DB 262 AATAAGAGAGACCAAGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCCTACC 321

QY 254 AAAGCTGTCAAAACACACAGG 273
DB 322 AAAGCTGTCAAAACACACAGG 341

RESULT 15

AF400601 787 bp mRNA linear PRI 19-NOV-2001
DEFINITION Homo sapiens beta-glucan receptor isoform G (BGR) mRNA, complete cds, alternatively spliced.
ACCESSION AF400601
VERSION AF400601.1 GI:15986711
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 787)
Willment, J.A., Gordon, S. and Brown, G.D.
Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
JOURNAL MEDLINE
PUBMED 21570237
REFERENCE 2 (bases 1 to 787)
Willment, J.A., Gordon, S. and Brown, G.D.
Direct Submission
AUTHORS
TITLE Submitted (18-JUN-2001) Sir William Dunn School of Pathology, Oxford University, South Parks Road, Oxford OX1 3RE, UK
JOURNAL Location/Qualifiers
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gene

CDS

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QY 134 GCTATTTCGAGATCCAAATTCAGGAGCAACCAACATCATCTTTAGAGACAGTGTGACTCCTACC 193
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
Run on: December 2, 2004, 00:55:08 ; Search time 534.388 Seconds
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                Post-processing: Minimum Match 0%
                               Maximum Match 100%

Database :
Listing first 1500 summaries
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12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID AAZ65094 standard; cDNA; 713 BP.
DE Membrane-bound protein PRO1159 encoding cDNA.
PN WO9631088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 2
ID AAC58634 standard; cDNA; 713 BP.
DE Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 3
ID AAS21480 standard; cDNA; 713 BP.
DE Human cDNA sequence encoding for PRO1159 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 4; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 4
ID AAF44240 standard; cDNA; 713 BP.
DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 5; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 5
ID ACA64409 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 713; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 6
ID ACA03839 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 7
ID ABX89377 standard; cDNA; 713 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1159.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 8
ID ABX80868 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 9
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DE cDNA encoding human PRO1159 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
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ID ACD42031 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #237.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 8; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 11
ID ABX79548 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 12
ID AC93569 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 13
ID ABX81251 standard; DNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2003032155-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 14
ID ACA04260 standard; cDNA; 713 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 473.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 15
ID ACA93067 standard; cDNA; 713 BP.
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DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
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Pred. No. 3.3e-155;
RESULT 16
ID ABX17151 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 8; Length 713;
Pred. No. 3.3e-155;
RESULT 17
ID ACA68006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 18
ID ACA88455 standard; cDNA; 713 BP.
DE Human secreted and transmembrane polypeptide PRO1159 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 19
ID ACD81962 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 20
ID ADA4592 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US200302328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 21
ID ADA76423 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 22
ID ADA19073 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 23
ID ADA61696 standard; cDNA; 713 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 24
ID ADB19481 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 25
ID ADB28022 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 26
ID ADA86501 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 27
ID ADB16065 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 28
ID ADA37887 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 29
ID ADA47851 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 30
ID ADA21573 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1159.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 31
ID ADA10360 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1159.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 32
ID ADA67646 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;
RESULT 33
ID ADB30653 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 9; Length 713;
Pred. No. 3.3e-155;

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 53
ID ADA85397 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 54
ID ADA84845 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 55
ID ADB30101 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 56
ID ADA80629 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 57
ID ADA75871 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 58
ID ADA38817 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 59
ID ADA47096 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 60
ID ADB25392 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 61
ID ADA93568 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;

Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 62
ID ADB26918 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 63
ID ADB31205 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 64
ID ADA92938 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 65
ID ADA61133 standard; cDNA; 713 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 66
ID ADB24280 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US2003077114-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 67
ID ADA96609 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 68
ID ADA81181 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 69
ID ADA96057 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 70
ID ADB26366 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 71
ID ADB26366 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;

ID ADB21851 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 72
ID ADA77630 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 73
ID ADB18370 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 74
ID ADA87053 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 75
ID ADA88156 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 76
ID ADA46544 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 77
ID ADB28574 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 78
ID ADB29126 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 79
ID ACH65523 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 80
ID ADA77078 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.

PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 81
ID ADA22499 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1159.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 82
ID ADA88708 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 83
ID ADA97713 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 84
ID ADB27470 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 85
ID ADB22403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 86
ID ACD39513 standard; cDNA; 713 BP.
DE Human cDNA encoding PRO1124.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 87
ID ADA06665 standard; cDNA; 713 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #118.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 88
ID ADA39358 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 89
ID ADA67094 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 90
ID ADB22955 standard; cDNA; 713 BP.

DE Human PRO polynucleotide #237.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 91
ID ADB23728 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 92
ID ADA92450 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 93
ID ADB15513 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 94
ID ADB38765 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 95
ID ADB96384 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 96
ID ADB38213 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 97
ID ADB66685 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 98
ID ADB89765 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 99
ID ADB90497 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082762-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 100
ID ADB39598 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 101
ID ADB47221 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082887-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 102
ID ADB86928 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 103
ID ADB77433 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 104
ID ADB34590 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 105
ID ADB35694 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 106
ID ADB34038 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 107
ID ADB35142 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 108
ID ADB36246 standard; cDNA; 713 BP.
DE Human PRO polynucleotide SEQ ID NO 473.
PN US200307720-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 109
ID ADB46641 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 110
ID ADC57856 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 111
ID ADC55220 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 112
ID ADC12087 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 113
ID ADC58509 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 114
ID ADC07564 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 115
ID ADC11554 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 116
ID ADC50514 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 117
ID ADC72061 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 118
ID ADC60040 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092105-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 119
ID ADC53047 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 120
ID ADC57401 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 121
ID ADC60592 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 122
ID ADC51067 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 123
ID ADC65594 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 124
ID ADC54692 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 125
ID ADC53653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 126
ID ADC59176 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 127
ID ADC56054 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087360-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 128
ID ADC58624 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID473.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 129
ID ADC14676 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 130
ID ADD08208 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 131
ID ADD03298 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 132
ID ADC90290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 133
ID ADC82033 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 134
ID ADC69709 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 135
ID ADC48598 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 136
ID ADD10127 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 137

ID ADD07675 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 138
ID ADD04702 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 139
ID ADC82566 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 140
ID ADC80658 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 141
ID ADD11165 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 142
ID ADC48046 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 143
ID ADD08746 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 144
ID ADC80106 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 145
ID ADD06995 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 146
ID ADD09575 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194775-A1.


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PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 147
ID ADC83242 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 148
ID ADD41288 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 149
ID ADD52427 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 150
ID ADD53167 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 151
ID ADD53719 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 152
ID ADD55349 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 153
ID ADD56307 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 154
ID ADD51875 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 155
ID ADD02674 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 156
ID ADD02108 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 157
ID ADD54290 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 158
ID ADD54745 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 159
ID ADD92607 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 160
ID ADD91503 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 161
ID ADE04117 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 162
ID ADE26899 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 163
ID ADE32414 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 164
ID ADE22346 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 165
ID ADD79570 standard; cDNA; 713 BP.
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DE cDNA encoding human PRO polypeptide #237.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 166
ID AD842106 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 167
ID AD817923 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 168
ID AD92055 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 169
ID AD83518 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 170
ID AD834070 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 171
ID AD80122 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 172
ID AD93159 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 173
ID AD819579 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 174
ID AD819027 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 175
ID AD843223 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 176
ID AD96012 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 177
ID AD822898 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 178
ID AD79016 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 179
ID AD826366 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 180
ID AD832966 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 181
ID AD842658 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 182
ID AD80674 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 183
ID AD89702 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199028-A1.
PD 23-OCT-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 184
ID ADE40986 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 185
ID ADE04785 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 186
ID ADE92914 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 187
ID ADF67303 standard; cDNA; 713 BP.
DE Human PRO1159 nucleotide sequence SEQ ID NO:376.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 188
ID ADG21623 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 189
ID ADG23264 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 190
ID ADF97599 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 191
ID ADG80663 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 192
ID ADG80111 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 193
ID ADH5403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 194
ID ADH55955 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 195
ID ADI35557 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 196
ID ADI64174 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 197
ID ADI65123 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 198
ID ADI63622 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 199
ID ADH82036 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 200
ID ADI00050 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 201
ID ADH81484 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 202
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ID ABX7952 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #118.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 203
ID ABX80364 standard; DNA; 713 BP.
DE Novel human secreted or transmembrane protein PRO1124 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 204
ID ACA69270 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 205
ID ACD24089 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 206
ID AEX90341 standard; cDNA; 713 BP.
DE Human secreted/transmembrane protein cDNA, #154.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 207
ID ABX64187 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 208
ID ACA67230 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 10; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 209
ID ADM82653 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 11; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 210
ID ADN16052 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 11; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 211
ID ADN16681 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087385-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 11; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 212
ID ADN15500 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 11; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 213
ID ADN14948 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 11; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 214
ID ADC81210 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 215
ID ADD76658 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 216
ID ADD88022 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 217
ID ADD86426 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 218
ID ADE75874 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 219
ID ADR23450 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 220
ID ADE24002 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092110-A1.
PD 15-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 221
ID ADE93466 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 222
ID ADE24645 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 223
ID ADE87470 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 224
ID ADE18475 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 225
ID ADE88784 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 226
ID ADE94804 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 227
ID ADE91215 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 228
ID ADF35502 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 229
ID ADE95356 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 230
ID ADE93466 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 231
ID ADF35047 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 232
ID ADE92362 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 233
ID ADE90663 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 234
ID ADE91810 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 235
ID ADG11752 standard; cDNA; 713 BP.
DE cDNA encoding human PRO1159 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 236
ID ADG02389 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 237
ID ADG22175 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 238
ID ADG20245 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
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RESULT 239
ID ADF98151 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 240
ID ADG24368 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 241
ID ADF98722 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 242
ID ADG03553 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 243
ID ADF99274 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 244
ID ADG16859 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 245
ID ADG05318 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 246
ID ADG19585 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 247
ID ADG13422 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 248
ID ADF98151 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 249
ID ADG15649 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 250
ID ADF97047 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 251
ID ADG06232 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 252
ID ADG23816 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 253
ID ADG04105 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 254
ID ADG25006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 255
ID ADG07303 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 256
ID ADG07855 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
  RESULT 257
ID ADG55350 standard; cDNA; 713 BP.
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DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 258
ID ADG61014 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 259
ID ADG62118 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 260
ID ADG82319 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 261
ID ADG57558 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 262
ID ADG57006 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 263
ID ADG55902 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 264
ID ADG58662 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 265
ID ADG71028 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 266
ID ADG58110 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.

PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 267
ID ADG53694 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 268
ID ADG71580 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 269
ID ADG81767 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 270
ID ADH19622 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 271
ID ADH30729 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 272
ID ADH12096 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 273
ID ADG52518 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 274
ID ADG54246 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 275
ID ADG81215 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003194793-A1.
PD 16-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 276
ID ADG56454 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 277
ID ADH12720 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 278
ID ADH21115 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 279
ID ADG61566 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 280
ID ADH20155 standard; cDNA; 713 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1159.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 281
ID ADH28653 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 282
ID ADG54798 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 283
ID ADG59838 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 284
ID ADH181262 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 285
ID ADG10005 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 286
ID ADH15476 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 287
ID ADG09353 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 288
ID ADH14808 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 289
ID ADH18403 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 290
ID ADJ63684 standard; cDNA; 713 BP.
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 291
ID ADJ77579 standard; cDNA; 713 BP.
DE Human PRO polynucleotide #237.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 292
ID ADJ65701 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
RESULT 293
ID ADM27837 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 713; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 3.3e-155;
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RESULT 294
ID ADM42561 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
Pred. No. 3.3e-155;
RESULT 295
ID ADM28423 standard; cDNA; 713 BP.
DE cDNA encoding human PRO polypeptide #237.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 713; DB 12; Length 713;
Pred. No. 3.3e-155;
RESULT 296
ID AAK81282 standard; DNA; 5709 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 99.0%; Score 705.6; DB 4; Length 5709;
Pred. No. 2.6e-153;
RESULT 297
ID AAC91481 standard; cDNA; 712 BP.
DE Human PRO1159 cDNA.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.3%; Score 701; DB 5; Length 712;
Pred. No. 1.9e-152;
RESULT 298
ID AAK81284 standard; DNA; 336 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36096.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 46.7%; Score 332.8; DB 4; Length 336;
Pred. No. 2.4e-67;
RESULT 299
ID AAX01260 standard; cDNA; 741 BP.
DE Human DC3' protein coding sequence.
PN JP11001497-A.
PD 06-JAN-1999.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 19.6%; Score 140; DB 2; Length 741;
Pred. No. 1.1e-22;
RESULT 300
ID AAZ07533 standard; cDNA; 1018 BP.
DE Human SDMP4 polypeptide encoding cDNA.
PN WO9447673-A2.
PD 23-SEP-1999.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Score 140; DB 2; Length 1018;
Pred. No. 1.2e-22;
RESULT 301
ID ADF60937 standard; cDNA; 1018 BP.
DE Human long Schering dendritic cell membrane protein 4 (SDCMP4) cDNA.
PN US2003162955-A1.
PD 28-AUG-2003.
PA (CHAL/) CHALUS L.
PA (QUAN/) QUAN A. B.
PA (BATE/) BATES E E M.
PA (GORM/) GORMAN D M.
PA (SAEL/) SAELAND S.
PA (LEBE/) LEBECQUE S J E.
PA (PHIL/) PHILLIPS J H.
Query Match
Best Local Similarity 19.8%; Score 140; DB 10; Length 1018;
Pred. No. 1.2e-22;
RESULT 302
ID ABV73351 standard; cDNA; 1153 BP.
DE LLR-J24-2 polypeptide encoding cDNA.

PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match
Best Local Similarity 19.6%; Score 140; DB 10; Length 1153;
Pred. No. 1.2e-22;
RESULT 303
ID AAS31409 standard; cDNA; 1281 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 223.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 19.6%; Score 140; DB 4; Length 1281;
Pred. No. 1.2e-22;
RESULT 304
ID ABQ66733 standard; cDNA; 1281 BP.
DE Human polynucleotide SEQ ID NO 223.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 19.6%; Score 140; DB 6; Length 1281;
Pred. No. 1.2e-22;
RESULT 305
ID ADC10755 standard; cDNA; 1281 BP.
DE Human cDNA from extracellular matrix gene 66 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 19.6%; Score 140; DB 10; Length 1281;
Pred. No. 1.2e-22;
RESULT 306
ID ABZ24041 standard; DNA; 1606 BP.
DE Human Dectin-1 polypeptide encoding cDNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match
Best Local Similarity 19.6%; Score 140; DB 8; Length 1606;
Pred. No. 1.3e-22;
RESULT 307
ID ABV73363 standard; cDNA; 138 BP.
DE LLR-J24-stalk peptide encoding cDNA.
PN WO200277216-A2.
PD 03-OCT-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match
Best Local Similarity 19.4%; Score 138; DB 10; Length 138;
Pred. No. 2.2e-22;
RESULT 308
ID AAC24137 standard; cDNA; 85 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 28212.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match
Best Local Similarity 11.6%; Score 83; DB 3; Length 85;
Pred. No. 1.1e-09;
RESULT 309
ID AAV42548 standard; cDNA; 2298 BP.
DE Mouse Dectin-1 cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 10.9%; Score 77.6; DB 2; Length 2298;
Pred. No. 3.7e-08;
RESULT 310
ID ABZ24043 standard; DNA; 2298 BP.
DE Mouse Dectin-1 polypeptide encoding cDNA.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match
Best Local Similarity 10.9%; Score 77.6; DB 8; Length 2298;
Pred. No. 3.7e-08;

RESULT 311
ID AAV42551 standard; cDNA; 528 BP.
DE Mouse dectin-1 extracellular domain cDNA.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 10.5%; Score 75.2; DB 2; Length 528;
Best Local Similarity 77.2%; Pred. No. 9.9e-08;
RESULT 312
ID ABL33920 standard; DNA; 12590 BP.
DE Human immune system associated gene SEQ ID NO: 1893.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 6.7%; Score 47.6; DB 6; Length 12590;
Best Local Similarity 45.6%; Pred. No. 0.46;
RESULT 313
ID AAF1371 standard; DNA; 335913 BP.
DE Soybean 240017 region G3, SEQ ID NO: 2.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 6.5%; Score 46.4; DB 5; Length 335913;
Best Local Similarity 45.4%; Pred. No. 1.7;
RESULT 314
ID AAF1372 standard; DNA; 335913 BP.
DE Soybean 240017 region G3, SEQ ID NO: 3.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 6.5%; Score 46.4; DB 5; Length 335913;
Best Local Similarity 45.4%; Pred. No. 1.7;
RESULT 315
ID AEN8067 standard; DNA; 7041 BP.
DE Human chemically modified disease associated gene SEQ ID NO 84.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 6.5%; Score 46; DB 6; Length 7041;
Best Local Similarity 48.2%; Pred. No. 0.96;
RESULT 316
ID ABA09212 standard; cDNA; 1204 BP.
DE Human juvenile hormone esterase binding protein homologue cDNA, SEQ:988.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 44.6; DB 4; Length 1204;
Best Local Similarity 49.4%; Pred. No. 1.4;
RESULT 317
ID AAK53107 standard; cDNA; 1204 BP.
DE Human polynucleotide SEQ ID NO 2636.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 44.6; DB 4; Length 1204;
Best Local Similarity 49.4%; Pred. No. 1.4;
RESULT 318
ID ADL63064 standard; DNA; 1675 BP.
DE Human ovarian cancer DNA marker #21276.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 6.2%; Score 44.4; DB 5; Length 1675;
Best Local Similarity 47.8%; Pred. No. 1.7;
RESULT 319
ID AAK52839 standard; cDNA; 5007 BP.
DE Human polynucleotide SEQ ID NO 2368.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 44.4; DB 4; Length 5007;
Best Local Similarity 47.8%; Pred. No. 2.1;
RESULT 320
ID ADN02625 standard; cDNA; 6497 BP.
DE Liver disease associated protein Obcl1 gene sequence.
PN WO2004029287-A2.
PD 08-APR-2004.
PA (ORID-) ORIDIS BIOMED FORSCHUNGS & ENTWICKLUNGS.
Query Match 6.2%; Score 44.4; DB 12; Length 6497;
Best Local Similarity 47.8%; Pred. No. 2.2;
RESULT 321
ID ADQ19685 standard; DNA; 115863 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2504.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.2%; Score 44.4; DB 12; Length 115863;
Best Local Similarity 58.2%; Pred. No. 4.1;
RESULT 322
ID ABZ35977 standard; cDNA; 3906 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 141.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.2%; Score 44.2; DB 8; Length 3906;
Best Local Similarity 47.0%; Pred. No. 2.2;
RESULT 323
ID ABZ36196 standard; cDNA; 5216 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 360.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.2%; Score 44.2; DB 8; Length 5216;
Best Local Similarity 47.0%; Pred. No. 2.4;
RESULT 324
ID ABL32227 standard; DNA; 6509 BP.
DE Human immune system associated gene SEQ ID NO: 200.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 6.1%; Score 43.2; DB 6; Length 6509;
Best Local Similarity 46.9%; Pred. No. 4.2;
RESULT 326
ID ADP75185 standard; DNA; 22693 BP.
DE Human NR2G gene fragment #1.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 43; DB 11; Length 22693;
Best Local Similarity 55.8%; Pred. No. 6.1;
RESULT 327
ID ADL38504 standard; DNA; 319 BP.
DE Human ovarian cancer DNA marker #12394.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 6.0%; Score 42.8; DB 5; Length 319;
Best Local Similarity 43.7%; Pred. No. 2.8;
RESULT 328
ID ADI73373 standard; DNA; 319 BP.
DE Human ovarian cancer DNA marker #6115.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 6.0%; Score 42.8; DB 5; Length 319;
Best Local Similarity 43.7%; Pred. No. 2.8;
RESULT 329
ID ABL34019 standard; DNA; 5304 BP.
DE Human immune system associated gene SEQ ID NO: 1992.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.9%; Score 42.4; DB 6; Length 5304;

Best Local Similarity 55.4%; Pred. No. 6.2;
RESULT 330
ID ABV56017 standard; cDNA; 592 BP.
DE Human prostate expression marker cDNA 56008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 41.4; DB 5; Length 592;
Best Local Similarity 48.1%; Pred. No. 6.6;
RESULT 340
ID ABL32058 standard; DNA; 8323 BP.
DE Human immune system associated gene SEQ ID NO: 31.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.9%; Score 42.4; DB 6; Length 5858;
Best Local Similarity 45.5%; Pred. No. 6.3;
RESULT 331
ID AAH19176 standard; cDNA; 1414 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HPWAY46, SEQ ID NO:17.
PN WO200132910-A2.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 41.8; DB 4; Length 1414;
Best Local Similarity 49.3%; Pred. No. 6.4;
RESULT 332
ID ADA40093 standard; cDNA; 1414 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 41.8; DB 8; Length 1414;
Best Local Similarity 49.3%; Pred. No. 6.4;
RESULT 333
ID ADC73667 standard; DNA; 1414 BP.
DE Human secreted protein-related DNA - SEQ ID 300.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 41.8; DB 10; Length 1414;
Best Local Similarity 49.3%; Pred. No. 6.4;
RESULT 334
ID ADD37667 standard; cDNA; 1414 BP.
DE Human secreted protein encoding sequence #149.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 41.8; DB 10; Length 1414;
Best Local Similarity 49.3%; Pred. No. 6.4;
RESULT 335
ID ADA56266 standard; DNA; 1414 BP.
DE Gene encoding human secreted protein #445.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 41.8; DB 10; Length 1414;
Best Local Similarity 49.3%; Pred. No. 6.4;
RESULT 336
ID ABK28419 standard; DNA; 5265 BP.
DE DNA transcription associated genomic DNA #147.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.8%; Score 41.6; DB 6; Length 5265;
Best Local Similarity 55.6%; Pred. No. 9.4;
RESULT 337
ID ABK40052 standard; DNA; 7058 BP.
DE Human chemically pretreated gene sequence #67 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.8%; Score 41.6; DB 6; Length 7058;
Best Local Similarity 49.5%; Pred. No. 10;
RESULT 338
ID ABV08830 standard; cDNA; 420 BP.
DE Human prostate expression marker cDNA 8821.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 41.4; DB 5; Length 420;
Best Local Similarity 40.8%; Pred. No. 6.2;

RESULT 339
ID ABV56017 standard; cDNA; 592 BP.
DE Human prostate expression marker cDNA 56008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 41.4; DB 5; Length 592;
Best Local Similarity 48.1%; Pred. No. 6.6;
RESULT 340
ID ABL32058 standard; DNA; 8323 BP.
DE Human immune system associated gene SEQ ID NO: 31.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.8%; Score 41.4; DB 6; Length 8323;
Best Local Similarity 57.3%; Pred. No. 12;
RESULT 341
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.8%; Score 41.4; DB 6; Length 11394;
Best Local Similarity 54.2%; Pred. No. 12;
RESULT 342
ID ABQ99653 standard; DNA; 104644 BP.
DE Human MS4A7, MS4A5 and MS4A2 genomic sequence.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 5.8%; Score 41.4; DB 6; Length 104644;
Best Local Similarity 56.1%; Pred. No. 20;
RESULT 343
ID ADI72870 standard; DNA; 348 BP.
DE Human ovarian cancer DNA marker #5612.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 41.2; DB 5; Length 348;
Best Local Similarity 53.7%; Pred. No. 6.6;
RESULT 344
ID ADL38009 standard; DNA; 348 BP.
DE Human ovarian cancer DNA marker #11899.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 41.2; DB 5; Length 348;
Best Local Similarity 53.7%; Pred. No. 6.6;
RESULT 345
ID ABX48619 standard; cDNA; 397 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13784.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.8%; Score 41.2; DB 8; Length 397;
Best Local Similarity 46.0%; Pred. No. 6.8;
RESULT 346
ID ADO25148 standard; DNA; 1533 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.8%; Score 41.2; DB 12; Length 1533;
Best Local Similarity 49.5%; Pred. No. 9;
RESULT 347
ID ABL33054 standard; DNA; 6294 BP.
DE Human immune system associated gene SEQ ID NO: 1027.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match
Best Local Similarity 5.8%; Score 41.2; DB 6; Length 6294;
RESULT 348
ID ABX41811 standard; cDNA; 337 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6976.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 5.8%; Score 41; DB 8; Length 337;
RESULT 349
ID ABN80169 standard; DNA; 6467 BP.
DE Human chemically modified disease associated gene SEQ ID NO 186.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.8%; Score 41; DB 6; Length 6467;
RESULT 350
ID ABS77273 standard; cDNA; 774 BP.
DE Fr3g embryonic gene sequence Q9925688.
PN US2002081610-A1.
PD 27-JUN-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match
Best Local Similarity 5.7%; Score 40.8; DB 6; Length 774;
RESULT 351
ID AAT129007 standard; cDNA; 298 BP.
DE Colon tumour related determined cDNA sequence for contig 71.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 4; Length 298;
RESULT 352
ID ABZ33193 standard; cDNA; 298 BP.
DE Human colon tumour cDNA contig 71 SEQ ID NO:556.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 8; Length 298;
RESULT 353
ID ABL38485 standard; cDNA; 301 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:2074.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 301;
RESULT 354
ID ABL37552 standard; cDNA; 301 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:1141.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 301;
RESULT 355
ID ABX46069 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11234.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 8; Length 419;
RESULT 356
ID ABX46069 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11234.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 588;
RESULT 357
ID AAZ98188 standard; cDNA; 1130 BP.
DE Human signal peptide containing protein HSPP-80 cDNA SEQ ID NO:214.
PN WO20000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 3; Length 1130;
RESULT 358
ID AAH98698 standard; cDNA; 1765 BP.
DE Human EST-derived coding sequence SEQ ID NO: 555.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 4; Length 1765;
RESULT 359
ID ABL34242 standard; DNA; 14429 BP.
DE Human immune system associated gene SEQ ID NO: 2215.
PN WO200200328-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 14429;
RESULT 360
ID ABQ67097 standard; DNA; 14429 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 127.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 14429;
RESULT 361
ID ABL56202 standard; DNA; 50000 BP.
DE AmEPV genome fragment#4.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match
Best Local Similarity 5.7%; Score 40.6; DB 6; Length 50000;
RESULT 362
ID ABL33655 standard; DNA; 5228 BP.
DE Human immune system associated gene SEQ ID NO: 1628.
PN WO200200328-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.7%; Score 40.4; DB 6; Length 5228;
RESULT 363
ID ABS58028 standard; DNA; 5847 BP.
DE Human serum amyloid A4 (SAA4) gene segment #1.
PN US6455308-B1.
PD 24-SEP-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 40.4; DB 8; Length 5847;
RESULT 364
ID ABL34589 standard; DNA; 7104 BP.
DE Human metastasis associated gene SEQ ID NO: 142.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.7%; Score 40.4; DB 6; Length 7104;
RESULT 365
ID ABL34589 standard; DNA; 7104 BP.
DE Human metastasis associated gene SEQ ID NO: 142.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 5.7%; Score 40.4; DB 6; Length 7104;
RESULT 365

ID ABL70396 standard; DNA; 7104 BP.
DE Chemically treated cell signalling DNA sequence complementary to#143.
PN WO200202807-A2.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.7%; Score 40.4; DB 6; Length 7104;
Best Local Similarity 46.2%; Pred. No. 19;
RESULT 366
ID ACF05254 standard; cDNA; 3197 BP.
DE Plasmodium falciparum cGMP dependent protein kinase cDNA.
PN WO2003054157-A2.
PD 03-JUL-2003.
PA (MERI) MERCK & CO INC.
Query Match 5.6%; Score 40.2; DB 9; Length 3197;
Best Local Similarity 44.5%; Pred. No. 18;
RESULT 367
ID AAA70170 standard; DNA; 4041 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:303.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 5.6%; Score 40.2; DB 3; Length 4041;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 368
ID AAS61094 standard; DNA; 6062 BP.
DE Human gene regulation-associated gene oligonucleotide #49.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40.2; DB 6; Length 6062;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 369
ID ABN80020 standard; DNA; 6561 BP.
DE Human chemically modified disease associated gene SEQ ID NO 37.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40.2; DB 6; Length 6561;
Best Local Similarity 45.2%; Pred. No. 21;
RESULT 370
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40.2; DB 6; Length 11394;
Best Local Similarity 50.8%; Pred. No. 23;
RESULT 371
ID AAL03268 standard; DNA; 1399 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5956.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 4; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 372
ID AAL03269 standard; DNA; 1399 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5957.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 4; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 373
ID ADA41621 standard; DNA; 1399 BP.
DE Human secreted protein related DNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 8; Length 1399;

Best Local Similarity 52.4%; Pred. No. 17;
RESULT 374
ID ADA41620 standard; DNA; 1399 BP.
DE Human secreted protein related DNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 8; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 375
ID ADC74693 standard; DNA; 1399 BP.
DE Human secreted protein-related DNA - SEQ ID 1326.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 376
ID ADC74694 standard; DNA; 1399 BP.
DE Human secreted protein-related DNA - SEQ ID 1327.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 377
ID ADD38147 standard; cDNA; 1399 BP.
DE cDNA clone in ATCC deposit #41.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 378
ID ADD38148 standard; cDNA; 1399 BP.
DE cDNA clone in ATCC deposit #42.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 379
ID ADA57757 standard; DNA; 1399 BP.
DE BAC fragment containing human secreted protein gene #455.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 380
ID ADA57756 standard; DNA; 1399 BP.
DE BAC fragment containing human secreted protein gene #455.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 40; DB 10; Length 1399;
Best Local Similarity 52.4%; Pred. No. 17;
RESULT 381
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40; DB 6; Length 13511;
Best Local Similarity 57.0%; Pred. No. 27;
RESULT 382
ID ABK40038 standard; DNA; 16258 BP.
DE Human chemically pretreated gene sequence #60 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40; DB 6; Length 16258;
Best Local Similarity 47.2%; Pred. No. 28;

RESULT 383
ID ABL70376 standard; DNA; 16258 BP.
DE Chemically treated cell signalling DNA sequence complementary to#133.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 40; DB 6; Length 16258;
Best Local Similarity 47.2%; Pred. No. 28;
RESULT 384
ID AAL24138 standard; cDNA; 874 BP.
DE Human breast cancer expressed polynucleotide 16595.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.6%; Score 39.8; DB 4; Length 874;
Best Local Similarity 46.0%; Pred. No. 17;
RESULT 385
ID AAC259161 standard; cDNA; 1131 BP.
DE Human secreted protein cDNA sequence #5.
PN WO200055201-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 39.8; DB 3; Length 1131;
Best Local Similarity 52.8%; Pred. No. 18;
RESULT 386
ID ABX77226 standard; DNA; 1940 BP.
DE DNA sequence of BAC clone /ctb-137N13.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Query Match 5.6%; Score 39.8; DB 10; Length 1940;
Best Local Similarity 47.7%; Pred. No. 20;
RESULT 387
ID ABU27546 standard; DNA; 2669 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 34111.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 39.8; DB 4; Length 2669;
Best Local Similarity 49.8%; Pred. No. 21;
RESULT 388
ID AD854117 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 41.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 10; Length 16579;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 389
ID ADB54245 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 169.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 10; Length 16579;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 390
ID ADB37772 standard; DNA; 16579 BP.
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:18.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 10; Length 16579;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 391
ID ADB37762 standard; DNA; 16579 BP.
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:8.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 10; Length 16579;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 392

ID AAS46313 standard; DNA; 16750 BP.
DE Tumour suppressor gene derived chemically modified sequence #35.
PN WO200168312-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 4; Length 16750;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 393
ID ABL32520 standard; DNA; 16750 BP.
DE Human immune system associated gene SEQ ID NO: 493.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.8; DB 6; Length 16750;
Best Local Similarity 52.8%; Pred. No. 31;
RESULT 394
ID AAK731165 standard; DNA; 20420 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 39.8; DB 4; Length 20420;
Best Local Similarity 46.5%; Pred. No. 33;
RESULT 395
ID ABK69933 standard; DNA; 20420 BP.
DE Human secreted protein gene 68 genomic DNA fragment #21.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 39.8; DB 6; Length 20420;
Best Local Similarity 46.5%; Pred. No. 33;
RESULT 396
ID AD059203 standard; DNA; 76406 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:40.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 5.6%; Score 39.8; DB 12; Length 76406;
Best Local Similarity 67.5%; Pred. No. 43;
RESULT 397
ID ABS4549 standard; DNA; 98472 BP.
DE Human multidrug resistance associated protein gene associated sequence.
PN WO200257410-A2.
PD 25-JUL-2002.
PA (DNAS-) DNA SCI LAB INC.
Query Match 5.6%; Score 39.8; DB 6; Length 98472;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 398
ID ACF62745 standard; DNA; 98472 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:673.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.6%; Score 39.8; DB 8; Length 98472;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 399
ID ADB20860 standard; DNA; 98472 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:673.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.6%; Score 39.8; DB 8; Length 98472;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 400
ID ADB87949 standard; DNA; 98472 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:673.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 5.6%; Score 39.8; DB 10; Length 98472;

Best Local Similarity 47.7%; Pred. No. 45;
RESULT 401
ID ADB96932 standard; DNA; 98472 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:673.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.6%; Score 39.8; DB 10; Length 98472;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 402
ID ADB92123 standard; DNA; 98472 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:673.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 5.6%; Score 39.8; DB 10; Length 98472;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 403
Query Match 5.6%; Score 39.8; DB 10; Length 110000;
Best Local Similarity 52.8%; Pred. No. 46;
RESULT 404
Query Match 5.6%; Score 39.8; DB 10; Length 110000;
Best Local Similarity 52.8%; Pred. No. 46;
RESULT 405
ID ACF65382 standard; DNA; 243072 BP.
DE Photorhabdus luminescens nucleotide sequence #35.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.6%; Score 39.8; DB 10; Length 243072;
Best Local Similarity 52.8%; Pred. No. 55;
RESULT 406
ID ABA93723 standard; cDNA; 1464 BP.
DE Human amygdala derived cDNA clone amy2_24k15.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.6%; Score 39.6; DB 6; Length 1464;
Best Local Similarity 49.6%; Pred. No. 21;
RESULT 407
ID ABL33702 standard; DNA; 18624 BP.
DE Human immune system associated gene SEQ ID NO: 1675.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.6%; Score 39.6; DB 6; Length 18624;
Best Local Similarity 51.1%; Pred. No. 36;
RESULT 408
ID AAC58017 standard; DNA; 20674 BP.
DE Arachidonic acid metabolism related genomic biallelic marker #651.
PN WO200047771-A2.
PD 17-AUG-2000.
PA (GEST) GENSET.
Query Match 5.6%; Score 39.6; DB 3; Length 20674;
Best Local Similarity 56.0%; Pred. No. 36;
RESULT 409
ID AAA96365 standard; DNA; 50000 BP.
DE Polymorphic repeat microsatellite sequences present in the CTLA4 locus.
PN WO200056856-A2.
PD 28-SEP-2000.
PA (GEMY) GENETICS INST INC.
Query Match 5.6%; Score 39.6; DB 3; Length 50000;
Best Local Similarity 56.0%; Pred. No. 44;
RESULT 410
ID AAI89341 standard; cDNA; 288 BP.
DE Human polynucleotide SEQ ID NO 9401.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 39.4; DB 4; Length 288;
Best Local Similarity 53.6%; Pred. No. 17;
RESULT 411

ID AAO25532 standard; DNA; 1648 BP.
DE Sequence of genomic clone contg. the entire Histidine-rich protein (HsRP) gene.
PN US5116965-A.
PD 26-MAY-1992.
PA (SLOK) SLOAN KETTERING INST CANCER.
Query Match 5.5%; Score 39.4; DB 2; Length 1648;
Best Local Similarity 52.1%; Pred. No. 24;
RESULT 412
ID ADQ23114 standard; DNA; 5798 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5934.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.5%; Score 39.4; DB 12; Length 5798;
Best Local Similarity 46.8%; Pred. No. 31;
RESULT 413
ID ABL33317 standard; DNA; 13574 BP.
DE Human immune system associated gene SEQ ID NO: 1290.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.4; DB 6; Length 13574;
Best Local Similarity 61.0%; Pred. No. 37;
RESULT 414
ID ABN80238 standard; DNA; 15121 BP.
DE Human chemically modified disease associated gene SEQ ID NO 255.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.4; DB 6; Length 15121;
Best Local Similarity 46.8%; Pred. No. 38;
RESULT 415
ID ABK39964 standard; DNA; 15479 BP.
DE Human chemically pretreated gene sequence #23 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.4; DB 6; Length 15479;
Best Local Similarity 55.5%; Pred. No. 38;
RESULT 416
ID ABL33998 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1971.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.4; DB 6; Length 21537;
Best Local Similarity 49.3%; Pred. No. 41;
RESULT 417
ID ABQ76617 standard; cDNA; 81440 BP.
DE C. albicans BAX-associated cDNA fragment SEQ ID 659.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.5%; Score 39.4; DB 6; Length 81440;
Best Local Similarity 48.4%; Pred. No. 54;
RESULT 418
Query Match 5.5%; Score 39.4; DB 6; Length 110000;
Best Local Similarity 48.8%; Pred. No. 57;
RESULT 419
Query Match 5.5%; Score 39.4; DB 12; Length 110000;
Best Local Similarity 48.8%; Pred. No. 57;
RESULT 420
Query Match 5.5%; Score 39.4; DB 12; Length 110000;
Best Local Similarity 48.8%; Pred. No. 57;
RESULT 421
Query Match 5.5%; Score 39.4; DB 12; Length 110000;
Best Local Similarity 48.8%; Pred. No. 57;
RESULT 422
ID ABK31540 standard; DNA; 6045 BP.
DE Signal transduction associated gene modified DNA #192.
PN WO200200926-A2.
PD 03-JAN-2002.

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PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.2; DB 6; Length 6045;
Best Local Similarity 52.4%; Pred. No. 35;
RESULT 423
ID ABL70623 standard; DNA; 6045 BP.
DE Chemically treated cell signalling DNA sequence#257.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39.2; DB 6; Length 6045;
Best Local Similarity 52.4%; Pred. No. 35;
RESULT 424
ID ARAQ62924 standard; cDNA; 8920 BP.
DE Carbamoyl-phosphate-synthetase II.
PN WO9412643-A1.
PD 09-JUN-1994.
PA (UNIX ) UNISEARCH LTD.
Query Match 5.5%; Score 39.2; DB 2; Length 8920;
Best Local Similarity 46.6%; Pred. No. 38;
RESULT 425
Query Match 5.5%; Score 39.2; DB 6; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 426
Query Match 5.5%; Score 39.2; DB 6; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 427
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 428
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 429
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 430
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 431
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 432
Query Match 5.5%; Score 39.2; DB 12; Length 110000;
Best Local Similarity 64.1%; Pred. No. 64;
RESULT 433
ID ABR83568 standard; DNA; 201143 BP.
DE Human DNA differentially expressed in granulocytic cells #139.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.5%; Score 39.2; DB 6; Length 201143;
Best Local Similarity 58.6%; Pred. No. 73;
RESULT 434
ID ABV44994 standard; cDNA; 309 BP.
DE Human prostate expression marker cDNA 44985.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.5%; Score 39; DB 5; Length 309;
Best Local Similarity 48.1%; Pred. No. 21;
RESULT 435
ID ADL37255 standard; DNA; 467 BP.
DE Human ovarian cancer DNA marker #11145.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.5%; Score 39; DB 5; Length 467;
Best Local Similarity 46.6%; Pred. No. 23;
RESULT 436
ID ADI72106 standard; DNA; 467 BP.
DE Human ovarian cancer DNA marker #4848.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.5%; Score 39; DB 6; Length 7450;
Best Local Similarity 49.7%; Pred. No. 40;
RESULT 440
ID AAK52123 standard; cDNA; 1182 BP.
DE Human polynucleotide SEQ ID NO 668.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 39; DB 4; Length 1182;
Best Local Similarity 50.6%; Pred. No. 27;
RESULT 441
ID ADL22698 standard; DNA; 3629 BP.
DE Human liver differentially expressed cDNA seq id 508.
PN US2003165854-A1.
PD 04-SEP-2003.
PA (CUNN/) CUNNINGHAM M J.
PA (KASE/) KASER M R.
Query Match 5.5%; Score 39; DB 10; Length 3629;
Best Local Similarity 50.6%; Pred. No. 35;
RESULT 442
ID ABL32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 5195;
Best Local Similarity 49.7%; Pred. No. 37;
RESULT 443
ID ABL32813 standard; DNA; 6059 BP.
DE Human immune system associated gene SEQ ID NO: 786.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 6059;
Best Local Similarity 55.6%; Pred. No. 39;
RESULT 444
ID ABR28131 standard; DNA; 7450 BP.
DE DNA transcription associated genomic DNA #3.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 7450;
Best Local Similarity 49.7%; Pred. No. 40;
RESULT 445
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Query Match 5.5%; Score 39; DB 5; Length 467;
Best Local Similarity 46.6%; Pred. No. 23;
RESULT 437
ID ADM90702 standard; DNA; 615 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 95.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAP-) DNAPFORM KK.
Query Match 5.5%; Score 39; DB 12; Length 615;
Best Local Similarity 59.5%; Pred. No. 24;
RESULT 438
ID ADM91120 standard; DNA; 615 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 513.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAP-) DNAPFORM KK.
Query Match 5.5%; Score 39; DB 12; Length 615;
Best Local Similarity 59.5%; Pred. No. 24;
RESULT 439
ID AAZ17651 standard; cDNA; 672 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:5124.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 39; DB 2; Length 672;
Best Local Similarity 50.6%; Pred. No. 24;
RESULT 440
ID AAK52123 standard; cDNA; 1182 BP.
DE Human polynucleotide SEQ ID NO 668.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 39; DB 4; Length 1182;
Best Local Similarity 50.6%; Pred. No. 27;
RESULT 441
ID ADL22698 standard; DNA; 3629 BP.
DE Human liver differentially expressed cDNA seq id 508.
PN US2003165854-A1.
PD 04-SEP-2003.
PA (CUNN/) CUNNINGHAM M J.
PA (KASE/) KASER M R.
Query Match 5.5%; Score 39; DB 10; Length 3629;
Best Local Similarity 50.6%; Pred. No. 35;
RESULT 442
ID ABL32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 5195;
Best Local Similarity 49.7%; Pred. No. 37;
RESULT 443
ID ABL32813 standard; DNA; 6059 BP.
DE Human immune system associated gene SEQ ID NO: 786.
PN WO20020928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 6059;
Best Local Similarity 55.6%; Pred. No. 39;
RESULT 444
ID ABR28131 standard; DNA; 7450 BP.
DE DNA transcription associated genomic DNA #3.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 7450;
Best Local Similarity 49.7%; Pred. No. 40;
RESULT 445
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ID ABL33964 standard; DNA; 9180 BP.
DE Human immune system associated gene SEQ ID NO: 1937.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 9180;
Best Local Similarity 56.7%; Pred. No. 42;
RESULT 446
ID ABL70480 standard; DNA; 9742 BP.
DE Chemically treated cell signalling DNA sequence complementary to#185.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 39; DB 6; Length 9742;
Best Local Similarity 48.7%; Pred. No. 43;
RESULT 447
ID AD056275 standard; DNA; 89500 BP.
DE Human presynaptic cytomatrix protein, PCLO, genomic sequence.
PN WO200404164-A2.
PD 27-MAY-2004.
Query Match 5.5%; Score 39; DB 12; Length 89500;
Best Local Similarity 45.1%; Pred. No. 68;
RESULT 448
ID ABX91637 standard; cDNA; 199 BP.
DE Murine gene trapped sequence (GTS) SEQ ID NO 981.
PN US2002161207-A1.
PD 31-OCT-2002.
PA (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 5.4%; Score 38.8; DB 8; Length 199;
Best Local Similarity 54.1%; Pred. No. 21;
RESULT 449
ID AD44393 standard; DNA; 263 BP.
DE Human ovarian cancer DNA marker #18283.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.4%; Score 38.8; DB 5; Length 263;
Best Local Similarity 54.1%; Pred. No. 22;
RESULT 450
ID ABX39417 standard; cDNA; 393 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4582.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.4%; Score 38.8; DB 8; Length 393;
Best Local Similarity 46.1%; Pred. No. 24;
RESULT 451
ID AD036005 standard; DNA; 3470 BP.
DE Novel mouse gene sequence #678.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.4%; Score 38.8; DB 12; Length 3470;
Best Local Similarity 58.8%; Pred. No. 38;
RESULT 452
ID AD019964 standard; cDNA; 5316 BP.
DE Human PRO polynucleotide #438.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH/) GENENTECH INC.
Query Match 5.4%; Score 38.8; DB 12; Length 5316;
Best Local Similarity 42.6%; Pred. No. 42;
RESULT 453
ID ABL33396 standard; DNA; 5641 BP.
DE Human immune system associated gene SEQ ID NO: 1369.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.4%; Score 38.6; DB 2; Length 4526;
Best Local Similarity 5.4%; Score 38.6; DB 2; Length 4526;
Query Match 5.4%; Score 38.8; DB 6; Length 5641;
Best Local Similarity 46.9%; Pred. No. 42;
RESULT 454
ID ADJ75955 standard; DNA; 5893 BP.
DE Marker gene SEQ ID NO:1207.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.4%; Score 38.8; DB 12; Length 5893;
Best Local Similarity 58.8%; Pred. No. 43;
RESULT 455
ID ADJ76057 standard; DNA; 5893 BP.
DE Marker gene SEQ ID NO:1309.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.4%; Score 38.8; DB 12; Length 5893;
Best Local Similarity 58.8%; Pred. No. 43;
RESULT 456
ID ABK28257 standard; DNA; 8170 BP.
DE DNA transcription associated genomic DNA #66.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.4%; Score 38.8; DB 6; Length 8170;
Best Local Similarity 45.9%; Pred. No. 46;
RESULT 457
ID ABL32062 standard; DNA; 9905 BP.
DE Human immune system associated gene SEQ ID NO: 35.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.4%; Score 38.8; DB 6; Length 9905;
Best Local Similarity 56.2%; Pred. No. 48;
RESULT 458
ID ADP91459 standard; cDNA; 256 BP.
DE Cotton expressed sequence tag, EST, #470.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 5.4%; Score 38.6; DB 12; Length 256;
Best Local Similarity 53.8%; Pred. No. 25;
RESULT 459
ID ADL37605 standard; DNA; 576 BP.
DE Human ovarian cancer DNA marker #11495.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.4%; Score 38.6; DB 5; Length 576;
Best Local Similarity 43.6%; Pred. No. 29;
RESULT 460
ID ADI72466 standard; DNA; 576 BP.
DE Human ovarian cancer DNA marker #5208.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.4%; Score 38.6; DB 5; Length 576;
Best Local Similarity 43.6%; Pred. No. 29;
RESULT 461
ID ABL18982 standard; DNA; 2279 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8419.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 5.4%; Score 38.6; DB 4; Length 2279;
Best Local Similarity 44.4%; Pred. No. 39;
RESULT 462
ID AAQ9780 standard; DNA; 4526 BP.
DE Prosystemin.
PN WO9319079-A1.
PD 30-SEP-1993.
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
Query Match 5.4%; Score 38.6; DB 2; Length 4526;

RESULT 472
ID ABU33999 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1972.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.4%; Score 38.6; DB 6; Length 21537;
Best Local Similarity 47.3%; Pred. No. 63;
RESULT 473
ID ADA14746 standard; DNA; 22118 BP.
DE Mouse 45S rRNA gene.
FN US2002160970-A1.
PD 31-OCT-2002.
PA (HADL/) HADIACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 5.4%; Score 38.6; DB 8; Length 22118;
Best Local Similarity 59.6%; Pred. No. 63;
RESULT 474
ID ADA37415 standard; DNA; 22118 BP.
DE Origin of replication DNA..
FN US2003108914-A1.
PD 12-JUN-2003.
PA (HADL/) HADIACZKY G.
Query Match 5.4%; Score 38.6; DB 9; Length 22118;
Best Local Similarity 59.6%; Pred. No. 63;
RESULT 475
ID AAD61410 standard; DNA; 22118 BP.
DE Mouse ribosomal DNA (rDNA) repeat region.
FN US2003101480-A1.
PD 29-MAY-2003.
PA (HADL/) HADIACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 5.4%; Score 38.6; DB 10; Length 22118;
Best Local Similarity 59.6%; Pred. No. 63;
RESULT 476
ID ADP10518 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene repeat unit.
FN WO2003093469-A2.
PD 13-NOV-2003.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 5.4%; Score 38.6; DB 10; Length 22118;
Best Local Similarity 59.6%; Pred. No. 63;
RESULT 477
ID ACC44629 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene (rDNA) nucleotide sequence SEQ ID NO:18.
FN WO200297059-A2.
PD 05-DEC-2002.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 5.4%; Score 38.6; DB 10; Length 22118;
Best Local Similarity 59.6%; Pred. No. 63;
RESULT 478
ID ADL43972 standard; DNA; 539 BP.
DE Human ovarian cancer DNA marker #17862.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC..
Query Match 5.4%; Score 38.4; DB 5; Length 539;
Best Local Similarity 53.3%; Pred. No. 32;
RESULT 479
ID AAL13462 standard; cDNA; 637 BP.
DE Human breast cancer expressed polynucleotide 5919.
FN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC..
Query Match 5.4%; Score 38.4; DB 4; Length 637;
Best Local Similarity 52.6%; Pred. No. 33;
RESULT 480
ID AAK68216 standard; DNA; 1402 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23028.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 38.4; DB 4; Length 1402;

Best Local Similarity 44.3%; Pred. No. 39;
RESULT 481
ID AAA37089 standard; cDNA; 1743 BP.
DE Human PRO1337 (UN0692) cDNA sequence SEQ ID NO:235.
PN WO200012708-A2.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 3; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 482
ID AAF54367 standard; DNA; 1743 BP.
DE Primer #140 used in the identification of proteins.
PN WO200078961-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 4; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 483
ID AAS46150 standard; cDNA; 1743 BP.
DE Human DNA encoding PRO polypeptide sequence #226.
PN WO200168848-A2.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 4; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 484
ID ABL88183 standard; cDNA; 1743 BP.
DE Human PRO1337 cDNA sequence SEQ ID NO:223.
PN WO200200690-A2.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 6; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 485
ID ABK11752 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO1337 protein.
PN WO200149715-A2.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 6; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 486
ID ABL95672 standard; cDNA; 1743 BP.
DE Human angiogenesis related cDNA PRO1337 SEQ ID NO: 223.
PN WO200208284-A2.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 6; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 487
ID ACAB9600 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003036141-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 488
ID ACA73610 standard; cDNA; 1743 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036146-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 489
ID ACA05925 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036162-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 490
ID ACA86759 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO protein #226.
PN US2003036137-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 491
ID ACF20334 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040063-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 492
ID ACF19720 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040064-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 493
ID ACD22008 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003027267-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 494
ID ACF13173 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036160-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 495
ID ACD25276 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044925-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 496
ID ACF00325 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054474-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 497
ID ACA72382 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003032114-A1.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 498
ID ACA73610 standard; cDNA; 1743 BP.

ID ACD04906 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 499
ID ACD18367 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 500
ID ACD08374 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 501
ID ACA88808 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 502
ID ACA70250 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 503
ID ACD12472 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 504
ID AC74387 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 505
ID ACD16015 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 506
ID ACD25583 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 507
ID ACD18060 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 508
ID ACC88347 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.

PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 509
ID ACD21701 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 510
ID ABX98378 standard; cDNA; 1743 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 451.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 511
ID ACD14129 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 512
ID ACD09909 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 513
ID ACC88654 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 514
ID ACD21394 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 515
ID ABX75766 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1337.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 516
ID ABX97969 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 517
ID ACA97445 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 518
ID ACA57908 standard; cDNA; 1743 BP.
DE Human PRO1337 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.

Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 519
ID AC1436 standard; cDNA; 1743 BP.
DE Human secreted polypeptide #226.
PN US200302130-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 520
ID ACC91219 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US200302138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 521
ID ACC8961 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US200302132-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 522
ID ACD07158 standard; cDNA; 1743 BP.
DE Human secreted polypeptide #226.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 523
ID ACA67609 standard; cDNA; 1743 BP.
DE Human secreted polypeptide #226.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 524
ID ACC81664 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US200302137-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 525
ID ACC89268 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 526
ID ACC86624 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 527
ID ACC9882 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 528
ID ACC93061 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US200302135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 529
ID ACA72689 standard; cDNA; 1743 BP.
DE Human secreted polypeptide #226.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 530
ID ACA89207 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 531
ID ACA69943 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US200302105-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 532
ID ACA97086 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003021223-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 533
ID ACA91082 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US200302108-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 534
ID ACA70864 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US200302111-A1.
PD 13-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 535
ID ACA95374 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US200302119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 536
ID ACC86317 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 537
ID ACC90189 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 538
ID ACD12797 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;

RESULT 539
ID ACF20027 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 540
ID ABX76971 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 541
ID ACA73303 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 542
ID ACA68946 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 543
ID ACA74690 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted/transmembrane protein (PRO) cDNA #226.
RESULT 544
ID ACA70557 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human PRO polynucleotide #226.
RESULT 545
ID ACD14743 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 546
ID ACA68415 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 547
ID ABX98880 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 548
ID ACC81357 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 549
ID ACA95681 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.

PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 550
ID ACD04599 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA, SEQ ID NO:451.
RESULT 551
ID ACC8040 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
RESULT 552
ID ACF12702 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
RESULT 553
ID ACA96417 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted/transmembrane protein (PRO) cDNA #226.
RESULT 554
ID ACA65191 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted/transmembrane protein (PRO) cDNA #226.
RESULT 555
ID ACA73917 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 556
ID ACA74329 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
RESULT 557
ID ACA96724 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
RESULT 558
ID ACD10830 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
RESULT 559
ID ACC91526 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032139-A1.
PD 13-FEB-2003.

Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 560
ID AC02861 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 561
ID ACC87426 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 562
ID ACC86010 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 563
ID ACA65498 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 564
ID ACA94315 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 565
ID ACA98059 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 566
ID ACA91561 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 567
ID ACA90775 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 568
ID ACD16322 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 569
ID ACC92140 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 570
ID ACA74997 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 571
ID ACA91868 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 572
ID ACA71512 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 573
ID ACC90912 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 574
ID ACA65922 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO protein #226.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 575
ID ACA95067 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 576
ID ACD16629 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 577
ID ACD15708 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 578
ID ABX16811 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein #226.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 579
ID ACA97752 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 580
ID ACA99201 standard; cDNA; 1743 BP.

RESULT 570
ID ACA74997 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 571
ID ACA91868 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 572
ID ACA71512 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 573
ID ACC90912 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 574
ID ACA65922 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO protein #226.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 575
ID ACA95067 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 576
ID ACD16629 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 577
ID ACD15708 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 8; Length 1743;
RESULT 578
ID ABX16811 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein #226.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 8; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 579
ID ACA97752 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
RESULT 580
ID ACA99201 standard; cDNA; 1743 BP.

DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2003032140-A1.
 PD 13-FEB-2003.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 581
 ID ACC91833 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003040076-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 582
 ID ACD11244 standard; cDNA; 1743 BP.
 DE Novel human secreted and transmembrane protein PRO1337 cDNA.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 583
 ID ACD15094 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003044922-A1.
 PD 06-MAR-2003.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 584
 ID ACD11858 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003032118-A1.
 PD 13-FEB-2003.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 585
 ID ACC95987 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003036135-A1.
 PD 20-FEB-2003.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 586
 ID ACF16550 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 587
 ID ACF02668 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 588
 ID ACF02975 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 589
 ID ACF21562 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;

Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 590
 ID ACF10246 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 591
 ID ACF78139 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 592
 ID ACD46844 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 593
 ID ACD49607 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003068725-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 594
 ID ACF28374 standard; cDNA; 1743 BP.
 DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
 PN US2003068752-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 595
 ID ACD89064 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003068682-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 596
 ID ACD84459 standard; cDNA; 1743 BP.
 DE Human PRO polynucleotide #226.
 PN US2003068701-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 597
 ID ACD99233 standard; cDNA; 1743 BP.
 DE cDNA encoding human PRO polypeptide #226.
 PN US2003068755-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;
 RESULT 598
 ID ADA78203 standard; cDNA; 1743 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #226.
 PN US2003073180-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 5.4%; Score 38.4; DB 9; Length 1743;
 Best Local Similarity 52.5%; Pred. No. 41;

RESULT 599
ID ACF48975 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US20030104539-A1.
PD 05-JUN-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 600
ID ACD09295 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 601
ID ACF12088 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 602
ID ACF41322 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 603
ID ACF15936 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 604
ID ACF16243 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 605
ID ACD32070 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 606
ID ACF18978 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 607
ID ACF09325 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 608
ID ACF78446 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054473-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 609
ID ACF52045 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 610
ID ACF26532 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 611
ID ACF24325 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 612
ID ACF63636 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 613
ID ACF50510 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 614
ID ACH07981 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 615
ID ACF13787 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 616
ID ACD41713 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 617
ID ACF32126 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;

Best Local Similarity 52.5%; Pred. No. 41;
RESULT 618
ID ACF23404 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 619
ID ACF40131 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO9741-encoding cDNA, SEQ ID NO:525.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 620
ID ACF40094 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 621
ID ACF45616 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 622
ID ACF53273 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 623
ID ACF27453 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 624
ID ACF45291 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 625
ID ACF29909 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 626
ID ACD89985 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 627
ID ACD84766 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 628
ID ACD98926 standard; cDNA; 1743 BP.
DE CDNA encoding human PRO polypeptide #226.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 629
ID ACF77218 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 630
ID ACF76911 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 631
ID ACF49896 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 632
ID ACF50203 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 633
ID ACD09602 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 634
ID ACD08681 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 635
ID ACF12395 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 636
ID ACC94903 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;

Best Local Similarity 52.5%; Pred. No. 41;
RESULT 637
ID ACD22622 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 638
ID ACF15322 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 639
ID ACC97417 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 640
ID ACC92447 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 641
ID ACF14094 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 642
ID ACF14401 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 643
ID ACF09632 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 644
ID ACD68406 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO1337 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 645
ID ACD45923 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 646
ID ACD48072 standard; cDNA; 1743 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 647
ID ACD67803 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 648
ID ACF25611 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 649
ID ACF29295 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 650
ID ACD85073 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 651
ID ACD84152 standard; cDNA; 1743 BP.
DE Human PRO polynucleotide #226.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 652
ID ACD88143 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 653
ID ACF30830 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 654
ID ACF32433 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 655
ID ACH12093 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.

PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 656
ID ACF12400 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 657
ID ACD40792 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 658
ID ACF18264 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 659
ID ACF08711 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 660
ID ACF31512 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 661
ID ACF52352 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 662
ID ACD50221 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 663
ID ACF38924 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 664
ID ACF26839 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068709-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 665
ID ACF24939 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 666
ID ACF46519 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 667
ID ACF28067 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 668
ID ACD89371 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 669
ID ACF63943 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 670
ID ACF60583 standard; cDNA; 1743 BP.
DE Human secreted polypeptide PRO1337-encoding cDNA, SEQ ID NO:451.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 671
ID ACH12707 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO polypeptide #226.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 672
ID ACH10130 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;
RESULT 673
ID ACD3985 standard; cDNA; 1743 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #226.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 38.4; DB 9; Length 1743;
Best Local Similarity 52.5%; Pred. No. 41;